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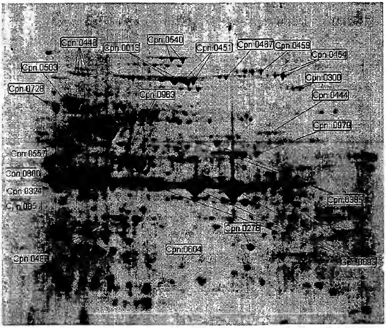
(54) Title: IMMUNISATION AGAINST *CHLAMYDIA PNEUMONIAE*



(57) Abstract: The published genomic of *Chlamydia pneumoniae* reveals over 1000 putative encoded proteins but does not itself indicate which of these might to useful antigens for immunisation and vaccination or for diagnosis. This difficulty is addressed by the invention, which provides a number of *C pneumoniae* protein sequences suitable for vaccine production and development and/or for diagnostic purposes.

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IMMUNISATION AGAINST *CHLAMYDIA PNEUMONIAE*

All documents cited herein are incorporated by reference in their entirety.

TECHNICAL FIELD

This invention is in the field of immunisation against chlamydial infection, in particular against infection by *Chlamydia pneumoniae*.

BACKGROUND ART

Chlamydiae are obligate intracellular parasites of eukaryotic cells which are responsible for endemic sexually transmitted infections and various other disease syndromes. They occupy an exclusive eubacterial phylogenic branch, having no close relationship to any other known organisms – they are classified in their own order (*Chlamydiales*) which contains a single family (*Chlamydiaceae*) which in turn contains a single genus (*Chlamydia*). A particular characteristic of the *Chlamydiae* is their unique life cycle, in which the bacterium alternates between two morphologically distinct forms: an extracellular infective form (elementary bodies, EB) and an intracellular non-infective form (reticulate bodies, RB). The life cycle is completed with the re-organization of RB into EB, which subsequently leave the disrupted host cell ready to infect further cells.

Four chlamydial species are currently known – *C.trachomatis, C.pneumoniae, C.pecorum* and *C.psittaci* [*e.g.* Raulston (1995) *Mol Microbiol* 15:607-616; Everett (2000) *Vet Microbiol* 75:109-126]. *C.pneumoniae* is closely related to *C.trachomatis*, as the whole genome comparison of at least two isolates from each species has shown [Kalman *et al.* (1999) *Nature Genetics* 21:385-389; Read *et al.* (2000) *Nucleic Acids Res* 28:1397-406; Stephens *et al.* (1998) *Science* 282:754-759]. Based on surface reaction with patient immune sera, the current view is that only one serotype of *C.pneumoniae* exists world-wide.

C.pneumoniae is a common cause of human respiratory disease. It was first isolated from the conjunctiva of a child in Taiwan in 1965, and was established as a major respiratory pathogen in 1983. In the USA, *C.pneumoniae* causes approximately 10% of community-acquired pneumonia and 5% of pharyngitis, bronchitis, and sinusitis.

More recently, the spectrum of *C.pneumoniae* infections has been extended to include atherosclerosis, coronary heart disease, carotid artery stenosis, myocardial infarction, cerebrovascular disease, aortic aneurysm, claudication, and stroke. The association of *C.pneumoniae* with atherosclerosis is corroborated by the presence of the organism in atherosclerotic lesions throughout the arterial tree and the near absence of the organism in healthy arterial tissue. *C.pneumoniae* has also been isolated from coronary and carotid atheromatous plaques. The bacterium has also been associated with other acute and chronic respiratory diseases (*e.g.* otitis media, chronic obstructive pulmonary disease, pulmonary exacerbation of cystic fibrosis) as a result of sero-epidemiologic observations, case reports, isolation or direct detection of the organism in specimens, and successful

response to anti-chlamydial antibiotics. To determine whether chronic infection plays a role in initiation or progression of disease, intervention studies in humans have been initiated, and animal models of *C.pneumoniae* infection have been developed.

Considerable knowledge of the epidemiology of *C.pneumoniae* infection has been derived from serologic studies using the *C.pneumoniae*-specific microimmunofluorescence test. Infection is ubiquitous, and it is estimated that virtually everyone is infected at some point in life, with common re-infection. Antibodies against *C.pneumoniae* are rare in children under the age of 5, except in developing and tropical countries. Antibody prevalence increases rapidly at ages 5 to 14, reaching 50% at the age of 20, and continuing to increase slowly to ~80% by age 70.

A current hypothesis is that *C.pneumoniae* can persist in an asymptomatic low-grade infection in very large sections of the human population. When this condition occurs, it believed that the presence of *C.pneumoniae*, and/or the effects of the host reaction to the bacterium, can cause or help progress of cardiovaseular illness.

It is not yet clear whether *C.pneumoniae* is actually a causative agent of cardiovascular disease, or whether it is just artefactually associated with it. It has been shown, however, that *C.pneumoniae* infection can induce LDL oxidation by human monocytes [Kalayoglu *et al.* (1999) *J. Infect. Dis.* 180:780-90; Kalayoglu *et al.* (1999) *Am. Heart J.* 138:S488-490]. As LDL oxidation products are highly atherogenic, this observation provides a possible mechanism whereby *C.pneumoniae* may cause atheromatous degeneration. If a causative effect is confirmed, vaccination (prophylactic and therapeutic) will be universally recommended.

Genomic sequence information has been published for *C.pneumoniae* [Kalman *et al.* (1999) *supra*; Read *et al.* (2000) *supra*; Shirai *et al.* (2000) *J. Infect. Dis.* 181(Suppl 3):S524-S527; WO99/27105; WO00/27994] and is available from GenBank. Sequencing efforts have not, however, focused on vaccination, and the availability of genomic sequence does not in itself indicate which of the >1000 genes might encode useful antigens for immunisation and vaccination. WO99/27105, for instance, implies that every one of the 1296 ORFs identified in the *C.pneumoniae* strain CM1 genome is a useful vaccine antigen.

It is thus an object of the present invention to identify antigens useful for vaccine production and development from amongst the many proteins present in *C.pneumoniae*. It is a further object to identify antigens useful for diagnosis (*e.g.* immunodiagnosis) of *C.pneumoniae*.

DISCLOSURE OF THE INVENTION

The invention provides proteins comprising the *C.pneumoniae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences which share at least *x*% sequence identity with the *C.pneumoniae* amino acid sequences disclosed in the examples. Depending on the particular

sequence, x is preferably 50% or more (*e.g.* 60%, 70%, 80%, 90%, 95%, 99% or more). These include mutants and allelic variants. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman homology search algorithm as implemented in the MPSRCH program (Oxford Molecular), using an affine gap search with parameters *gap open penalty=12* and *gap extension penalty=1*.

The invention further provides proteins comprising fragments of the *C.pneumoniae* amino acid sequences disclosed in the examples. The fragments should comprise at least n consecutive amino acids from the sequences and, depending on the particular sequence, n is 7 or more (*e.g.* 8, 10, 12, 14, 16, 18, 20, 30, 40, 50, 75, 100 or more). Preferably the fragments comprise one or more epitope(s) from the sequence. Other preferred fragments omit a signal peptide.

The proteins of the invention can, of course, be prepared by various means (*e.g.* native expression, recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (*e.g.* native, fusions *etc.*). They are preferably prepared in substantially pure form (*ie.* substantially free from other *C.pneumoniae* or host cell proteins). Heterologous expression in *E.coli* is a preferred preparative route.

According to a further aspect, the invention provides nucleic acid comprising the *C.pneumoniae* nucleotide sequences disclosed in the examples. In addition, the invention provides nucleic acid comprising sequences which share at least x% sequence identity with the *C.pneumoniae* nucleotide sequences disclosed in the examples. Depending on the particular sequence, x is preferably 50% or more (*e.g.* 60%, 70%, 80%, 90%, 95%, 99% or more).

Furthermore, the invention provides nucleic acid which can hybridise to the *C.pneumoniae* nucleic acid disclosed in the examples, preferably under "high stringency" conditions (*e.g.* 65°C in a 0.1xSSC, 0.5% SDS solution).

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least n consecutive nucleotides from the *C.pneumoniae* sequences and, depending on the particular sequence, n is 10 or more (*e.g.* 12, 14, 15, 18, 20, 25, 30, 35, 40, 50, 75, 100, 200, 300 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (*e.g.* for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (*e.g.* by chemical synthesis, from genomic or cDNA libraries, from the organism itself *etc.*) and can take various forms (*e.g.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also peptide nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*e.g.* cloning or expression vectors) and host cells transformed therewith.

According to a further aspect, the invention provides immunogenic compositions comprising protein and/or nueleic acid according to the invention. These compositions are suitable for immunisation and vaccination purposes. Vaccines of the invention may be prophylactic or therapeutic, and will typically comprise an antigen which can induce antibodies capable of inhibiting (a) chlamydial adhesion, (b) ehlamydial entry, and/or (c) successful replication within the host cell. The vaccines preferably induce any cell-mediated T-cell responses which are necessary for chlamydial clearance from the host.

The invention also provides nucleic acid or protein according to the invention for use as medicaments (*e.g.* as vaccines). It also provides the use of nucleic acid or protein according to the invention in the manufacture of a medicament (*e.g.* a vaccine or an immunogenic composition) for treating or preventing infection due to *C.pneumoniae*.

The invention also provides a method of treating (*e.g.* immunising) a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid or protein according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for produeing protein or nucleic acid of the invention is provided, wherein the protein or nucleie acid is synthesised in part or in whole using chemieal means.

A proeess for detecting *C.pneumoniae* in a sample is provided, wherein the sample is contacted with an antibody which binds to a protein of the invention .

A summary of standard techniques and procedures which may be employed in order to perform the invention (*e.g.* to utilise the disclosed sequences for immunisation) follows. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

General

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature *e.g.* Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989) and *Third Edition* (2001); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I.

Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C. C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

The term "comprising" means "including" as well as "consisting" *e.g.* a composition "comprising" X may consist exclusively of X or may include something additional to X, such as X+Y.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a Chlamydial sequence is heterologous to a mouse host cell. A further examples would be two epitopes from the same or different proteins which have been assembled in a single protein in an arrangement not found in nature.

An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as DNA, RNA or amino acid sequence differing from but having sequence identity with the native or disclosed sequence. Depending on the particular sequence, the degree of sequence identity between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (*e.g.* 60%, 70%, 80%, 90%, 95%, 99% or more, calculated using the Smith-Waterman algorithm as described above). As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs essentially at the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions (*e.g.* see US patent 5,753,235).

Expression systems

The Chlamydial nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, baculoviruses, plants, bacteria, and yeast.

i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (*e.g.* structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can aet in either orientation [Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual, 2nd ed.]*.

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallotheionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible), depending on the promoter can be induced with glucocorticoid in hormone-responsive cells.

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter [Maniatis et al. (1987) *Science 236*:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.]. Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer [Dijkema et al (1985) *EMBO J. 4*:761] and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus [Gorman et al. (1982) *PNAS USA* 79:6777] and from human cytomegalovirus [Boshart et al. (1985) *Cell 41*:521]. Additionally, some enhaneers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion [Sassone-Corsi and Borelli (1986) *Trends Genet. 2*:215; Maniatis et al. (1987) *Science* 236:1237].

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader

fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus triparite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation [Birnstiel et al. (1985) *Cell 41*:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M. Glover); Proudfoot (1989) *Trends Biochem. Sci. 14*:105]. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminater/polyadenylation signals include those derived from SV40 [Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*].

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (*e.g.* plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 [Gluzman (1981) *Cell 23*:175] or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replicaton systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 [Kaufman et al. (1989) *Mol. Cell. Biol. 9*:946] and pHEBO [Shimizu et al. (1986) *Mol. Cell. Biol. 6*:1074].

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene-mediated transfection, protoplast fusion, electroporation, encapsulation of polynucleotide(s) in liposomes, direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (*e.g.* Hep G2), and a number of other cell lines.

ii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the eomponents of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence

homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its owned set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (*e.g.* plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These inelude, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from thc ATT; see Luckow and Summers, *Virology* (1989) *17*:31.

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, *42*:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli.*

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (*e.g.* structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* *69*:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, *73*:409). Alternatively, since the signals

for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human α-interferon, Maeda et al., (1985), *Nature* *315*:592; human gastrin-releasing peptide, Lebacq-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, *82*:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* *58*:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally seereted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) *3*:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* *4*:91.The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between ~1% and ~5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuelei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15μm in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus)

or absence (indicative of recombinant virus) of occlusion bodies. "Current Protocols in Microbiology" Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers & Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti* , *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (WO 89/046699; Carbonell et al., (1985) *J. Virol. 56*:153; Wright (1986) *Nature 321*:718; Smith et al., (1983) *Mol. Cell. Biol. 3*:2156; and see generally, Fraser, *et al.* (1989) *In Vitro Cell. Dev. Biol. 25*:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. *See, e.g.* Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible eontrol, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the produet of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g. HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g. proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

iii. Plant Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: US 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., Nucleic Acids Research 15:2515-2535 (1987); Wirsel et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, Gibberellins: in: *Advanced Plant Physiology*,. Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for Agrobacterium transformations, T DNA sequences for Agrobacterium-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a seleetable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Reptr*, 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the eells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet*, 202:179-185, 1985. The genetic material may also be

transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

iv. Baeterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (*e.g.* structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps initiate transcription of the lac operon in Escherichia coli (E. coli) [Raibaud *et al.* (1984) *Annu. Rev. Genet. 18*:173]. Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) [Chang *et al.* (1977) *Nature 198*:1056], and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) [Goeddel *et al.* (1980) *Nuc. Acids Res. 8*:4057; Yelverton *et al.* (1981) *Nucl. Acids Res. 9*:731; US patent 4,738,921; EP-A-0036776 and EP-A-0121775]. The g-laotamase (*bla*) promoter system [Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)], bacteriophage lambda PL [Shimatake *et al.* (1981) *Nature 292*:128] and T5 [US patent 4,689,406] promoter systems also provide useful promoter sequences.

In addition, synthetic promoters whieh do not occur in nature also function as bacterial promoters. For example, transcription aetivation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequenees of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter [US patent 4,551,433]. For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor [Amann *et al.* (1983) *Gene 25*:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci. 80*:21]. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system [Studier *et al.* (1986) *J. Mol. Biol. 189*:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci. 82*:1074]. In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO-A-0 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon [Shine *et al.* (1975) *Nature 254*:34]. The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' and of *E. coli* 16S rRNA [Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological*

Regulation and Development: Gene Expression (ed. R.F. Goldberger)]. To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site [Sambrook *et al.* (1989) "Expression of cloned genes in Escherichia coli." In *Molecular Cloning: A Laboratory Manual*].

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino aeid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be eleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* on *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO-A-0 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene [Nagai *et al.* (1984) *Nature 309*:810]. Fusion proteins can also be made with sequences from the *lacZ* [Jia *et al.* (1987) *Gene 60*:197], *trpE* [Allen et al. (1987) J. Biotechnol. 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol. 135*:11], and *Chey* [EP-A-0 324 647] genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (*e.g.* ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated [Miller *et al.* (1989) *Bio/Technology* 7:698].

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria [US patent 4,336,336]. The signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) [Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghrayeb *et al.* (1984) *EMBO J. 3*:2437] and the *E. coli* alkaline phosphatase signal sequence (*phoA*) [Oka *et al.* (1985) *Proc. Natl. Acad. Sci. 82*:7212]. As an additional example, the signal sequence of the alpha-amylase gene from various Bacillus strains can be used to secrete heterologous proteins from *B. subtilis* [Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA 79*:5582; EP-A-0 244 042].

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (*e.g.* plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually eontain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various Bacillus strains integrate into the Bacillus chromosome (EP-A- 0 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline [Davies *et al.* (1978) *Annu. Rev. Microbiol. 32*:469]. Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable market that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: Bacillus subtilis [Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA 79*:5582; EP-A-0 036 259 and EP-A-0 063 953; WO 84/04541], Escherichia coli [Shimatake *et al.* (1981) *Nature 292*:128; Amann *et al.* (1985) *Gene 40*:183; Studier *et al.* (1986) *J. Mol. Biol. 189*:113; EP-A-0 036 776,EP-A-0 136 829 and EP-A-0 136 907], Streptococcus cremoris [Powell *et al.* (1988) *Appl. Environ. Microbiol. 54*:655]; Streptococcus lividans [Powell *et al.* (1988) *Appl. Environ. Microbiol. 54*:655], Streptomyces lividans [US patent 4,745,056].

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with $CaCl_2$ or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by electroporation. Transformation procedures usually vary with the bacterial species to be transformed. See *e.g.* [Masson *et al.* (1989) *FEMS Microbiol. Lett. 60*:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA 79*:5582; EP-A-0 036 259 and EP-A-0 063 953; WO 84/04541, Bacillus], [Miller *et al.* (1988) *Proc. Natl. Acad. Sci. 85*:856; Wang *et al.* (1990) *J. Bacteriol. 172*:949, Campylobacter], [Cohen *et al.* (1973) *Proc. Natl. Acad. Sci. 69*:2110; Dower *et al.* (1988) *Nucleic Acids Res. 16*:6127; Kushner (1978) "An improved method for transformation of Escherichia coli with ColE1-derived plasmids. In *Genetic*

Engineering: Proceedings of the International Symposium on Genetic Engineering (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol. 53*:159; Taketo (1988) *Biochim. Biophys. Acta 949*:318; Escherichia], [Chassy *et al.* (1987) *FEMS Microbiol. Lett. 44*:173 Lactobacillus]; [Fiedler *et al.* (1988) *Anal. Biochem 170*:38, Pseudomonas]; [Augustin *et al.* (1990) *FEMS Microbiol. Lett. 66*:203, Staphylococcus], [Barany *et al.* (1980) *J. Bacteriol. 144*:698; Harlander (1987) "Transformation of Streptococcus lactis by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun. 32*:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol. 54*:655; Somkuti *et al.* (1987) *Proc. 4th Evr. Cong. Biotechnology 1*:412, Streptococcus].

v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (*e.g.* structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences. Examples include alcohol dehydrogenase (ADH) (EP-A-0 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO-A-0 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences [Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA 80*:1].

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (US Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters inelude promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EP-A-0 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, [Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA 77*:1078; Henikoff *et al.* (1981) *Nature 283*:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol. 96*:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast Saccharomyces cerevisiae," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene 11*:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;].

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always

be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See *e.g.* EP-A-0 196 056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (*e.g.* ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (*e.g.* WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the genes for invertase (EP-A-0012873; JPO 62,096,086) and A-factor (US patent 4,588,684). Alternatively, leaders of non-yeast origin exit, such as an interferon leader, that also provide for secretion in yeast (EP-A-0060057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino aeid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (US Patents 4,546,083 and 4,870,008; EP-A-0 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-faetor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (*e.g.* see WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (*e.g.* plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 [Botstein *et al.* (1979) *Gene 8*:17-24], pCl/1 [Brake *et al.* (1984) *Proc. Natl. Acad. Sci USA 81*:4642-4646], and YRp17 [Stinchcomb *et al.* (1982) *J. Mol. Biol. 158*:157]. In addition, a replicon may be either a high or low eopy number plasmid. A high copy

number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See *e.g.* Brake *et al., supra.*

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome [Orr-Weaver *et al.* (1983) *Methods in Enzymol. 101*:228-245]. An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al., supra.* One or more expression construct may integrate, possibly affecting levels of recombinant protein produced [Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA 80*:6750]. The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions [Butt *et al.* (1987) *Microbiol, Rev. 51*:351].

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors have been developed for, *inter alia*, the following yeasts:Candida albicans [Kurtz, *et al.* (1986) *Mol. Cell. Biol. 6*:142], Candida maltosa [Kunze, *et al.* (1985) *J. Basic Microbiol. 25*:141]. Hansenula polymorpha [Gleeson, *et al.* (1986) *J. Gen. Microbiol. 132*:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet. 202*:302], Kluyveromyces fragilis [Das, *et al.* (1984) *J. Bacteriol. 158*:1165], Kluyveromyces lactis [De Louvencourt *et al.* (1983) *J. Bacteriol. 154*:737; Van den Berg *et al.* (1990) *Bio/Technology 8*:135], Pichia guillerimondii [Kunze *et al.* (1985) *J. Basic Microbiol. 25*:141], Pichia pastoris [Cregg, *et al.* (1985) *Mol. Cell. Biol. 5*:3376; US Patent Nos. 4,837,148 and 4,929,555], Saccharomyces cerevisiae [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA 75*:1929; Ito *et al.* (1983) *J. Bacteriol. 153*:163], Schizosaccharomyces pombe [Beach and Nurse (1981) *Nature 300*:706], and Yarrowia lipolytica [Davidow, *et al.* (1985) *Curr. Genet. 10*:380471 Gaillardin, *et al.* (1985) *Curr. Genet. 10*:49].

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See *e.g.* [Kurtz *et al.* (1986) *Mol. Cell. Biol. 6*:142; Kunze *et al.* (1985) *J. Basic Microbiol. 25*:141; Candida]; [Gleeson *et al.* (1986) *J. Gen. Microbiol. 132*:3459;

Roggenkamp *et al.* (1986) *Mol. Gen. Genet. 202*:302; Hansenula]; [Das *et al.* (1984) *J. Bacteriol. 158*:1165; De Louvencourt *et al.* (1983) *J. Bacteriol. 154*:1165; Van den Berg *et al.* (1990) *Bio/Technology 8*:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol. 5*:3376; Kunze *et al.* (1985) *J. Basic Microbiol. 25*:141; US Patents 4,837,148 & 4,929,555; Pichia]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA 75*;1929; Ito *et al.* (1983) *J. Bacteriol. 153*:163 Saccharomyces]; [Beach & Nurse (1981) *Nature 300*:706; Schizosaccharomyces]; [Davidow *et al.* (1985) *Curr. Genet. 10*:39; Gaillardin *et al.* (1985) *Curr. Genet. 10*:49; Yarrowia].

Pharmaceutical Compositions

Pharmaceutical compositions can comprise polypeptides and/or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgement of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal or transcutaneous applications (*e.g.* see WO98/20734), needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (*ie.* to prevent infection) or therapeutic (*ie.* to treat disease after infection).

Such vaccines comprise immunising antigen(s), immunogen(s), polypeptide(s), protein(s) or nucleic acid, usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the antigen or immunogen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, *etc.* pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59™ (WO 90/14837; Chapter 10 in *Vaccine design: the subunit and adjuvant approach*, eds. Powell & Newman, Plenum Press 1995), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi™ adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox™); (3) saponin adjuvants, such as Stimulon™ (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (*e.g.* IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, *etc.*), interferons (*e.g.* gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; and (6) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59™ are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), *etc.*

The immunogenic compositions (*e.g.* the immunising antigen/immunogen/polypeptide/protein/ nucleic acid, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles.

Typically, the immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

Immunogenic compositions used as vaccines comprise an immunologically effective amount of the antigenic or immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (*e.g.* nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

The immunogenic compositions are conventionally administered parenterally, *e.g.* by injection, either subcutaneously, intramuscularly, or transdermally/transcutaneously (*e.g.* WO98/20734). Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed [*e.g.* Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648; see later herein].

Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence in vivo can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art and we contemplate that any retroviral gene therapy vector is employable in the invention, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses *e.g.* MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (*e.g.* HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia, Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC Nol VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671,

WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102, WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (*ie.* there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 & WO92/07945, HSV Us3::pgC-laeZ described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in US Serial No. 08/405,627, filed March 15, 1995,WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems.

Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, Nature 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Triniti virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral veetors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationie condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu & Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed. Exemplary naked DNA introduction methods are described in WO90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in US 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in US 5,149,655; use of ionizing radiation for activating transferred gene, as described in US 5,206,152 and WO92/11033

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP-0524968; and in Stryer, Biochemistry, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for recombinant protein expression. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal or transcutaneous applications (*e.g.* see WO98/20734), needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *e.g.* WO93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoetic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

A.Polypeptides

One example are polypeptides which include, without limitation: asioloorosomucoid (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

B.Hormones, Vitamins, *etc.*

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

C.Polyalkylenes, Polysaccharides, *etc.*

Also, polyalkylene glycol can be included with the desired polynucleotides/polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethlylene glycol. In addition, mono-, di-, or polysaecharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D.Lipids, and Liposomes

The desired polynucleotide/polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See,

also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boerhinger). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, *e.g.* Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphoshatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilammelar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See *e.g.* Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77); Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348); Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E.Lipoproteins

In addition, lipoproteins can be included with the polynucleotide/polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, & E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, & E apoproteins, LDL comprises apoprotein B; HDL comprises apoproteins A, C, & E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) Annu Rev. Biochem 54:699; Law (1986) Adv. Exp Med. Biol. 151:162; Chen (1986) J Biol Chem 261:12918; Kane (1980) Proc Natl Acad Sci USA 77:2465; and Utermann (1984) Hum Genet 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in

conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol. (supra)*; Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750. Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host ccll. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443. Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Techniologies, Inc., Stoughton, Massachusetts, USA. Further description of lipoproteins can be found in Zuckermann *et al.* PCT/US97/14465.

F.Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide/polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, eoat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic aid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and purtrescine.

The dimensions and of the physical propertics of a polycationic agent ean be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin™, and lipofectAMINE™ are monomers that form polycationic complexes when combined with polynucleotides/polypeptides.

Nucleic Acid Hybridisation

"Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affeet this bonding include: the type and volume of solvent; reaetion temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequcnces; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] vol.2, chapt.9, pp.9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated Tm of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1µg for a plasmid or phage digest to 10^{-9} to 10^{-8} g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy yeast gene can be detected with an exposure time of only 1 hour starting with 1 µg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/µg. For a single-copy mammalian gene a conservative approach would start with 10 µg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/µg, resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature (Tm) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$Tm = 81 + 16.6(\log_{10}Ci) + 0.4[\%(G + C)] - 0.6(\%formamide) - 600/n - 1.5(\%mismatch).$$

where Ci is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe with is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be washed at high stringency and

reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Chlamydial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Chlamydial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Chlamydial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Chlamydial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Chlamydial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Chlamydial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably $\geq$30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *e.g.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*e.g.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*e.g.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patents 4,683,195 & 4,683,202. Two 'primers' hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its

complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Chlamydial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Chlamydial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1-189 show data pertaining to examples 1-189.

Figure 190 shows a representative 2D gel of proteins in elementary bodies.

Figure 191 shows an alignment of sequences in five (six) proteins of the invention.

EXAMPLES

The examples indicate *C.pneumoniae* proteins, together with evidence to support the view that the proteins are useful antigens for vaccine production and development or for diagnostic purposes. This evidence takes the form of:

- Computer prediction based on sequence information from CWL029 strain (*e.g.* using the PSORT algorithm available from *www.psort.nibb.ac.jp*).
- Data on recombinant expression and purification of the proteins cloned from IOL207 strain.
- Western blots to demonstrate immunoreactivity in serum (typically a blot of an EB extract of *C.pneumoniae strain* FB/96 stained with mouse antiserum against the recombinant protein).
- FACS analysis of *C.pneumoniae* bacteria or purified EBs to confirm aecessibility of the antigen to the immune system (see also table III).
- An indication if the protein was identified by MALDI-TOF from a 2D gel electrophoresis map of proteins from purified elementary bodies from strain FB/96. This confirms that the protein is expressed *in vivo* (see also table V).

Various tests can be used to assess the *in vivo* immunogenicity of the proteins identified in the examples. For example, the proteins can be expressed recombinantly and used to screen patient sera by immunoblot. A positive reaction between the protein and patient serum indicates that the patient has previously mounted an immune response to the protein in question *ie.* the protein is an immunogen. This method can also be used to identify immunodominant proteins.

The recombinant protein can also be conveniently used to prepare antibodies *e.g.* in a mouse. These can bc used for direct confirmation that a protein is located on the cell-surface. Labelled antibody (*e.g.* fluorescent labelling for FACS) can be incubated with intact bacteria and the presence of label on the bacterial surface confirms the location of the protein.

In particular, the following methods (A) to (O) were used to express, purify and biochemically characterise the proteins of the invention:

CLONING OF CPN ORFs FOR EXPRESSION IN *E.COLI*

ORFs of *Chlamydia pneumoniae* (Cpn) were cloned in such a way as to potentially obtain three different kind of proteins:

a) proteins having an hexa-histidine tag at the C-terminus (epn-His)
b) proteins having a GST fusion partner at the N-terminus (Gst-cpn)
c) proteins having both hexa-histidine tag at the C-terminus and GST at the N-terminus (GST/His fusion; NH_2-GST-cpn-$(His)_6$-COOH)

The type a) proteins were obtained upon cloning in the pET21b+ (Novagen). The type b) and c) proteins were obtained upon cloning in modified pGEX-KG vectors [Guan & Dixon (1991) *Anal. Biochem.* 192:262]. For instance pGEX-KG was modified to obtain pGEX-NN, then by modifying pGEX-NN to obtain pGEX-NNH. The Gst-cpn and Gst-cpn-His proteins were obtained in pGEX-NN and pGEX-NNH respectively.

The modified versions of pGEX-KG vector were made with the aim of allowing the cloning of single amplification produets in all three vectors after only one double restriction enzyme digestion and to minimise the presence of extraneous amino acids in the final recombinant proteins.

(A) Construction of pGEX-NN and pGEX-NNH expression vectors

Two couples of complementary oligodeoxyribonucleotidcs were synthesised using the DNA synthesiser ABI394 (Perkin Elmer) and the reagents from Cruachem (Glasgow, Scotland). Equimolar amounts of the oligo pairs (50 ng each oligo) were annealed in T4 DNA ligase buffer (New England Biolabs) for 10 min in a final volume of 50µl and then were left to cool slowly at room temperature. With the described procedure he following DNA linkers were obtained:

gexNN linker:

```
NdeI  NheI XmaI  EcoRI   NcoI        SalI     XhoI       SacI            NotI
GATCCCATATGGCTAGCCCGGGGAATTCGTCCATGGAGTGAGTCGACTGACTCGAGTGATCGAGCTCCTGAGCGGCCGCATGAA
    GGTATACCGATCGGGCCCCTTAAGCAGGTACCTCACTCAGCTGACTGAGCTCACTAGCTCGAGGACTCGCCGGCGTACTTTCGA
```

gexNNH linker:

```
          HindIII NotI  XhoI   --Hexa-Histidine--
     TCGACAAGCTTGCGGCCGCACTCGAGCATCACCATCACCATCACTGAT
         GTTCGAACGCCGGCGTGAGCACGTAGAGGTAGTGGTAGTGACTATCGA
```

The plasmid pGEX-KG was digested with BamHI and HindIII and 100 ng were ligated overnight at 16 °C to the linker gexNN with a molar ratio of 3:1 linker/plasmid using 200 units of T4 DNA ligase

(New england Biolabs). After transformation of the ligation product in *E. coli* DH5, a clone containing the pGEX-NN plasmid, having the correct linker, was selected by means of restriction enzyme analysis and DNA sequencing.

The new plasmid pGEX-NN was digested with SalI and HindIII and ligated to the linker gexNNH. After transformation of the ligation product in *E. coli* DH5, a clone containing the pGEX-NNH plasmid, having the correct linker, was selected by means of restriction enzyme analysis and DNA sequencing.

(B) Chromosomal DNA preparation

The chromosomal DNA of elementary bodies (EB) of *C.pneumoniae* strain 10L-207 was prepared by adding 1.5 ml of lysis buffer (10 mM Tris-HCl, 150 mM NaCl, 2 mM EDTA, 0,6 % SDS, 100 µg/ml Proteinase K, pH 8) to 450 µl EB suspension (400.000/µl) and incubating overnight at 37 °C. After sequential extraction with phenol, phenol-chloroform, and chloroform, the DNA was precipitated with 0,3 M sodium acetate, pH 5,2 and 2 volumes of absolute ethanol. The DNA pellet was washed with 70 % ethanol. After solubilization with distilled water and treatment with 20 µg/ml RNAse A for 1 hour at RT, the DNA was extracted again with phenol-chloroform, alcohol precipitated and suspended with 300 µl 1 mM Tris-HCl pH 8,5. The DNA concentration was evaluated by measuring OD_{260} of the sample.

(C) Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF using the sequence of *C.pneumoniae* strain CWL029. Any predicted signal peptide were omitted, by deducing the 5' end amplification primer sequence immediately downstream from the predicted leader sequenee. For most ORFs, the 5' tail of the primers (table I) included only one restriction enzyme recognition site (NdeI, or NheI, or SpeI depending on the gene's own restriction pattern); the 3' primer tails (tableI) included a XhoI or a NotI or a HindIII restriction site.

5' tails		3' tails	
NdeI	5' GTGCGT**CATATG** 3'	XhoI	5' GCGT**CTCGAG** 3'
NheI	5' GTGCGT**GCTAGC** 3'	NotI	5' ACTCGCTA**GCGGCCGC** 3'
SpeI	5' GTGCGT**ACTAGT** 3'	HindIII	5' GCGT**AAGCTT** 3'

Table I. Oligonucleotide tails of the primers used to amplify Cpn genes.

As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridized to the sequence to be amplified. The number of hybridizing nucleotides depended on the melting temperature of the primers which was determined as described [(Breslauer *et al.* (1986) *PNAS USA* 83:3746-50]. The average melting temperature of the selected oligos was 50-55°C for the hybridizing region alone and 65-75°C for the whole oligos. Table II shows the forward and reverse primers used for each amplification.

(D) Amplification

The standard PCR protocol was as follow: 50 ng genomic DNA were used as template in the presence of 0,2 µM each primer, 200 µM each dNTP, 1,5 mM $MgCl_2$, 1x PCR buffer minus Mg (Gibco-BRL), and 2 units of Taq DNA polymerase (Platinum Taq, Gibco-BRL) in a final volume of 100 µl. Each sample underwent a double-step amplification: the first 5 cycles were performed using as the hybridizing temperature the one of the oligos excluding the restriction enzyme tail, followed by 25 cycles performed according to the hybridization temperature of the whole lenght primers. The standard cycles were as follow:

denaturation : 94 °C, 2 min

denaturation: 94 °C, 30 seconds
hybridization: 51 °C, 50 seconds } 5 cycles
elongation: 72 °C, 1 min or 2 min and 40 sec

denaturation: 94 °C, 30 seconds
hybridization: 70 °C, 50 seeonds } 25 cycles
elongation: 72 °C, 1 min or 2 min and 40 sec

72 °C, 7 min
4 °C

The elongation time was 1 min for ORFs shorter than 2000 bp, and 2 min and 40 seconds for ORFs longer than 2000 bp. The amplifications were performed using a Gene Amp PCR system 9600 (Perkin Elmer).

To check the amplification results, 4 µl of eaeh PCR product was loaded onto 1-1.5 agarose gel and the size of amplified fragments compared with DNA molecular weight standards (DNA markers III or IX, Roche). The PCR products were loaded on agarose gel and after eleetrophoresis the right size bands were excised from the gel. The DNA was purified from the agarose using the Gel Extraction Kit (Qiagen) following the instruction of the manufacturer. The final elution volume of the DNA was 50 µl TE (10 mM Tris-HCl, 1 mM EDTA, pH 8). One µl of each purified DNA was loaded onto agarose gel to evaluate the yield.

(E) Digestion of PCR fragments

One-two µg of purified PCR product were double digested overnight at 37 °C with the appropriate restriction enzymes (60 units of each enzyme) using the appropriate restriction buffer in 100 µl final volume. The restriction enzymes and the digestion buffers were from New England Biolabs. After

purification of the digested DNA (PCR purification Kit, Qiagen) and elution with 30 µl TE, 1 µl was subjected to agarose gel electrophoresis to evaluate the yield in comparison to titrated molecular weight standards (DNA markers III or IX, Roche).

(F) Digestion of the cloning vectors (pET21b+, pGEX-NN, and pGEX-NNH)

10 µg of plasmid was double digested with 100 units of each restriction enzyme in 400 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37 °C. After electrophoresis on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen Qiaex II Gel Extraction Kit and the DNA was eluted with 50 µl TE. The DNA concentration was evaluated by measuring OD_{260} of the sample.

(G) Cloning

75ng of the appropriately digested and purified vectors and the digested and purified fragments corresponding to each ORF, were ligated in final volumes of 10-20 µl with a molar ratio of 1:1 fragment/vector, using 400 units T4 DNA ligase (New England Biolabs) in the presence of the buffer supplied by the manufacturer. The reactions were incubated overnight at 16 °C.

Transformation in *E coli* DH5 competent cells was performed as follow: the ligation reaction was mixed with 200 µl of competent DH5 cells and incubated on ice for 30 min and then at 42 °C for 90 seconds. After cooling on ice, 0.8 ml LB was added and the cells were incubated for 45 min at 37 °C under shaking. 100 and 900 µl of cell suspensions were plated on separate plates of agar LB 100 µg/ml Ampicillin and the plates were incubated overnight at 37 °C. The screening of the transformants was done by growing randomly chosen clones in 6 ml LB 100 µg/ml Ampicillin, by extracting the DNA using the Qiagen Qiaprep Spin Miniprep Kit following the manufacturer instructions, and by digesting 2 µl of plasmid minipreparation with the restrietion enzymes specific for the restriction cloning sites. After agarose gel electrophoresis of the digested plasmid mini-preparations, positive clones were chosen on the basis of the eorrect size of the restriction fragments, as evaluated by comparison with appropriate molecular weight markers (DNA markers III or IX, Roche).

(H) Expression

1 µl of each right plasmid mini-preparation was transformed in 200 µl of competent *E. coli* strain suitable for expression of the recombinant protein. All pET21b+ recombinant plasmids were transformed in BL21 DE3 (Novagen) *E. coli* cells, whilst all pGEX-NN and all pGEX-NNH recombinant plasmids were transformed in BL21 cells (Novagen). After plating transformation mixtures on LB/Amp agar plates and incubation overnight at 37 °C, single colonies were inoculated in 3 ml LB 100 µg/ml Ampicillin and grown at 37 °C overnight. 70 µl of the overnight culture was inoculated in 2 ml LB/Amp and grown at 37 °C until OD_{600} of the pET clones reached the 0,4-0,8 value or until OD_{600} of the pGEX elones reached the 0,8-1 value. Protein expression was then

induced by adding IPTG (Isopropil β-D thio-galacto-piranoside) to the mini-cultures. pET clones were induced using 1 mM IPTG, whilst pGEX clones were induced using 0.2 mM IPTG. After 3 hours incubation at 37 °C the final OD_{600} was checked and the cultures were cooled on ice. After eentrifugation of 0.5 ml culture, the cell pellet was suspended in 50 μl of protein Loading Sample Buffer (60 mM TRIS-HCl pH 6.8, 5% w/v SDS, 10% v/v glycerin, 0.1% w/v Bromophenol Blue, 100 mM DTT) and incubated at 100 °C for 5 min. A volume of boiled sample corresponding to 0.1 OD_{600} culture was analysed by SDS-PAGE and Coomassie Blue staining to verify the presence of induced protein band.

PURIFICATION OF THE RECOMBINANT PROTEINS

Single colonies were inoculated in 25 ml LB 100 μg/ml Ampicillin and grown at 37 °C overnight. The overnight culture was inoculated in 500 ml LB/Amp and grown under shaking at 25 °C until OD_{600} 0,4-0,8 value for the pET clones, or until OD_{600} 0,8-1 value for the pGEX clones. Protein expression was then induced by adding IPTG to the cultures. pET clones were induced using 1 mM IPTG, whilst pGEX clones were induced using 0.2 mM IPTG. After 4 hours incubation at 25 °C the final OD_{600} was checked and the cultures were cooled on ice. After centrifugation at 6000 rpm (JA10 rotor, Beckman), the cell pellet was processed for purification or frozen at –20 °C.

(I) Procedure for the purification of soluble His-tagged proteins from *E.coli*

1. Transfer the pellets from –20°C to ice bath and reconstitute with 10 ml 50 mM $NaHPO_4$ buffer, 300 mM NaCl, pH 8,0, pass in 40-50 ml centrifugation tubes and break the cells as per the following outline:
2. Break the pellets in the French Press performing <u>three</u> passages with in-line washing.
3. Centrifuge at about 30-40000 x g per 15-20 min. If possible use rotor JA 25.50 (21000 rpm, 15 min.) or JA-20 (18000 rpm, 15 min.)
4. Equilibrate the Poly-Prep columns with 1 ml Fast Flow Chelating Sepharose resin with 50 mM phosphate buffer, 300 mM NaCl, pH 8,0.
5. Store the centrifugation pellet at –20°C, and load the supernatant in the columns.
6. Collect the flow through.
7. Wash the columns with 10 ml (2 ml + 2 ml + 4 ml) 50 mM phosphate buffer, 300 mM NaCl, pH 8,0.
8. Wash again with 10 ml 20 mM imidazole buffer, 50 mM phosphate, 300 mM NaCl, pH 8,0.
9. Elute the proteins bound to the columns with 4,5 ml (1,5 ml + 1,5 ml + 1,5 ml) 250 mM imidazole buffer, 50 mM phosphate, 300 mM NaCl, pH 8,0 and collect the 3 corresponding fractions of ~1,5 ml each. Add to each tube 15 μl DTT 200 mM (final concentration 2 mM)

10. Measure the protein concentration of the first two fractions with the Bradford method, collect a 10 μg aliquot of proteins from each sample and analyse by SDS-PAGE. (N.B.: should the sample be too diluted, load 21 μl + 7 μl loading buffer).
11. Store the collected fractions at +4°C while waiting for the results of the SDS-PAGE analysis.
12. For immunisation prepare 4-5 aliquots of 100 μg each in 0,5 ml in 40% glycerol. The dilution buffer is the above elution buffer, plus 2 mM DTT. Store the aliquots at –20°C until immunisation.

(J) Purification of His-tagged proteins from Inclusion bodies

Purifications were carried out essentially according the following protocol:

1. Bacteria are collected from 500 ml cultures by centrifugation. If required store bacterial pellets at -20°C. For extraction, resuspend each bacterial pellet in 10 ml 50 mM TRIS-HCl buffer, pH 8,5 on an ice bath.
2. Disrupt the resuspended bacteria with a French Press, performing two passages.
3. Centrifuge at 35000 x g for 15 min and collect the pellets. Use a Beckman rotor JA 25.50 (21000 rpm, 15 min.) or JA-20 (18000 rpm, 15 min.).
4. Dissolve the centrifugation pellets with 50 mM TRIS-HCl, 1 mM TCEP {Tris(2-carboxyethyl)-phosphine hydrochloride, Pierce} , 6M guanidium chloride, pH 8,5. Stir for ~ 10 min. with a magnetic bar.
5. Centrifuge as described above, and collect the supernatant..
6. Prepare an adequate number of Poly-Prep (Bio-Rad) columns containing 1 ml of Fast Flow Chelating Sepharose (Pharmacia) saturated with Nichel according to manufacturer reeommendations.. Wash the columns twiee with 5 ml of H_20 and equilibrate with 50 mM TRIS-HCl, 1 mM TCEP, 6M guanidinium chloride, pH 8,5.
7. Load the supernatants from step 5 onto the columns, and wash with 5 ml of 50 mM TRIS-Hcl buffer, 1 mM TCEP, 6M urea, pH 8,5
8. Wash the columns with 10 ml of 20 mM imidazole, 50 mM TRIS-HCl , 6M urea, 1 mM TCEP, pH 8,5. Collect and set aside the first 5 ml for possible further controls.
9. Elute the proteins bound to the columns with 4,5 ml of a buffer containing 250 mM imidazole, 50 mM TRIS-HCl, 6M urea, 1 mM TCEP, pH 8,5. Add the elution buffer in three 1,5 ml aliquots, and collect the corresponding 3 fractions. Add to each fraction 15 μl DTT (final concentration 2 mM) .
10. Measure eluted protein concentration with the Bradford method, and analyze aliquots of ca 10 μg of protein by SDS-PAGE.
11. Store proteins at -20°C in 40% (v/v) glycerol, 50 mM TRIS-HCl, 2M urea, 0.5 M arginine, 2 mM DTT, 0.3 mM TCEP, 83.3 mM imidazole, pH 8,5

(K) Procedure for the purification of GST-fusion proteins from *E.coli*

1. Transfer the bactcrial pellets from –20°C to an ice bath and resuspend with 7,5 ml PBS, pH 7,4 to which a mixture of protease inhibitors (C∅MPLETE™ - Boehringer Mannheim, 1 tablet every 25 ml of buffer) has been added. Transfer to 40-50 ml centrifugation tubes and sonicate according to the following procedure:
   a) Position the probe at about 0,5 cm from the bottom of the tube
   b) Block the tube with the elamp
   c) Dip the tube in an ice bath
   d) Set the sonicator as follows: Timer → Hold, Duty Cycle → 55, Out. Control → 6.
   e) perform 5 cycles of 10 impulses at a time lapse of 1 minute (i.e. one cycle = 10 impulses + ~45" hold; b. 10 impulses + ~45" hold; c. 10 impulses + ~45" hold; d. 10 impulses + ~45" hold; e. 10 impulses + ~45" hold)
2. Centrifuge at about 30-40000 x g for 15-20 min. E.g.: use rotor Beckman JA 25.50 at 21000 rpm, for 15 min.
3. Store the centrifugation pellets at –20°C, and load the supernatants on the chromatography columns, as follows
4. Equilibrate the Poly-Prep (Bio-Rad) columns with 0,5 ml (≅1 ml suspension) of Glutathione-Sepharose 4B resin, wash with 2 ml (1 + 1) H_2O, and then with 10 ml (2 + 4 + 4) PBS, pH 7,4.
5. Load the supernatants on the columns and discard the flow through.
6. Wash the eolumns with 10 ml (2 + 4 + 4) PBS, pH 7,4.
7. Elute the proteins bound to the columns with 4,5 ml of 50 mM TRIS buffer, 10 mM reduced glutathione, pH 8.0, adding 1,5 ml + 1,5 ml + 1,5 ml and collecting the respective 3 fractions of ~1,5 ml each.
8. Measure the protein concentration of the first two fraetions with the Bradford method, analyse a 10 µg aliquot of proteins from each sample by SDS-PAGE. (N.B.: if the sample is too diluted load 21 µl (+ 7 µl loading buffer).
9. Store the collected fractions at +4°C while waiting for the results of the SDS-PAGE analysis.
10. For each protein destined to the immunisation prepare 4-5 aliquots of 100 µg each in 0,5 ml of 40% glycerol. The dilution buffer is 50 mM TRIS.HCl, 2 mM DTT, pH 8,0. Store the aliquots at –20°C until immunisation..

SEROLOGY

(L) Protocol of immunization

1. Groups of four CD1 female mice aged between 6 and 7 weeks were immunized with 20 µg of recombinant protein resuspended in 100 µl.

2. Four mice for each group received 3 doses with a 14 days interval schedule.

3. Immunization was performed through intra-peritoneal injection of the protein with an equal volume of Complete Freund's Adjuvant (CFA) for the first dose and Incomplete Freund's Adjuvant (IFA) for the following two doses.

4. Sera were collected before each immunization. Mice were sacrified 14 days after the third immunization and the collected sera were pooled and stored at –20°C.

(M) Western blot analysis of Cpn elementary body proteins with mouse sera

Aliquots of elementary bodies containing approximately 4 μg of proteins, mixed with SDS loading buffer (1x: 60 mM TRIS-HCl pH 6.8, 5% w/v SDS, 10% v/v glycerin, 0.1% Bromophenol Blue, 100 mM DTT) and boiled 5 minutes at 95° C, were loaded on a 12% SDS-PAGE gel. The gel was run using a SDS-PAGE running buffer containing 250 mM TRIS, 2.5 mM Glycine and 0.1 %SDS. The gel was electroblotted onto nitrocellulose membrane at 200 mA for 30 minutes. The membrane was blocked for 30 minutes with PBS, 3% skimmed milk powder and incubated O/N at 4° C with the appropriate dilution (1/100) of the sera. After washing twice with PBS + 0.1% Tween (Sigma) the membrane was incubated for 2 hours with peroxidase-conjugated secondary anti-mouse antibody (Sigma) diluted 1:3000. The nitrocellulose was washed twice for 10 minutes with PBS + 0.1% Tween-20 and once with PBS and thereafter developed by Opti-4CN Substrate Kit (Biorad).

Lanes shown in Western blots are: (P) = pre-immune control serum; (I) = immune serum.

(N) FACS analysis of *Chlamydia pneumoniae* elementary bodies with mouse sera

1. $2x10^5$ Elementary Bodies (EB)/well were washed with 200 μl of PBS-0.1%BSA in a 96 wells U bottom plate and centrifuged for 10 min. at 1200rpm, at 4°C.
2. The supernatant was discarded and the E.B. resuspended in 10 μl of PBS-0.1%BSA.
3. 10μl mouse sera diluted in PBS-0.1%BSA were added to the E.B. suspention to a final dilution of 1:400, and ineubated on ice for 30 min.
4. EB were washed by adding 180μl PBS-0.1%BSA and centrifuged for 10min. at 1200rpm, 4°C.
5. The supernatant was discarded and the E.B. resuspended in 10 1 of PBS-0.1%BSA.
6. 10μl of a goat anti-mouse IgG, $F(ab')_2$ fragment specific-R-Phycoerythrin-conjugated (Jackson Immunoresearch Laboratories Inc., cat.N°115-116-072) was added to the EB suspension to a final dilution of 1:100, and incubated on ice for 30 min. in the dark.
7. EB were washed by adding 180μl PBS-0.1%BSA and centrifuged for 10min. at 1200rpm, 4°C.
8. The supernatant was discarded and the E.B. resuspended in 150 μl of PBS-0.1%BSA.
9. E.B. suspension was passed through a cytometric chamber of a FACS Calibur (Becton Dikinson, Mountain View, CA USA) and 10.000 events were acquired.

10. Data were analysed using Cell Quest Software (Becton Dikinson, Mountain View, CA USA) by drawing a morphological dot plot (using forward and side scatter parameters) on E.B. signals. An histogram plot was then created on FL2 intensity of fluorescence log scale recalling the morphological region of EB.

NB: the results of FACS depend not only on the extent of accessibility of the native antigens but also on the quality of the antibodies elicited by the recombinant antigens, which may have structures with a variable degree of correct folding as compared with the native protein structures. Therefore, even if a FACS assay appears negative this does not necessarily mean that the protein is not abundant or accessible on the surface. PorB antigen, for instance, gave negative results in FACS but is a surface-exposed neutralising antigen [Kubo & Stephens (2000) *Mol. Microbiol.* 38:772-780].

(O) Mass Spectrometry analysis of two-dimensional electrophoretic protein maps

Gradient purified EBs from strain FB/96 were solubilized at a final concentration of 5.5mg/ml with immobiline rehydratation buffer (7M urea, 2M thiourea, 2% (w/v) CHAPS, 2% (w/v) ASB 14 [Chevallet *et al.* (1998) *Electrophor.* 19:1901-9], 2% (v/v) C.A 3-10NL (Amersham Pharmacia Biotech), 2 mM tributyl phosphine, 65 mM DTT). Samples (250μg protein) were adsorbed overnight on Immobiline DryStrips (7 cm, pH 3-10 non linear). Electrophocusing was performed in a IPGphor Isoelectric Focusing Unit (Amersham Pharmacia Biotech). Before PAGE separation, the focused strips were incubated in 4M urea, 2M thiourea, 30% (v/v) glycerol, 2% (w/v) SDS, 5mM tributyl phosphine 2.5%(w/v) acrylamide, 50mM Tris-HCl pH 8.8, as described [Herbert *et al.* (1998) *Electrophor.* 19:845-51]. SDS-PAGE was performed on linear 9-16% acrylamide gradients. Gels were stained with colloidal Coomassie (Novex, San Diego) [Doherty *et al.* (1998) *Electrophor.* 19:355-63]. Stained gels were scanned with a Personal Densitometer SI (Molecular Dynamics) at 8 bits and 50μm per pixel. Map images were annotated with the software Image Master 2D Elite, version 3.10 (Amersham Pharmacia Biotech). Protein spots were excised from the gel, using an Ettan Spot picker (Amersham Pharmacia Biotech), and dried in a vacuum centrifuge. In-gel digestion of samples for mass spectrometry and extraction of peptides were performed as described by Wilm *et al.* [*Nature* (1996) 379:466-9]. Samples were desalted with a ZIP TIP (Millipore), eluted with a saturated solution of alpha-cyano-4-hydroxycinnamic acid in 50% acetonitrile, 0.1% TFA and directly loaded onto a SCOUT 381 multiprobe plate (Bruker). Spectra were acquired on a Bruker Biflex II MALDI-TOF. Spectra were calibrated using a combination of known standard peptides, located in spots adjacent to the samples. Resulting values for monoisotopic peaks were used for database searches using the computer program Mascot (www.matrixscienee.com). All searches were performed using an error of 200-500ppm as constraint. A representative gel is shown in Figure 190.

Example 1

The following *C.pneumoniae* protein (PID 4376552) was expressed <SEQ ID 1; cp6552>:

1 **MKKKLSLLVG LIFVLSS**CHK EDAQNKIRIV ASPTPHAELL ESLQEEAKDL

```
 51  GIKLKILPVD DYRIPNRLLL DKQVDANYFQ HQAFLDDECE RYDCKGELVV
101  IAKVHLEPQA IYSKKHSSLE RLKSQKKLTI AIPVDRTNAQ RALHLLEECG
151  LIVCKGPANL NMTAKDVCGK ENRSINILEV SAPLLVGSLP DVDAAVIPGN
201  FAIAANLSPK KDSLCLEDLS VSKYTNLVVI RSEDVGSPKM IKLQKLFQSP
251  SVQHFFDTKY HGNILTMTQD NG*
```

A predicted signal peptide is highlighted.

The cp6552 nucleotide sequence <SEQ ID 2> is:

```
  1  ATGAAAAAAA AATTATCATT ACTTGTAGGT TTAATTTTTG TTTTGAGTTC
 51  TTGCCATAAG GAAGATGCTC AGAATAAAAT ACGTATTGTA GCCAGTCCGA
101  CACCTCATGC GGAATTATTG GAGAGTTTAC AGGAAGAGGC TAAAGATCTT
151  GGAATCAAGC TGAAAATACT TCCAGTAGAT GATTATCGTA TTCCTAATCG
201  TTTGCTTTTG GATAAACAAG TAGATGCAAA TTACTTTCAA CATCAAGCTT
251  TTCTTGATGA CGAATGCGAG CGTTATGATT GTAAGGGTGA ATTAGTTGTT
301  ATCGCTAAAG TTCATTTGGA ACCTCAAGCA ATTTATTCTA AGAAACATTC
351  TTCTTTAGAG CGCTTAAAAA GCCAGAAGAA ACTGACTATA GCGATTCCTG
401  TGGATCGTAC GAATGCTCAG CGTGCTCTAC ACTTGTTAGA AGAGTGCGGA
451  CTCATTGTTT GCAAAGGGCC TGCTAATTTA AATATGACAG CTAAAGATGT
501  CTGTGGGAAA GAAAATAGAA GTATCAACAT ATTAGAGGTG TCAGCTCCTC
551  TTCTTGTCGG ATCTCTTCCT GACGTTGATG CTGCTGTCAT TCCTGGAAAT
601  TTTGCTATAG CAGCAAACCT TTCTCCAAAG AAAGATAGTC TTTGTTTAGA
651  GGATCTTTCG GTATCTAAGT ATACAAACCT TGTTGTCATT CGTTCTGAAG
701  ACGTAGGTTC TCCTAAAATG ATAAAATTAC AGAAGCTGTT TCAATCTCCT
751  TCTGTACAAC ATTTTTTTGA TACAAAATAT CATGGGAATA TTTTGACAAT
801  GACTCAAGAC AATGGTTAG
```

The PSORT algorithm predicts an inner membrane location (0.127).

The protein was expressed in *E.coli* and purified as a his-tag product, as shown in Figure 1A, and also as a GST-fusion. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 1B) and for FACS analysis (Figure 1C).

The cp6552 protein was also identified in the 2D-PAGE experiment (Cpn0278).

These experiments show that cp6552 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 2

The following *C.pneumoniae* protein (PID 4376736) was expressed <SEQ ID 3; cp6736>:

```
  1  MKTSIRKFLI STTLAPCFAS TAFTVEVIMP SENFDGSSGK IFPYTTLSDP
 51  RGTLCIFSGD LYIANLDNAI SRTSSSCFSN RAGALQILGK GGVFSFLNIR
101  SSADGAAISS VITQNPELCP LSFSGFSQMI FDNCESLTSD TSASNVIPHA
151  SAIYATTPML FTNNDSILFQ YNRSAGFGAA IRGTSITIEN TKKSLLFNGN
201  GSISNGGALT GSAAINLINN SAPVIFSTNA TGIYGGAIYL TGGSMLTSGN
251  LSGVLFVNNS SRSGGAIYAN GNVTFSNNSD LTFQNNTASP QNSLPAPTPP
301  PTPPAVTPLL GYGGAIFCTP PATPPPTGVS LTISGENSVT FLENIASEQG
351  GALYGKKISI DSNKSTIFLG NTAGKGGAIA IPESGELSLS ANQGDILFNK
401  NLSITSGTPT RNSIHFGKDA KFATLGATQG YTLYFYDPIT SDDLSAASAA
451  ATVVVNPKAS ADGAYSGTIV FSGETLTATE AATPANATST LNQKLELEGG
501  TLALRNGATL NVHNFTQDEK SVVIMDAGTT LATTNGANNT DGAITLNKLV
551  INLDSLDGTK AAVVNVQSTN GALTISGTLG LVKNSQDCCD NHGMFNKDLQ
601  QVPILELKAT SNTVTTTDFS LGTNGYQQSP YGYQGTWEFT IDTTTHTVTG
651  NWKKTGYLPH PERLAPLIPN SLWANVIDLR AVSQASAADG EDVPGKQLSI
701  TGITNFFHAN HTGDARSYRH MGGGYLINTY TRITPDAALS LGFGQLFTKS
751  KDYLVGHGHS NVYFATVYSN ITKSLFGSSR FFSGGTSRVT YSRSNEKVKT
801  SYTKLPKGRC SWSNNCWLGE LEGNLPITLS SRILNLKQII PFVKAEVAYA
851  THGGIQENTP EGRIFGHGHL LNVAVPVGVR FGKNSHNRPD FYTIIVAYAP
901  DVYRHNPDCD TTLPINGATW TSIGNNLTRS TLLVQASSHT SVNDVLEIFG
951  HCGCDIRRTS RQYTLDIGSK LRF*
```

A predicted signal peptide is highlighted.

The cp6736 nucleotide sequence <SEQ ID 4> is:

```
   1 ATGAAAACGT CTATTCGTAA GTTCTTAATT TCTACCACAC TGGCGCCATG
  51 TTTTGCTTCA ACAGCGTTTA CTGTAGAAGT TATCATGCCT TCCGAGAACT
 101 TTGATGGATC GAGTGGGAAG ATTTTTCCTT ACACAACACT TTCTGATCCT
 151 AGAGGGACAC TCTGTATTTT TTCAGGGGAT CTCTACATTG CGAATCTTGA
 201 TAATGCCATA TCCAGAACCT CTTCCAGTTG CTTTAGCAAT AGGGCGGGAG
 251 CACTACAAAT CTTAGGAAAA GGTGGGGTTT TCTCCTTCTT AAATATCCGT
 301 TCTTCAGCTG ACGGAGCCGC GATTAGTAGT GTAATCACCC AAAATCCTGA
 351 ACTATGTCCC TTGAGTTTTT CAGGATTTAG TCAGATGATC TTCGATAACT
 401 GTGAATCTTT GACTTCAGAT ACCTCAGCGA GTAATGTCAT ACCTCACGCA
 451 TCGGCGATTT ACGCTACAAC GCCCATGCTC TTTACAAACA ATGACTCCAT
 501 ACTATTCCAA TACAACCGTT CTGCAGGATT TGGAGCTGCC ATTCGAGGCA
 551 CAAGCATCAC AATAGAAAAT ACGAAAAAGA GCCTTCTCTT TAATGGTAAT
 601 GGATCCATCT CTAATGGAGG GGCCCTCACG GGATCTGCAG CGATCAACCT
 651 CATCAACAAT AGCGCTCCTG TGATTTTCTC AACGAATGCT ACAGGGATCT
 701 ATGGTGGGGC TATTTACCTT ACCGGAGGAT CTATGCTCAC CTCTGGGAAC
 751 CTCTCAGGAG TCTTGTTCGT TAATAATAGC TCGCGCTCAG GAGGCGCTAT
 801 CTATGCTAAC GGAAATGTCA CATTTTCTAA TAACAGCGAC CTGACTTTCC
 851 AAAACAATAC AGCATCTCCA CAAAACTCCT TACCTGCACC TACACCTCCA
 901 CCTACACCAC CAGCAGTCAC TCCTTTGTTA GGATATGGAG GCGCCATCTT
 951 CTGTACTCCT CCAGCTACCC CCCCACCAAC AGGTGTTAGC CTGACTATAT
1001 CTGGAGAAAA CAGCGTTACA TTCCTAGAAA ACATTGCCTC CGAACAAGGA
1051 GGAGCCCTCT ATGGCAAAAA GATCTCTATA GATTCTAATA AATCTACAAT
1101 ATTTCTTGGA AATACAGCTG GAAAAGGAGG CGCTATTGCT ATTCCCGAAT
1151 CTGGGGAGCT CTCTCTATCC GCAAATCAAG GTGATATCCT CTTTAACAAG
1201 AACCTCAGCA TCACTAGTGG GACACCTACT CGCAATAGTA TTCACTTCGG
1251 AAAAGATGCC AAGTTTGCCA CTCTAGGAGC TACGCAAGGC TATACCCTAT
1301 ACTTCTATGA TCCGATTACA TCTGATGATT TATCTGCTGC ATCCGCAGCC
1351 GCTACTGTGG TCGTCAATCC CAAAGCCAGT GCAGATGGTG CGTATTCAGG
1401 GACTATTGTC TTTTCAGGAG AAACCCTCAC TGCTACCGAA GCAGCAACCC
1451 CTGCAAATGC TACATCTACA TTAAACCAAA AGCTAGAACT TGAAGGCGGT
1501 ACTCTCGCTT TAAGAAACGG TGCTACCTTA AATGTTCATA ACTTCACGCA
1551 AGATGAAAAG TCCGTCGTCA TCATGGATGC AGGGACCACA TTAGCAACTA
1601 CAAATGGAGC TAATAATACT GACGGTGCTA TCACCTTAAA CAAGCTTGTA
1651 ATCAATCTGG ATTCTTTGGA TGGCACTAAA GCGGCTGTCG TTAATGTGCA
1701 GAGTACCAAT GGAGCTCTCA CTATATCCGG AACTTTAGGA CTTGTGAAAA
1751 ACTCTCAAGA TTGCTGTGAC AACCACGGGA TGTTTAATAA AGATTTACAG
1801 CAAGTTCCGA TTTTAGAACT CAAAGCGACT TCAAATACTG TAACCACTAC
1851 GGACTTCAGT CTCGGCACAA ACGGCTATCA GCAATCTCCC TATGGGTATC
1901 AAGGAACTTG GGAGTTTACC ATAGACACGA CAACCCATAC GGTCACAGGA
1951 AATTGGAAAA AAACCGGTTA TCTTCCTCAT CCGGAGCGTC TTGCTCCCCT
2001 CATTCCTAAT AGCCTATGGG CAAACGTCAT AGATTTACGA GCTGTAAGTC
2051 AAGCGTCAGC AGCTGATGGC GAAGATGTCC CTGGGAAGCA ACTGAGCATC
2101 ACAGGAATTA CAAATTTCTT CCATGCGAAT CATACCGGTG ATGCACGCAG
2151 CTACCGCCAT ATGGGTGGAG GCTACCTCAT CAATACCTAC ACACGCATCA
2201 CTCCAGATGC TGCGTTAAGT CTAGGTTTTG GACAGCTGTT TACAAAATCT
2251 AAGGATTACC TCGTAGGTCA CGGTCATTCT AACGTTTATT TCGCTACAGT
2301 ATACTCTAAC ATCACCAAGT CTCTGTTTGG ATCATCGAGA TTCTTCTCAG
2351 GAGGCACTTC TCGAGTTACC TATAGCCGTA GCAATGAGAA AGTAAAGACT
2401 TCATATACAA AATTGCCTAA AGGGCGCTGC TCTTGGAGTA ACAATTGCTG
2451 GTTAGGAGAA CTCGAAGGGA ACCTTCCCAT CACTCTCTCT TCTCGCATCT
2501 TAAACCTCAA GCAGATCATT CCCTTTGTAA AAGCTGAAGT TGCTTACGCG
2551 ACTCATGGGG GCATCCAAGA AAATACCCCC GAGGGGAGGA TTTTTGGACA
2601 CGGTCATCTA CTCAACGTTG CAGTTCCCGT AGGCGTCCGC TTTGGTAAAA
2651 ATTCTCATAA TCGACCAGAT TTTTACACTA TAATCGTAGC CTATGCTCCT
2701 GATGTCTATC GTCACAATCC TGATTGCGAT ACGACATTAC CTATTAATGG
2751 AGCTACGTGG ACCTCTATAG GGAATAATCT AACCAGAAGT ACTTTGCTAG
2801 TACAAGCATC CAGCCATACT TCAGTAAATG ATGTTCTAGA GATCTTCGGG
2851 CACTGTGGAT GTGATATTCG CAGAACCTCC CGTCAATATA CTCTAGATAT
2901 AGGAAGCAAA TTACGATTTT AA
```

The PSORT algorithm predicts an outer membrane location (0.917).

The protein was expressed in *E.coli* and purified as a his-tag product, as shown in Figure 2A, and also as a GST-fusion. Both proteins were used to immunise mice, whose sera were used in a Western blot (Figure 2B) and for FACS analysis (Figure 2C).

The cp6736 protein was also identified in the 2D-PAGE experiment (Cpn0453) and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6736 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 3

The following *C.pneumoniae* protein (`PID 4376751`) was expressed <SEQ ID 5; cp6751>:

```
  1  MRFFCFGMLL PFTFVLANEG LQLPLETYIT LSPEYQAAPQ VGFTHNQNQD
 51  LAIVGNHNDF ILDYKYYRSN GGALTCKNLL ISENIGNVFF EKNVCPNSGG
101  AIYAAQNCTI SKNQNYAFTT NLVSDNPTAT AGSLLGGALF AINCSITNNL
151  GQGTFVDNLA LNKGGALYTE TNLSIKDNKG PIIIKQNRAL NSDSLGGGIY
201  SGNSLNIEGN SGAIQITSNS SGSGGGIFST QTLTISSNKK LIEISENSAF
251  ANNYGSNFNP GGGGLTTTFC TILNNREGVL FNNNQSQSNG GAIHAKSIII
301  KENGPVYFLN NTATRGGALL NLSAGSGNGS FILSADNGDI IFNNNTASKH
351  ALNPPYRNAI HSTPNMNLQI GARPGYRVLF YDPIEHELPS SFPILFNFET
401  GHTGTVLFSG EHVHQNFTDE MNFFSYLRNT SELRQGVLAV EDGAGLACYK
451  FFQRGGTLLL GQGAVITTAG TIPTPSSTPT TVGSTITLNH IAIDLPSILS
501  FQAQAPKIWI YPTKTGSTYT EDSNPTITIS GTLTLRNSNN EDPYDSLDLS
551  HSLEKVPLLY IVDVAAQKIN SSQLDLSTLN SGEHYGYQGI WSTYWVETTT
601  ITNPTSLLGA NTKHKLLYAN WSPLGYRPHP ERRGEFITNA LWQSAYTALA
651  GLHSLSSWDE EKGHAASLQG IGLLVHQKDK NGFKGFRSHM TGYSATTEAT
701  SSQSPNFSLG FAQFFSKAKE HESQNSTSSH HYFSGMCIEN TLFKEWIRLS
751  VSLAYMFTSE HTHTMYQGLL EGNSQGSFHN HTLAGALSCV FLPQPHGESL
801  QIYPFITALA IRGNLAAFQE SGDHAREFSL HRPLTDVSLP VGIRASWKNH
851  HRVPLVWLTE ISYRSTLYRQ DPELHSKLLI SQGTWTTQAT PVTYNALGIK
901  VKNTMQVFPK VTLSLDYSAD ISSSTLSHYL NVASRMRF*
```

A predicted signal peptide is highlighted.

The cp6751 nucleotide sequence <SEQ ID 6> is:

```
   1  ATGCGCTTTT TTTGCTTCGG AATGTTGCTT CCTTTTACTT TTGTATTGGC
  51  TAATGAAGGT CTCCAACTTC CTTTGGAGAC CTATATTACA TTAAGTCCTG
 101  AATATCAAGC AGCCCCTCAA GTAGGGTTTA CTCATAACCA AAATCAAGAT
 151  CTCGCAATTG TCGGGAATCA CAATGATTTC ATCTTGGACT ATAAGTACTA
 201  TCGGTCGAAT GGAGGTGCTC TTACCTGTAA GAATCTTCTG ATCTCTGAAA
 251  ATATAGGGAA TGTCTTCTTT GAGAAGAATG TCTGTCCCAA TTCTGGCGGG
 301  GCAATTTATG CTGCTCAAAA TTGCACGATC TCCAAGAATC AGAACTATGC
 351  ATTTACTACA AACTTGGTCT CTGACAATCC TACAGCCACT GCGGGATCAC
 401  TATTGGGTGG AGCTCTCTTT GCCATAAATT GCTCTATTAC TAATAACCTA
 451  GGACAGGGAA CTTTCGTTGA CAATCTCGCT TTAAATAAGG GGGGTGCCCT
 501  CTATACTGAG ACGAACTTAT CTATTAAAGA CAATAAAGGC CCGATCATAA
 551  TCAAGCAGAA TCGGGCACTA AATTCGGACA GTTTAGGAGG AGGGATTTAT
 601  AGTGGGAACT CTCTAAATAT AGAGGGAAAT TCTGGAGCTA TACAGATCAC
 651  AAGCAACTCT TCAGGATCTG GGGGAGGCAT ATTTTCTACC CAAACACTCA
 701  CGATCTCCTC GAATAAAAAA CTCATAGAAA TCAGTGAAAA TTCCGCGTTC
 751  GCAAATAACT ATGGATCGAA CTTCAATCCA GGAGGAGGAG GTCTTACTAC
 801  CACCTTTTGC ACGATATTGA ACAACCGAGA AGGGGTACTC TTTAACAATA
 851  ACCAAAGCCA GAGCAACGGT GGAGCCATTC ATGCGAAATC TATCATTATC
 901  AAAGAAAATG GTCCTGTATA CTTTTTAAAT AACACTGCAA CTCGGGGAGG
 951  GGCTCTCCTC AACTTATCAG CAGGTTCTGG AAACGGAAGC TTCATCTTAT
1001  CTGCAGATAA TGGAGATATT ATCTTTAACA ATAATACGGC CTCCAAGCAT
1051  GCCCTCAATC CTCCATACAG AAACGCCATT CACTCGACTC CTAATATGAA
1101  TCTGCAAATA GGAGCCCGTC CCGGCTATCG AGTGCTGTTC TATGATCCCA
1151  TAGAACATGA GCTCCCTTCC TCCTTCCCCA TACTCTTTAA TTTCGAAACC
1201  GGTCATACAG GTACAGTTTT ATTTTCAGGG GAACATGTAC ACCAGAACTT
```

```
1251  TACCGATGAA ATGAATTTCT TTTCCTATTT AAGGAACACT TCGGAACTAC
1301  GTCAAGGAGT CCTTGCTGTT GAAGATGGTG CGGGGCTGGC CTGCTATAAG
1351  TTCTTCCAAC GAGGAGGCAC TCTACTTCTA GGTCAAGGTG CGGTGATCAC
1401  GACAGCAGGA ACGATTCCCA CACCATCCTC AACACCAACG ACAGTAGGAA
1451  GTACTATAAC TTTAAATCAC ATTGCCATTG ACCTTCCTTC TATTCTTTCT
1501  TTTCAAGCTC AGGCTCCAAA AATTTGGATT TACCCCACAA AAACAGGATC
1551  TACCTATACT GAAGATTCCA ACCCGACAAT CACAATCTCA GGAACTCTCA
1601  CCTTACGCAA CAGCAACAAC GAAGATCCCT ACGATAGTCT GGATCTCTCG
1651  CACTCTCTTG AGAAAGTTCC CCTTCTTTAT ATTGTCGATG TCGCTGCACA
1701  AAAAATTAAC TCTTCGCAAC TGGATCTATC CACATTAAAT TCTGGCGAAC
1751  ACTATGGGTA TCAAGGCATC TGGTCGACCT ATTGGGTAGA AACTACAACA
1801  ATCACGAACC CTACATCTCT ACTAGGCGCG AATACAAAAC ACAAGCTGCT
1851  CTATGCAAAC TGGTCTCCTC TAGGCTACCG TCCTCATCCC GAACGTCGAG
1901  GAGAATTCAT TACGAATGCC TTGTGGCAAT CGGCATATAC GGCTCTTGCA
1951  GGACTCCACT CCCTCTCCTC CTGGGATGAA GAGAAGGGTC ATGCAGCTTC
2001  CCTACAAGGC ATTGGTCTTC TGGTTCATCA AAAAGACAAA AACGGTTTTA
2051  AGGGATTTCG TAGTCATATG ACAGGTTATA GTGCTACCAC CGAAGCAACC
2101  TCTTCTCAAA GTCCGAATTT CTCTTTAGGA TTTGCTCAGT TCTTCTCCAA
2151  AGCTAAAGAA CATGAATCTC AAAATAGCAC GTCCTCTCAC CACTATTTCT
2201  CTGGAATGTG CATAGAAAAT ACTCTCTTCA AAGAGTGGAT ACGTCTATCT
2251  GTGTCTCTTG CTTATATGTT TACCTCGGAA CATACCCATA CAATGTATCA
2301  GGGTCTCCTG GAAGGGAACT CTCAGGGATC TTTCCACAAC CATACCTTAG
2351  CAGGGGCTCT CTCCTGTGTT TTCTTACCTC AACCTCACGG CGAGTCCCTG
2401  CAGATCTATC CCTTTATTAC TGCCTTAGCC ATCCGAGGAA ATCTTGCTGC
2451  GTTTCAAGAA TCTGGAGACC ATGCTCGGGA ATTTTCCCTA CACCGCCCCC
2501  TAACGGACGT CTCCCTCCCT GTAGGAATCC GCGCTTCTTG GAAGAACCAC
2551  CACCGAGTTC CCCTAGTCTG GCTCACAGAA ATTTCCTATC GCTCTACTCT
2601  CTATAGGCAA GATCCTGAAC TCCACTCGAA ATTACTGATT AGCCAAGGTA
2651  CGTGGACGAC GCAGGCCACT CCTGTGACCT ACAATGCTTT AGGGATCAAA
2701  GTGAAAAATA CCATGCAGGT GTTTCCTAAA GTCACTCTCT CCTTAGATTA
2751  CTCTGCGGAT ATTTCTTCCT CCACGCTGAG TCACTACTTA AACGTGGCGA
2801  GTAGAATGAG ATTTTAA
```

The PSORT algorithm predicts an outer membrane location (0.923).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 3A, and also in his-tagged form. The GST-fusion recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 3B) and for FACS analysis (Figure 3C).

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6751 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 4

The following *C.pneumoniae* protein (PID 4376752) was expressed <SEQ ID 7; cp6752>:

```
  1  MFGMTPAVYS LQTDSLEKFA LERDEEFRTS FPLLDSLSTL TGFSPITTFV
 51  GNRHNSSQDI VLSNYKSIDN ILLLWTSAGG AVSCNNFLLS NVEDHAFFSK
101  NLAIGTGGAI ACQGACTITK NRGPLIFFSN RGLNNASTGG ETRGGAIACN
151  GDFTISQNQG TFYFVNNSVN NWGGALSTNG HCRIQSNRAP LLFFNNTAPS
201  GGGALRSENT TISDNTRPIY FKNNCGNNGG AIQTSVTVAI KNNSGSVIFN
251  NNTALSGSIN SGNGSGGAIY TTNLSIDDNP GTILFNNNYC IRDGGAICTQ
301  FLTIKNSGHV YFTNNQGNWG GALMLLQDST CLLFAEQGNI AFQNNEVFLT
351  TFGRYNAIHC TPNSNLQLGA NKGYTTAFFD PIEHQHPTTN PLIFNPNANH
401  QGTILFSSAY IPEASDYENN FISSSKNTSE LRNGVLSIED RAGWQFYKFT
451  QKGGILKLGH AASIATTANS ETPSTSVGSQ VIINNLAINL PSILAKGKAP
501  TLWIRPLQSS APFTEDNNPT ITLSGPLTLL NEENRDPYDS IDLSEPLQNI
551  HLLSLSDVTA RHINTDNFHP ESLNATEHYG YQGIWSPYWV ETITTTNNAS
601  IETANTLYRA LYANWTPLGY KVNPEYQGDL ATTPLWQSFH TMFSLLRSYN
651  RTGDSDIERP FLEIQGIADG LFVHQNSIPG APGFRIQSTG YSLQASSETS
```

```
701  LHQKISLGFA QFFTRTKEIG SSNNVSAHNT VSSLYVELPW FQEAFATSTV
751  LAYGYGDHHL HSLHPSHQEQ AEGTCYSHTL AAAIGCSFPW QQKSYLHLSP
801  FVQAIAIRSH QTAFEEIGDN PRKFVSQKPF YNLTLPLGIQ GKWQSKFHVP
851  TEWTLELSYQ PVLYQQNPQI GVTLLASGGS WDILGHNYVR NALGYKVHNQ
901  TALFRSLDLF LDYQGSVSSS TSTHHLQAGS TLKF*
```

The cp6752 nucleotide sequence <SEQ ID 8> is:

```
   1  ATGTTCGGGA TGACTCCTGC AGTGTATAGT TTACAAACGG ACTCCCTTGA
  51  AAAGTTTGCT TTAGAGAGGG ATGAAGAGTT TCGTACGAGC TTTCCTCTCT
 101  TAGACTCTCT CTCCACTCTT ACAGGATTTT CTCCAATAAC TACGTTTGTT
 151  GGAAATAGAC ATAATTCCTC TCAAGACATT GTACTTTCTA ACTACAAGTC
 201  TATTGATAAC ATCCTTCTTC TTTGGACATC GGCTGGGGGA GCTGTGTCCT
 251  GTAATAATTT CTTATTATCA AATGTTGAAG ACCATGCCTT CTTCAGTAAA
 301  AATCTCGCGA TTGGGACTGG AGGCGCGATT GCTTGCCAGG GAGCCTGCAC
 351  AATCACGAAG AATAGAGGAC CCCTTATTTT TTTCAGCAAT CGAGGTCTTA
 401  ACAATGCGAG TACAGGAGGA GAAACTCGTG GGGGTGCGAT TGCCTGTAAT
 451  GGAGACTTCA CGATTTCTCA AAATCAAGGG ACTTTCTACT TTGTCAACAA
 501  TTCCGTCAAC AACTGGGGAG GAGCCCTCTC CACCAATGGA CACTGCCGCA
 551  TCCAAAGCAA CAGGGCACCT CTACTCTTTT TTAACAATAC AGCCCCTAGT
 601  GGAGGGGGTG CGCTTCGTAG TGAAAATACA ACGATCTCTG ATAACACGCG
 651  TCCTATTTAT TTTAAGAACA ACTGTGGGAA CAATGGCGGG GCCATTCAAA
 701  CAAGCGTTAC TGTTGCGATA AAAAATAACT CCGGGTCGGT GATTTTCAAT
 751  AACAACACAG CGTTATCTGG TTCGATAAAT TCAGGAAATG GTTCAGGAGG
 801  GGCGATTTAT ACAACAAACC TATCCATAGA CGATAACCCT GGAACTATTC
 851  TTTTCAATAA TAACTACTGC ATTCGCGATG GCGGAGCTAT CTGTACACAA
 901  TTTTTGACAA TCAAAAATAG TGGCCACGTA TATTTCACCA ACAATCAAGG
 951  AAACTGGGGA GGTGCTCTTA TGCTCCTACA GGACAGCACC TGCCTACTCT
1001  TCGCGGAACA AGGAAATATC GCATTTCAAA ATAATGAGGT TTTCCTCACC
1051  ACATTTGGTA GATACAACGC CATACATTGT ACACCAAATA GCAACTTACA
1101  ACTTGGAGCT AATAAGGGGT ATACGACTGC TTTTTTTGAT CCTATAGAAC
1151  ACCAACATCC AACTACAAAT CCTCTAATCT TTAATCCCAA TGCGAACCAT
1201  CAGGGAACGA TCTTATTTTC TTCAGCCTAT ATCCCAGAAG CTTCTGACTA
1251  CGAAAATAAT TTCATTAGCA GCTCGAAAAA TACCTCTGAA CTTCGCAATG
1301  GTGTCCTCTC TATCGAGGAT CGTGCGGGAT GGCAATTCTA TAAGTTCACT
1351  CAAAAAGGAG GTATCCTTAA ATTAGGGCAT GCGGCGAGTA TTGCAACAAC
1401  TGCCAACTCT GAGACTCCAT CAACTAGTGT AGGCTCCCAG GTCATCATTA
1451  ATAACCTTGC GATTAACCTC CCCTCGATCT TAGCAAAAGG AAAAGCTCCT
1501  ACCTTGTGGA TCCGTCCTCT ACAATCTAGT GCTCCTTTCA CAGAGGACAA
1551  TAACCCTACA ATTACTTTAT CAGGTCCTCT GACACTCTTA AATGAGGAAA
1601  ACCGCGATCC CTACGACAGT ATAGATCTCT CTGAGCCTTT ACAAAACATT
1651  CATCTTCTTT CTTTATCGGA TGTAACAGCA CGTCATATCA ATACCGATAA
1701  CTTTCATCCT GAAAGCTTAA ATGCGACTGA GCATTACGGT TATCAAGGCA
1751  TCTGGTCTCC TTATTGGGTA GAGACGATAA CAACAACAAA TAACGCTTCT
1801  ATAGAGACGG CAAACACCCT CTACAGAGCT CTGTATGCCA ATTGGACTCC
1851  CTTAGGATAT AAGGTCAATC CTGAATACCA AGGAGATCTT GCTACGACTC
1901  CCCTATGGCA ATCCTTTCAT ACTATGTTCT CTCTATTAAG AAGTTATAAT
1951  CGAACTGGTG ATTCTGATAT CGAGAGGCCT TTCTTAGAAA TTCAAGGGAT
2001  TGCCGACGGC CTCTTTGTTC ATCAAAATAG CATCCCCGGG GCTCCAGGAT
2051  TCCGTATCCA ATCTACAGGG TATTCCTTAC AAGCATCCTC CGAAACTTCT
2101  TTACATCAGA AAATCTCCTT AGGTTTTGCA CAGTTCTTCA CCCGCACTAA
2151  AGAAATCGGA TCAAGCAACA ACGTCTCGGC TCACAATACA GTCTCTTCAC
2201  TTTATGTTGA GCTTCCGTGG TTCCAAGAGG CCTTTGCAAC ATCCACAGTG
2251  TTAGCGTATG GCTATGGGGA CCATCACCTC CACAGCCTAC ATCCCTCACA
2301  TCAAGAACAG GCAGAAGGGA CGTGTTATAG CCATACATTA GCAGCAGCTA
2351  TCGGCTGTTC TTTCCCTTGG CAACAGAAAT CCTATCTTCA CCTCAGCCCG
2401  TTCGTTCAGG CAATTGCAAT ACGTTCTCAC CAAACAGCGT TCGAAGAGAT
2451  TGGTGACAAT CCCCGAAAGT TTGTCTCTCA AAAGCCTTTC TATAATCTGA
2501  CCTTACCTCT AGGAATCCAA GGAAAATGGC AGTCAAAATT CCACGTACCT
2551  ACAGAATGGA CTCTAGAACT TTCTTACCAA CCGGTACTCT ATCAACAAAA
2601  TCCCCAAATC GGTGTCACGC TACTTGCGAG CGGAGGTTCC TGGGATATCC
2651  TAGGCCATAA CTATGTTCGC AATGCTTTAG GGTACAAAGT CCACAATCAA
2701  ACTGCGCTCT TCCGTTCTCT CGATCTATTC TTGGATTACC AAGGATCGGT
2751  CTCCTCCTCG ACATCTACGC ACCATCTCCA AGCAGGAAGT ACCTTAAAAT
2801  TCTAA
```

The PSORT algorithm predicts a cytoplasmic location (0.138).

The protein was expressed in *E.coli* and purified as a his-tag product, as shown in Figure 4A, and also as a GST-fusion. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (4B) and the his-tagged protein was used for FACS analysis (4C).

The cp6752 protein was also identified in the 2D-PAGE experiment (Cpn0467).

These experiments show that cp6752 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 5

The following *C.pneumoniae* protein (PID 4376850) was expressed <SEQ ID 9; ep6850>:

```
  1 MKKAVLIAAM FCGVVSLSSC CRIVDCCFED PCAPSSCNPC EVIRKKERSC
 51 GGNACGSYVP SCSNPCGSTE CNSQSPQVKG CTSPDGRCKQ *
```

A predicted signal peptide is highlighted.

The cp6850 nucleotide sequence <SEQ ID 10> is:

```
  1 ATGAAGAAAG CTGTTTTAAT TGCTGCAATG TTTTGTGGAG TAGTTAGCTT
 51 AAGTAGCTGC TGCCGCATTG TAGATTGTTG TTTTGAGGAT CCTTGCGCAC
101 CCTCTTCTTG CAATCCTTGT GAAGTAATAA GAAAAAAAGA AAGATCTTGC
151 GGCGGTAATG CTTGTGGGTC CTACGTTCCT TCTTGTTCTA ATCCATGTGG
201 TTCAACAGAG TGTAACTCTC AAAGCCCACA AGTTAAAGGT TGTACATCAC
251 CTGATGGCAG ATGCAAACAG TAA
```

The PSORT algorithm predicts an inner membrane location (0.329).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 5A. The recombinant protein was used to immunise miee, whose sera were used in a Western blot (Figure 5B) and for FACS analysis (Figure 5B). A his-tagged protein was also expressed.

These experiments show that ep6850 is a surface-exposed and immunoaecessible protein, and that it is a useful immunogen. These properties are not evident from the sequenee alone.

Example 6

The following *C.pneumoniae* protein (PID 4376900) was expressed <SEQ ID 11; cp6900>:

```
  1 MKIKFSWKVN FLICLLAVGL IFFGCSRVKR EVLVGRDATW FPKQFGIYTS
 51 DTNAFLNDLV SEINYKENLN INIVNQDWVH LFENLDDKKT QGAFTSVLPT
101 LEMLEHYQFS DPILLTGPVL VVAQDSPYQS IEDLKGRLIG VYKFDSSVLV
151 AQNIPDAVIS LYQHVPIALE ALTSNCYDAL LAPVIEVTAL IETAYKGRLK
201 IISKPLNADG LRLAILKGTN GDLLEGFNAG LVKTRRSGKY DAIKQRYRLP
```

The cp6900 nucleotide sequence <SEQ ID 12> is:

```
  1 GTGAAGATAA AATTTTCTTG GAAGGTAAAT TTTTTAATAT GTTTACTGGC
 51 TGTGGGACTG ATCTTTTTCG GGTGCTCTCG AGTAAAAAGA GAAGTTCTCG
101 TAGGTCGTGA TGCCACCTGG TTTCCAAAAC AATTCGGCAT TTATACATCC
151 GATACCAACG CATTTTTAAA CGATCTTGTT TCTGAGATTA ACTATAAAGA
201 GAATCTAAAT ATTAATATTG TAAATCAAGA TTGGGTGCAT CTCTTTGAGA
251 ATTTAGATGA TAAAAAGACC CAAGGAGCAT TTACATCTGT ATTGCCTACT
301 CTTGAGATGC TCGAACACTA TCAATTTTCT GATCCCATTT TACTCACAGG
351 TCCTGTCCTT GTCGTCGCTC AAGACTCTCC TTACCAATCT ATAGAGGATC
401 TTAAAGGTCG TCTTATTGGA GTGTATAAGT TTGACTCTTC AGTTCTTGTA
451 GCTCAAAATA TCCCTGACGC TGTGATTAGC CTCTACCAAC ATGTTCCAAT
501 AGCATTGGAA GCCTTAACAT CGAATTGTTA CGACGCTCTT CTAGCTCCTG
551 TAATTGAAGT GACCGCGCTA ATAGAAACAG CATATAAAGG AAGACTGAAA
601 ATTATTTCAA AACCCTTAAA CGCAGATGGT TTGCGGCTTG CAATACTGAA
```

```
651  AGGGACAAAC GGAGATTTGC TTGAAGGGTT TAACGCAGGA CTTGTGAAAA
701  CACGACGCTC AGGAAAATAC GATGCTATAA AACAGCGGTA TCGTCTTCCC
751  TAA
```

The PSORT algorithm predicts an inner membrane location (0.452).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 6A. The recombinant protein was used to immunise mice, whose sera were used for FACS analysis (Figure 6B). A his-tagged protein was also expressed.

The cp6900 protein was also identified in the 2D-PAGE experiment (Cpn0604).

These experiments show that cp6900 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 7

The following *C.pneumoniae* protein (PID 4377033) was expressed <SEQ ID 13; cp7033>:

```
  1  MVNPIGPGPI DETERTPPAD LSAQGLEASA ANKSAEAQRI AGAEAKPKES
 51  KTDSVERWSI LRSAVNALMS LADKLGIASS NSSSSTSRSA DVDSTTATAP
101  TPPPPTFDDY KTQAQTAYDT IFTSTSLADI QAALVSLQDA VTNIKDTAAT
151  DEETAIAAEW ETKNADAVKV GAQITELAKY ASDNQAILDS LGKLTSFDLL
201  QAALLQSVAN NNKAAELLKE MQDNPVVPGK TPAIAQSLVD QTDATATQIE
251  KDGNAIRDAY FAGQNASGAV ENAKSNNSIS NIDSAKAAIA TAKTQIAEAQ
301  KKFPDSPILQ EAEQMVIQAE KDLKNIKPAD GSDVPNPGTT VGGSKQQGSS
351  IGSIRVSMLL DDAENETASI LMSGFRQMIH MFNTENPDSQ AAQQELAAQA
401  RAAKAAGDDS AAAALADAQK ALEAALGKAG QQQGILNALG QIASAAVVSA
451  GVPPAAASSI GSSVKQLYKT SKSTGSDYKT QISAGYDAYK SINDAYGRAR
501  NDATRDVINN VSTPALTRSV PRARTEARGP EKTDQALARV ISGNSRTLGD
551  VYSQVSALQS VMQIIQSNPQ ANNEEIRQKL TSAVTKPPQF GYPYVQLSND
601  STQKFIAKLE SLFAEGSRTA AEIKALSFET NSLFIQQVLV NIGSLYSGYL
651  Q*
```

The cp7033 nucleotide sequence <SEQ ID 14> is:

```
   1  ATGGTTAATC CTATTGGTCC AGGTCCTATA GACGAAACAG AACGCACACC
  51  TCCCGCAGAT CTTTCTGCTC AAGGATTGGA GGCGAGTGCA GCAAATAAGA
 101  GTGCGGAAGC TCAAAGAATA GCAGGTGCGG AAGCTAAGCC TAAAGAATCT
 151  AAGACCGATT CTGTAGAGCG ATGGAGCATC TTGCGTTCTG CAGTGAATGC
 201  TCTCATGAGT CTGGCAGATA AGCTGGGTAT TGCTTCTAGT AACAGCTCGT
 251  CTTCTACTAG CAGATCTGCA GACGTGGACT CAACGACAGC GACCGCACCT
 301  ACGCCTCCTC CACCCACGTT TGATGATTAT AAGACTCAAG CGCAAACAGC
 351  TTACGATACT ATCTTTACCT CAACATCACT AGCTGACATA CAGGCTGCTT
 401  TGGTGAGCCT CCAGGATGCT GTCACTAATA TAAAGGATAC AGCGGCTACT
 451  GATGAGGAAA CCGCAATCGC TGCGGAGTGG GAAACTAAGA ATGCCGATGC
 501  AGTTAAAGTT GGCGCGCAAA TTACAGAATT AGCGAAATAT GCTTCGGATA
 551  ACCAAGCGAT TCTTGACTCT TTAGGTAAAC TGACTTCCTT CGACCTCTTA
 601  CAGGCTGCTC TTCTCCAATC TGTAGCAAAC AATAACAAAG CAGCTGAGCT
 651  TCTTAAAGAG ATGCAAGATA ACCCAGTAGT CCCAGGGAAA ACGCCTGCAA
 701  TTGCTCAATC TTTAGTTGAT CAGACAGATG CTACAGCGAC ACAGATAGAG
 751  AAAGATGGAA ATGCGATTAG GGATGCATAT TTTGCAGGAC AGAACGCTAG
 801  TGGAGCTGTA GAAAATGCTA AATCTAATAA CAGTATAAGC AACATAGATT
 851  CAGCTAAAGC AGCAATCGCT ACTGCTAAGA CACAAATAGC TGAAGCTCAG
 901  AAAAAGTTCC CCGACTCTCC AATTCTTCAA GAAGCGGAAC AAATGGTAAT
 951  ACAGGCTGAG AAAGATCTTA AAAATATCAA ACCTGCAGAT GGTTCTGATG
1001  TTCCAAATCC AGGAACTACA GTTGGAGGCT CCAAGCAACA AGGAAGTAGT
1051  ATTGGTAGTA TTCGTGTTTC CATGCTGTTA GATGATGCTG AAAATGAGAC
1101  CGCTTCCATT TTGATGTCTG GGTTTCGTCA GATGATTCAC ATGTTCAATA
1151  CGGAAAATCC TGATTCTCAA GCTGCCCAAC AGGAGCTCGC AGCACAAGCT
1201  AGAGCAGCGA AAGCCGCTGG AGATGACAGT GCTGCTGCAG CGCTGGCAGA
1251  TGCTCAGAAA GCTTTAGAAG CGGCTCTAGG TAAAGCTGGG CAACAACAGG
1301  GCATACTCAA TGCTTTAGGA CAGATCGCTT CTGCTGCTGT TGTGAGCGCA
1351  GGAGTTCCTC CCGCTGCAGC AAGTTCTATA GGGTCATCTG TAAAACAGCT
1401  TTACAAGACC TCAAAATCTA CAGGTTCTGA TTATAAAACA CAGATATCAG
```

```
1451  CAGGTTATGA TGCTTACAAA TCCATCAATG ATGCCTATGG TAGGGCACGA
1501  AATGATGCGA CTCGTGATGT GATAAACAAT GTAAGTACCC CCGCTCTCAC
1551  ACGATCCGTT CCTAGAGCAC GAACAGAAGC TCGAGGACCA GAAAAAACAG
1601  ATCAAGCCCT CGCTAGGGTG ATTTCTGGCA ATAGCAGAAC TCTTGGAGAT
1651  GTCTATAGTC AAGTTTCGGC ACTACAATCT GTAATGCAGA TCATCCAGTC
1701  GAATCCTCAA GCGAATAATG AGGAGATCAG ACAAAAGCTT ACATCGGCAG
1751  TGACAAAGCC TCCACAGTTT GGCTATCCTT ATGTGCAACT TTCTAATGAC
1801  TCTACACAGA AGTTCATAGC TAAATTAGAA AGTTTGTTTG CTGAAGGATC
1851  TAGGACAGCA GCTGAAATAA AAGCACTTTC CTTTGAAACG AACTCCTTGT
1901  TTATTCAGCA GGTGCTGGTC AATATCGGCT CTCTATATTC TGGTTATCTC
1951  CAATAA
```

The PSORT algorithm predicts a cytoplasmic location (0.272).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 7A. A his-tagged protein was also expressed. The recombinant proteins were used to immunise mice, whose sera were used for FACS (Figure 7B) and Western blot (7C) analyses.

The cp7033 protein was also identified in the 2D-PAGE experiment (Cpn0728) and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp7033 a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 8

The following *C.pneumoniae* protein (PID 6172321) was expressed <SEQ ID 15; cp0017>:

```
  1  MGIKGTGIIV WVDDATAKTK NATLTWTKTG YKPNPERQGP LVPNSLWGSF
 51  VDVRSIQSLM DRSTSSLSSS TNLWVSGIAD FLHEDQKGNQ RSYRHSSAGY
101  ALGGGFFTAS ENFFNFAFCQ LFGYDKDHLV AKNHTHVYAG AMSYRHLGES
151  KTLAKILSGN SDSLPFVFNA RFAYGHTDNN MTTKYTGYSP VKGSWGNDAF
201  GIECGGAIPV VASGRRSWVD THTPFLNLEM IYAHQNDFKE NGTEGRSFQS
251  EDLFNLAVPV GIKFEKFSDK STYDLSIAYV PDVIRNDPGC TTTLMVSGDS
301  WSTCGTSLSR QALLVRAGNH HAFASNFEVF SQFEVELRGS SRSYAIDLGG
351  RFGF*
```

The cp0017 nueleotide sequence <SEQ ID 16> is:

```
   1  ATGGGTATCA AGGGAACTGG AATAATTGTT TGGGTCGACG ATGCAACTGC
  51  AAAAACAAAA AATGCTACCT TAACTTGGAC TAAAACAGGA TACAAGCCGA
 101  ATCCAGAACG TCAGGGACCT TTGGTTCCTA ATAGCCTGTG GGGTTCTTTT
 151  GTCGATGTCC GCTCCATTCA GAGCCTCATG GACCGGAGCA CAAGTTCGTT
 201  ATCTTCGTCA ACAAATTTGT GGGTATCAGG AATCGCGGAC TTTTTGCATG
 251  AAGATCAGAA AGGAAACCAA CGTAGTTATC GTCATTCTAG CGCGGGTTAT
 301  GCATTAGGAG GAGGATTCTT CACGGCTTCT GAAAATTTCT TTAATTTTGC
 351  TTTTTGTCAG CTTTTTGGCT ACGACAAGGA CCATCTTGTG GCTAAGAACC
 401  ATACCCATGT ATATGCAGGG GCAATGAGTT ACCGACACCT CGGAGAGTCT
 451  AAGACCCTCG CTAAGATTTT GTCAGGAAAT TCTGACTCCC TACCTTTTGT
 501  CTTCAATGCT CGGTTTGCTT ATGGCCATAC CGACAATAAC ATGACCACAA
 551  AGTACACTGG CTATTCTCCT GTTAAGGGAA GCTGGGGAAA TGATGCCTTC
 601  GGTATAGAAT GTGGAGGAGC TATCCCGGTA GTTGCTTCAG GACGTCGGTC
 651  TTGGGTGGAT ACCCACACGC CATTTCTAAA CCTAGAGATG ATCTATGCAC
 701  ATCAGAATGA CTTTAAGGAA AACGGCACAG AAGGCCGTTC TTTCCAAAGT
 751  GAAGACCTCT TCAATCTAGC GGTTCCTGTA GGGATAAAAT TTGAGAAATT
 801  CTCCGATAAG TCTACGTATG ATCTCTCCAT AGCTTACGTT CCCGATGTGA
 851  TTCGTAATGA TCCAGGCTGC ACGACAACTC TTATGGTTTC TGGGGATTCT
 901  TGGTCGACAT GTGGTACAAG CTTGTCTAGA CAAGCTCTTC TTGTACGTGC
 951  TGGAAATCAT CATGCCTTTG CTTCAAACTT TGAAGTTTTC AGTCAGTTTG
1001  AAGTCGAGTT GCGAGGTTCT TCTCGTAGCT ATGCTATCGA TCTTGGAGGA
1051  AGATTCGGAT TTTAA
```

This sequence is frame-shifted with respect to cp0016.

The PSORT algorithm predicts a cytoplasmic location (0.075).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 8A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 8B) and for FACS analysis (Figure 8C). A his-tagged protein was also expressed.

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp0017 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 9

The following *C.pneumoniae* protein (PID 6172315) was expressed <SEQ ID 17; cp0014>:

```
  1  MKSSFPKFVF STFAIFPLSM IATETVLDSS ASFDGNKNGN FSVRESQEDA
 51  GTTYLFKGNV TLENIPGTGT AITKSCFNNT KGDLTFTGNG NSLLFQTVDA
101  GTVAGAAVNS SVVDKSTTFI GFSSLSFIAS PGSSITTGKG AVSCSTGSLS
151  LTKMSVCSSA KTFQRIMAVL SPQKLFH*
```

The cp0014 nucleotide sequence <SEQ ID 18> is:

```
  1  ATGAAGTCTT CTTTCCCCAA GTTTGTATTT TCTACATTTG CTATTTTCCC
 51  TTTGTCTATG ATTGCTACCG AGACAGTTTT GGATTCAAGT GCGAGTTTCG
101  ATGGGAATAA AAATGGTAAT TTTTCAGTTC GTGAGAGTCA GGAAGATGCT
151  GGAACTACCT ACCTATTTAA GGGAAATGTC ACTCTAGAAA ATATTCCTGG
201  AACAGGCACA GCAATCACAA AAAGCTGTTT TAACAACACT AAGGGCGATT
251  TGACTTTCAC AGGTAACGGG AACTCTCTAT TGTTCCAAAC GGTGGATGCA
301  GGGACTGTAG CAGGGGCTGC TGTTAACAGC AGCGTGGTAG ATAAATCTAC
351  CACGTTTATA GGGTTTTCTT CGCTATCTTT TATTGCGTCT CCTGGAAGTT
401  CGATAACTAC CGGCAAAGGA GCCGTTAGCT GCTCTACGGG TAGCTTGAGT
451  TTGACAAAAA TGTCAGTTTG CTCTTCAGCA AAAACTTTTC AACGGATAAT
501  GGCGGTGCTA TCACCGCAAA AACTCTTTCA TTAA
```

This protein is frame-shifted with respect to cp0015.

The PSORT algorithm predicts an inner membrane location (0.047).

The protein was expressed in *E.coli* and purified as a his-tag product, as shown in Figure 9A. A GST-fusion was also expressed. The recombinant proteins were used to immunise mice, whose sera were used in an immunoassay (Figure 9B) and for FACS analysis (Figure 9C).

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments suggest that cp0014 is a useful immunogen. These properties are not evident from the sequence alone.

Example 10

The following *C.pneumoniae* protein (PID 6172317) was expressed <SEQ ID 19; cp0015>:

```
  1  MSALFSENTS SKKGGAIQTS DALTITGNQG EVSFSDNTSS DSGAAIFTEA
 51  SVTISNNAKV SFIDNKVTGA SSSTTGDMSG GAICAYKTST DTKVTLTGNQ
101  MLLFSNNTST TAGGAIYVKK LELASGGLTL FSRNSVNGGT APKGGAIAIE
151  DSGELSLSAD SGDIVFLGNT VTSTTPGTNR SSIDLGTSAK MTALRSAAGR
```

```
201  AIYFYDPITT GSSTTVTDVL KVNETPADSA LQYTGNIIFT GEKLSETEAA
251  DSKNLTSKLL QPVTLSGGTL SLKHGVTLQT QAFTQQADSR LEMDVGTTLE
301  PADTSTINNL VINISSIDGA KKAKIETKAT SKNLTLSGTI TLLDPTGTFY
351  ENHSLRNPQS YDILELKASG TVTSTAVTPD PIMGEKFHYG YQGTWGPIVW
401  GTGASTTATF NWTKTGYIPN PERIGSLVPN SLWNAFIDIS SLHYLMETAN
451  EGLQGDRAFW CAGLSNFFHK DSTKTRRGFR HLSGGYVIGG NLHTCSDKIL
501  SAAFCQLFGR DRDYFVAKNQ GTVYGGTLYY QHNETYISLP CKLRPCSLSY
551  VPTEIPVLFS GNLSYTHTDN DLKTKYTTYP TVKGSWGNDS FALEFGGRAP
601  ICLDESALFE QYMPFMKLQF VYAHQEGFKE QGTEAREFGS SRLVNLALPI
651  GIRFDKESDC QDATYNLTLG YTVDLVRSNP DCTTTLRISG DSWKTFGTNL
701  ARQALVLRAG NHFCFNSNFE AFSQFSFELR GSSRNYNVDL GAKYQF*
```

This sequence is frame-shifted with respect to cp0014.

The cp0015 nucleotide sequence <SEQ ID 20> is:

```
   1  ATGTCAGCTC TGTTTTCTGA AAATACCTCC TCAAAGAAAG GCGGAGCCAT
  51  TCAGACTTCC GATGCCCTTA CCATTACTGG AAACCAAGGG GAAGTCTCTT
 101  TTTCTGACAA TACTTCTTCG GATTCTGGAG CTGCAATTTT TACAGAAGCC
 151  TCGGTGACTA TTTCTAATAA TGCTAAAGTT TCCTTTATTG ACAATAAGGT
 201  CACAGGAGCG AGCTCCTCAA CAACGGGGGA TATGTCAGGA GGTGCTATCT
 251  GTGCTTATAA AACTAGTACA GATACTAAGG TCACCCTCAC TGGAAATCAG
 301  ATGTTACTCT TCAGCAACAA TACATCGACA ACAGCGGGAG GAGCTATCTA
 351  TGTGAAAAAG CTCGAACTGG CTTCCGGAGG ACTTACCCTA TTCAGTAGAA
 401  ATAGTGTCAA TGGAGGTACA GCTCCTAAAG GTGGAGCCAT AGCTATCGAA
 451  GATAGTGGGG AATTGAGTTT ATCCGCCGAT AGTGGTGACA TTGTCTTTTT
 501  AGGGAATACA GTCACTTCTA CTACTCCTGG GACGAATAGA AGTAGTATCG
 551  ACTTAGGAAC GAGTGCAAAG ATGACAGCTT TGCGTTCTGC TGCTGGTAGA
 601  GCCATCTACT TCTATGATCC CATAACTACA GGATCATCCA CAACAGTTAC
 651  AGATGTCTTA AAAGTTAATG AGACTCCGGC AGATTCTGCA CTACAATATA
 701  CAGGGAACAT CATCTTCACA GGAGAAAAGT TATCAGAGAC AGAGGCCGCA
 751  GATTCTAAAA ATCTTACTTC GAAGCTACTA CAGCCTGTAA CTCTTTCAGG
 801  AGGTACTCTA TCTTTAAAAC ATGGAGTGAC TCTGCAGACT CAGGCATTCA
 851  CTCAACAGGC AGATTCTCGT CTCGAAATGG ACGTAGGAAC TACTCTAGAA
 901  CCTGCTGATA CTAGCACCAT AAACAATTTG GTCATTAACA TCAGTTCTAT
 951  AGACGGTGCA AAGAAGGCAA AAATAGAAAC CAAAGCTACG TCAAAAAATC
1001  TGACTTTATC TGGAACCATC ACTTTATTGG ACCCGACGGG CACGTTTTAT
1051  GAAAATCATA GTTTAAGAAA TCCTCAGTCC TACGACATCT TAGAGCTCAA
1101  AGCTTCTGGA ACTGTAACAA GCACCGCAGT GACTCCAGAT CCTATAATGG
1151  GTGAGAAATT CCATTACGGC TATCAGGGAA CTTGGGGCCC AATTGTTTGG
1201  GGGACAGGGG CTTCTACGAC TGCAACCTTC AACTGGACTA AAACTGGCTA
1251  TATTCCTAAT CCCGAGCGTA TCGGCTCTTT AGTCCCTAAT AGCTTATGGA
1301  ATGCATTTAT AGATATTAGC TCTCTCCATT ATCTTATGGA GACTGCAAAC
1351  GAAGGGTTGC AGGGAGACCG TGCTTTTTGG TGTGCTGGAT TATCTAACTT
1401  CTTCCATAAG GATAGTACAA AAACACGACG CGGGTTTCGC CATTTGAGTG
1451  GCGGTTATGT CATAGGAGGA AACCTACATA CTTGTTCAGA TAAGATTCTT
1501  AGTGCTGCAT TTTGTCAGCT CTTTGGAAGA GATAGAGACT ACTTTGTAGC
1551  TAAGAATCAA GGTACAGTCT ACGGAGGAAC TCTCTATTAC CAGCACAACG
1601  AAACCTATAT CTCTCTTCCT TGCAAACTAC GGCCTTGTTC GTTGTCTTAT
1651  GTTCCTACAG AGATTCCTGT TCTCTTTTCA GGAAACCTTA GCTACACCCA
1701  TACGGATAAC GATCTGAAAA CCAAGTATAC AACATATCCT ACTGTTAAAG
1751  GAAGCTGGGG GAATGATAGT TTCGCTTTAG AATTCGGTGG AAGAGCTCCG
1801  ATTTGCTTAG ATGAAAGTGC TCTATTTGAG CAGTACATGC CCTTCATGAA
1851  ATTGCAGTTT GTCTATGCAC ATCAGGAAGG TTTTAAAGAA CAGGGAACAG
1901  AAGCTCGTGA ATTTGGAAGT AGCCGTCTTG TGAATCTTGC CTTACCTATC
1951  GGGATCCGAT TTGATAAGGA ATCAGACTGC CAAGATGCAA CGTACAATCT
2001  AACTCTTGGT TATACTGTGG ATCTTGTTCG TAGTAACCCC GACTGTACGA
2051  CAACACTGCG AATTAGCGGT GATTCTTGGA AAACCTTCGG TACGAATTTG
2101  GCAAGACAAG CTTTAGTCCT TCGTGCAGGG AACCATTTTT GCTTTAACTC
2151  AAATTTTGAA GCCTTTAGCC AATTTTCTTT TGAATTGCGT GGGTCATCTC
2201  GCAATTACAA TGTAGACTTA GGAGCAAAAT ACCAATTCTA A
```

The PSORT algorithm predicts a cytoplasmic location (0.274).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 10A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 10B) and for FACS analysis. A his-tagged protein was also expressed.

These experiments show that cp0015 is a useful immunogen. These properties are not evident from the sequence alone.

Example 11

The following *C.pneumoniae* protein (PID 6172325) was expressed <SEQ ID 21; cp0019>:

```
  1 LQDSQDYSFV KLSPGAGGTI ITQDASQKPL EVAPSRPHYG YQGHWNVQVI
 51 PGTGTQPSQA NLEWVRTGYL PNPERQGSLV PNSLWGSFVD QRAIQEIMVN
101 SSQILCQERG VWGAGIANFL HRDKINEHGY RHSGVGYLVG VGTHAFSDAT
151 INAAFCQLFS RDKDYVVSKN HGTSYSGVVF LEDTLEFRSP QGFYTDSSSE
201 ACCNQVVTID MQLSYSHRNN DMKTKYTTYP EAQGSWANDV FGLEFGATTY
251 YYPNSTFLFD YYSPFLRLQC TYAHQEDFKE TGGEVRHFTS GDLFNLAVPI
301 GVKFERFSDC KRGSYELTLA YVPDVIRKDP KSTATLASGA TWSTHGNNLS
351 RQGLQLRLGN HCLINPGIEV FSHGAIELRG SSRNYNINLG GKYRF*
```

This sequence is frame-shifted with respect to cp0018.

The cp0019 nucleotide sequence <SEQ ID 22> is:

```
   1 TTGCAAGACT CTCAAGACTA TAGCTTTGTA AAGTTATCTC CAGGAGCGGG
  51 AGGGACTATA ATTACTCAAG ATGCTTCTCA GAAGCCTCTT GAAGTAGCTC
 101 CTTCTAGACC ACATTATGGC TATCAAGGAC ATTGGAATGT GCAAGTCATC
 151 CCAGGAACGG GAACTCAACC GAGCCAGGCA AATTTAGAAT GGGTGCGGAC
 201 AGGATACCTT CCGAATCCCG AACGGCAAGG ATCTTTAGTT CCCAATAGCC
 251 TGTGGGGTTC TTTTGTTGAT CAGCGTGCTA TCCAAGAAAT CATGGTAAAT
 301 AGTAGCCAAA TCTTATGTCA GGAACGGGGA GTCTGGGGAG CTGGAATTGC
 351 TAATTTCCTA CATAGAGATA AAATTAATGA GCACGGCTAT CGCCATAGCG
 401 GTGTCGGTTA TCTTGTGGGA GTTGGCACTC ATGCTTTTTC TGATGCTACG
 451 ATAAATGCGG CTTTTTGCCA GCTCTTCAGT AGAGATAAAG ACTACGTAGT
 501 ATCCAAAAAT CATGGAACTA GCTACTCAGG GGTCGTATTT CTTGAGGATA
 551 CCCTAGAGTT TAGAAGTCCA CAGGGATTCT ATACTGATAG CTCCTCAGAA
 601 GCTTGCTGTA ACCAAGTCGT CACTATAGAT ATGCAGTTGT CTTACAGCCA
 651 TAGAAATAAT GATATGAAAA CCAAATACAC GACATATCCA GAAGCTCAGG
 701 GATCTTGGGC AAATGATGTT TTTGGTCTTG AGTTTGGAGC GACTACATAC
 751 TACTACCCTA ACAGTACTTT TTTATTTGAT TACTACTCTC CGTTTCTCAG
 801 GCTGCAGTGC ACCTATGCTC ACCAGGAAGA CTTCAAAGAG ACAGGAGGTG
 851 AGGTTCGTCA CTTTACTAGC GGAGATCTTT TCAATTTAGC AGTTCCTATT
 901 GGCGTGAAGT TTGAGAGATT TTCAGACTGT AAAAGGGGAT CTTATGAACT
 951 TACCCTTGCT TATGTTCCTG ATGTGATTCG CAAAGATCCC AAGAGCACGG
1001 CAACATTGGC TAGTGGAGCT ACGTGGAGCA CCCACGGAAA CAATCTCTCC
1051 AGACAAGGAT TACAACTGCG TTTAGGGAAC CACTGTCTCA TAAATCCTGG
1101 AATTGAGGTG TTCAGTCACG GAGCTATTGA ATTGCGGGGA TCCTCTCGTA
1151 ATTATAACAT CAATCTCGGG GGTAAATACC GATTTTAA
```

The PSORT algorithm predicts a cytoplasmic location (0.189).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 11A. This protein was used to immunise mice, whose sera were used in a Western blot (Figure 11B) and an immunoblot assay (Figure 11C). A his-tagged protein was also expressed.

These experiments show that cp0019 is a useful immunogen. These properties are not evident from the sequence alone.

Example 12

The following *C.pneumoniae* protein (PID 4376466) was expressed <SEQ ID 23; cp6466>:

```
  1 MRKISVGICI TILLSLSVVL QGCKESSHSS TSRGELAINI RDEPRSLDPR
 51 QVRLLSEISL VKHIYEGLVQ ENNLSGNIEP ALAEDYSLSS DGLTYTFKLK
101 SAFWSNGDPL TAEDFIESWK QVATQEVSGI YAFALNPIKN VRKIQEGHLS
151 IDHFGVHSPN ESTLVVTLES PTSHFLKLLA LPVFFPVHKS QRTLQSKSLP
201 IASGAFYPKN IKQKQWIKLS KNPHYYNQSQ VETKTITIHF IPDANTAAKL
```

```
251  FNQGKLNWQG PPWGERIPQE TLSNLQSKGH LHSFDVAGTS WLTFNINKFP
301  LNNMKLREAL ASALDKEALV STIFLGRAKT ADHLLPTNIH SYPEHQKQEM
351  AQRQAYAKKL FKEALEELQI TAKDLEHLNL IFPVSSSASS LLVQLIREQW
401  KESLGFAIPI VGKEFALLQA DLSSGNFSLA TGGWFADFAD PMAFLTIFAY
451  PSGVPPYAIN HKDFLEILQN IEQEQDHQKR SELVSQASLY LETFHIIEPI
501  YHDAFQFAMN KKLSNLGVSP TGVVDFRYAK EN*
```

A predicted signal peptide is highlighted.

The cp6466 nucleotide sequence <SEQ ID 24> is:

```
   1  ATGCGCAAGA TATCAGTGGG AATCTGTATC ACCATTCTCC TTAGCCTCTC
  51  CGTAGTCCTC CAAGGCTGCA AGGAGTCCAG TCACTCCTCT ACATCTCGGG
 101  GAGAACTCGC TATTAATATA AGAGATGAAC CCCGTTCTTT AGATCCAAGA
 151  CAAGTGCGAC TTCTTTCAGA AATCAGCCTT GTCAAACATA TCTATGAGGG
 201  ATTAGTTCAA GAAAATAATC TTTCAGGAAA TATAGAGCCT GCTCTTGCAG
 251  AAGACTACTC TCTTTCCTCG GACGGACTCA CTTATACTTT TAAACTGAAA
 301  TCAGCTTTTT GGAGTAATGG CGACCCCTTA ACAGCTGAAG ACTTTATAGA
 351  ATCTTGGAAA CAAGTAGCTA CTCAAGAAGT CTCAGGAATC TATGCTTTTG
 401  CCTTGAATCC AATTAAAAAT GTACGAAAGA TCCAAGAGGG ACACCTCTCC
 451  ATAGACCATT TTGGAGTGCA CTCTCCTAAT GAATCTACAC TTGTTGTTAC
 501  CCTGGAATCC CCAACCTCGC ATTTCTTAAA ACTTTTAGCT CTTCCAGTCT
 551  TTTTCCCCGT TCATAAATCT CAAAGAACCC TGCAATCCAA ATCTCTACCT
 601  ATAGCAAGCG GAGCTTTCTA TCCTAAAAAT ATCAAACAAA AACAATGGAT
 651  AAAACTCTCA AAAAACCCTC ACTACTATAA TCAAAGTCAG GTGGAAACTA
 701  AAACGATTAC GATTCACTTC ATTCCCGATG CAAACACAGC AGCAAAACTA
 751  TTTAATCAGG GAAAACTCAA TTGGCAAGGA CCTCCTTGGG GAGAACGCAT
 801  TCCTCAAGAA ACCCTATCCA ATTTACAGTC TAAGGGGCAC TTACACTCTT
 851  TTGATGTCGC AGGAACCTCA TGGCTCACCT TCAATATCAA TAAATTCCCC
 901  CTCAACAATA TGAAGCTTAG AGAAGCCTTA GCATCAGCCT TAGATAAGGA
 951  AGCTCTTGTC TCAACTATAT TCTTAGGCCG TGCAAAAACT GCCGATCATC
1001  TCCTACCTAC AAATATTCAT AGCTATCCCG AACATCAAAA ACAAGAGATG
1051  GCACAACGCC AAGCTTACGC TAAAAAACTC TTTAAAGAAG CTTTAGAAGA
1101  ACTCCAAATC ACTGCTAAAG ATCTCGAACA TCTTAATCTT ATCTTTCCCG
1151  TTTCCTCGTC AGCAAGTTCT TTACTAGTCC AACTTATACG AGAACAGTGG
1201  AAAGAAAGTT TAGGGTTCGC TATCCCTATT GTCGGAAAGG AATTTGCTCT
1251  TCTCCAAGCA GACCTATCTT CAGGGAACTT CTCTTTAGCT ACAGGAGGAT
1301  GGTTCGCAGA CTTTGCTGAT CCTATGGCAT TTCTAACGAT CTTTGCTTAT
1351  CCATCAGGAG TTCCTCCTTA TGCAATCAAC CATAAGGACT TCCTAGAAAT
1401  TCTACAAAAC ATAGAACAAG AGCAAGATCA CCAAAAACGC TCGGAATTAG
1451  TGTCGCAAGC TTCTCTTTAC CTAGAGACCT TTCATATTAT TGAGCCGATC
1501  TACCACGACG CATTTCAATT TGCTATGAAT AAAAAACTTT CTAATCTAGG
1551  AGTCTCACCA ACAGGAGTTG TGGACTTCCG TTATGCTAAG GAAAATTAG
```

The PSORT algorithm predicts that the protein is an outer membrane lipoprotein (0.790).

The protein was expressed in *E.coli* and purified both as a GST-fusion product and a His-tag fusion product. Purification of the protein as a GST-fusion product is shown in Figure 12A. The recombinant proteins were used to immunise mice, whose sera were used in Western blots (Figures 12B and 12C). FACS analysis was also performed.

These experiments show that cp6466 is a useful immunogen. These properties are not evident from the sequence alone.

Example 13

The following *C.pneumoniae* protein (PID 4376468) was expressed <SEQ ID 25; cp6468>:

```
  1  MFSRWITLFL LFISLTGCSS YSSKHKQSLI IPIHDDPVAF SPEQAKRAMD
 51  LSIAQLLFDG LTRETHRESN DLELAIASRY TVSEDFCSYT FFIKDSALWS
101  DGTPITSEDI RNAWEYAQEN SPHIQIFQGL NFSTPSSNAI TIHLDSPNPD
151  FPKLLAFPAF AIFKPENPKL FSGPYTLVEY FPGHNIHLKK NPNYYDYHCV
201  SINSIKLLII PDIYTAIHLL NRGKVDWVGQ PWHQGIPWEL HKQSQYHYYT
251  YPVEGAFWLC LNTKSPHLND LQNRHRLATC IDKRSIIEEA LQGTQQPAET
```

```
301  LSRGAPQPNQ YKKQKPLTPQ EKLVLTYPSD ILRCQRIAEI LKEQWKAAGI
351  DLILEGLEYH LFVNKRKVQD YAIATQTGVA YYPGANLISE EDKLLQNFEI
401  IPIYYLSYDY LTQDFIEGVI YNASGAVDLK YTYFP*
```

A predicted signal peptide is highlighted.

The cp6468 nucleotide sequence <SEQ ID 26> is:

```
   1  ATGTTTTCAC GATGGATCAC CCTCTTTTTA TTATTCATTA GCCTTACTGG
  51  ATGCTCCTCC TACTCTTCAA AACATAAACA ATCTTTAATT ATTCCCATAC
 101  ATGACGACCC TGTAGCTTTT TCTCCTGAAC AAGCAAAACG GGCCATGGAC
 151  CTTTCTATTG CCCAACTTCT TTTTGATGGT CTGACTAGAG AAACTCATCG
 201  CGAATCCAAT GATTTGGAAT TAGCGATTGC CAGTCGCTAT ACAGTCTCTG
 251  AAGACTTTTG CTCTTATACG TTCTTTATCA AAGACAGCGC TTTATGGAGC
 301  GACGGAACAC CAATCACCTC CGAAGATATC CGTAACGCTT GGGAGTATGC
 351  ACAGGAGAAC TCTCCCCACA TACAGATCTT CCAAGGACTT AACTTCTCAA
 401  CTCCTTCATC AAATGCAATT ACGATTCATC TCGACTCGCC CAACCCCGAT
 451  TTTCCTAAGC TTCTTGCCTT TCCTGCATTT GCTATCTTTA AACCAGAAAA
 501  CCCGAAGCTC TTTAGCGGTC CGTATACTCT TGTAGAGTAT TTCCCAGGGC
 551  ATAACATTCA TTTAAAGAAA AACCCTAACT ATTACGACTA CCACTGCGTC
 601  TCCATCAACT CCATCAAACT GCTCATTATT CCTGATATAT ATACAGCCAT
 651  CCACCTCCTA AACAGAGGCA AGGTGGACTG GGTAGGACAA CCCTGGCATC
 701  AAGGGATTCC TTGGGAGCTC CATAAACAAT CGCAATATCA CTACTACACC
 751  TATCCTGTAG AAGGTGCCTT CTGGCTTTGT CTAAATACAA AATCCCCACA
 801  CTTAAATGAT CTTCAAAACA GACATAGACT CGCTACTTGT ATTGATAAAC
 851  GTTCTATCAT TGAAGAAGCT CTTCAAGGAA CCCAACAACC AGCGGAAACA
 901  CTGTCCCGAG GAGCTCCACA ACCAAATCAA TATAAAAAAC AAAAGCCTCT
 951  AACTCCACAA GAAAAACTCG TGCTTACCTA TCCCTCAGAT ATTCTAAGAT
1001  GCCAACGCAT AGCAGAAATC TTAAAGGAAC AATGGAAAGC TGCTGGAATA
1051  GATTTAATCC TTGAAGGACT CGAATACCAT CTGTTTGTTA ACAAACGAAA
1101  AGTCCAAGAC TACGCCATAG CAACACAGAC TGGAGTTGCT TATTACCCAG
1151  GAGCAAATCT AATTTCTGAA GAAGACAAGC TCCTGCAAAA CTTTGAGATT
1201  ATCCCGATCT ACTATCTGAG CTATGACTAT CTCACTCAAG ATTTTATAGA
1251  GGGAGTAATC TATAATGCTT CTGGAGCTGT AGATCTCAAA TATACCTATT
1301  TCCCCTAG
```

The PSORT algorithm predicts that this protein is an outer membrane lipoprotein (0.790).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 13A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 13B) and for FACS analysis. A his-tagged protein was also expressed.

These experiments show that cp6468 is a useful immunogen. These properties are not evident from the sequence alone.

Example 14

The following *C.pneumoniae* protein (PID 4376469) was expressed <SEQ ID 27; cp6469>:

```
  1  MKMHRLKPTL KSLIPNLLFL LLTLSSCSKQ KQEPLGKHLV IAMSHDLADL
 51  DPRNAYLSRD ASLAKALYEG LTRETDQGIA LALAESYTLS KDHKVYTFKL
101  RPSVWSDGTP LTAYDFEKSI KQLYFEEFSP SIHTLLGVIK NSSAIHNAQK
151  SLETLGIQAK DDLTLVITLE QPFPYFLTLI ARPVFSPVHH TLRESYKKGT
201  PPSTYISNGP FVLKKHEHQN YLILEKNPHY YDHESVKLDR VTLKIIPDAS
251  TATKLFKSKS IDWIGSPWSA PISNEDQKVL SQEKILTYSV SSTTLLIYNL
301  QKPLIQNKAL RKAIAHAIDR KSILRLVPSG QEAVTLVPPN LSQLNLQKEI
351  STEERQTKAR AYFQEAKETL SEKELAELSI LYPIDSSNSS IIAQEIQRQL
401  KDTLGLKIKI QGMEYHCFLK KRRQGDFFIA TGGWIAEYVS PVAFLSILGN
451  PRDLTQWRNS DYEKTLEKLY LPHAYKENLK RAEMIIEEET PIIPLYHGKY
501  IYAIHPKIQN TFGSLLGHTD LKNIDILS*
```

A predicted signal peptide is highlighted.

The cp6469 nucleotide sequence <SEQ ID 28> is:

```
   1  ATGAAGATGC ATAGGCTTAA ACCTACCTTA AAAAGTCTGA TCCCTAATCT
  51  TCTTTTCTTA TTGCTCACTC TTTCAAGCTG CTCAAAGCAA AAACAAGAAC
 101  CCTTAGGAAA ACATCTCGTT ATTGCGATGA GCCATGATCT CGCCGACCTA
 151  GATCCTCGCA ATGCCTATTT AAGCAGAGAT GCTTCCCTAG CAAAAGCCCT
 201  CTATGAAGGA CTGACAAGAG AAACTGATCA AGGAATCGCA CTGGCTCTTG
 251  CAGAAAGTTA TACCCTGTCA AAAGATCATA AGGTCTATAC CTTTAAACTC
 301  AGACCTTCTG TGTGGAGCGA TGGCACTCCA CTCACTGCTT ATGACTTTGA
 351  AAAATCTATA AAACAACTGT ACTTCGAAGA ATTTTCACCT TCCATACATA
 401  CTTTACTCGG CGTGATTAAA AATTCTTCGG CAATCCACAA TGCTCAAAAA
 451  TCTCTGGAAA CTCTTGGGAT ACAGGCAAAA GATGATCTTA CTTTGGTGAT
 501  TACCCTAGAG CAACCTTTCC CATACTTTCT CACACTTATC GCTCGCCCCG
 551  TATTCTCCCC TGTTCATCAC ACCCTTAGGG AATCCTATAA GAAAGGAACA
 601  CCCCCATCCA CATACATCTC CAATGGGCCC TTTGTCTTAA AAAAACATGA
 651  ACACCAAAAC TACTTAATTT TAGAAAAAAA TCCTCACTAC TATGATCATG
 701  AATCAGTAAA GTTAGACCGA GTCACCTTAA AAATTATCCC AGACGCCTCC
 751  ACAGCCACGA AACTTTTCAA AAGTAAATCT ATAGATTGGA TTGGCTCACC
 801  TTGGAGCGCT CCGATATCTA ACGAAGACCA AAAAGTTCTC TCCCAAGAAA
 851  AGATTCTTAC CTATTCTGTT TCAAGCACCA CCCTTCTTAT CTATAACCTG
 901  CAAAAACCTC TAATACAAAA TAAAGCCCTC AGGAAAGCCA TTGCTCATGC
 951  TATTGATAGA AAATCTATCT TAAGACTCGT GCCTTCAGGA CAAGAAGCTG
1001  TAACTCTAGT TCCCCCAAAT CTTTCACAAC TCAATCTTCA AAAAGAGATC
1051  TCAACAGAAG AACGACAAAC AAAAGCCAGA GCATATTTTC AAGAAGCTAA
1101  AGAAACACTT TCTGAAAAAG AACTCGCAGA ACTCAGCATC CTCTATCCTA
1151  TAGATTCCTC GAATTCCTCC ATCATAGCTC AAGAAATCCA AAGACAACTT
1201  AAAGATACCT TAGGATTGAA AATCAAAATC CAAGGCATGG AGTACCACTG
1251  CTTTTTAAAG AAACGTCGTC AAGGAGATTT CTTCATAGCG ACAGGAGGAT
1301  GGATTGCGGA ATACGTAAGC CCCGTAGCCT TCCTATCTAT TCTAGGCAAC
1351  CCCAGAGACC TCACACAATG GAGAAACAGT GATTACGAAA AGACTTTAGA
1401  GAAACTCTAT CTCCCTCATG CCTACAAAGA GAATTTAAAA CGCGCAGAAA
1451  TGATAATAGA AGAAGAAACC CCGATTATCC CCCTGTATCA CGGCAAATAT
1501  ATTTACGCTA TACATCCTAA AATCCAGAAT ACATTCGGAT CTCTTCTAGG
1551  CCACACAGAT CTCAAAAATA TCGATATCTT AAGTTAG
```

The PSORT algorithm predicts a periplasmic location (0.934).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 14A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 14B) and for FACS analysis. A his-tagged protein was also expressed.

These experiments show that cp6469 is a useful immunogen. These properties are not evident from the sequence alone.

Example 15

The following *C.pneumoniae* protein (PID 4376602) was expressed <SEQ ID 29; cp6602>:

```
   1  MAASGGTGGL GGTQGVNLAA VEAAAAKADA AEVVASQEGS EMNMIQQSQD
  51  LTNPAAATRT KKKEEKFQTL ESRKKGEAGK AEKKSESTEE KPDTDLADKY
 101  ASGNSEISGQ ELRGLRDAIG DDASPEDILA LVQEKIKDPA LQSTALDYLV
 151  QTTPPSQGKL KEALIQARNT HTEQFGRTAI GAKNILFASQ EYADQLNVSP
 201  SGLRSLYLEV TGDTHTCDQL LSMLQDRYTY QDMAIVSSFL MKGMATELKR
 251  QGPYVPSAQL QVLMTETRNL QAVLTSYDYF ESRVPILLDS LKAEGIQTPS
 301  DLNFVKVAES YHKIINDKFP TASKVEREVR NLIGDDVDSV TGVLNLFFSA
 351  LRQTSSRLFS SADKRQQLGA MIANALDAVN INNEDYPKAS DFPKPYPWS*
```

The cp6602 nucleotide sequence <SEQ ID 30> is:

```
   1  ATGGCAGCAT CAGGAGGCAC AGGTGGTTTA GGAGGCACTC AGGGTGTCAA
  51  CCTTGCAGCT GTAGAAGCTG CAGCTGCAAA AGCAGATGCA GCAGAAGTTG
 101  TAGCCAGCCA AGAAGGTTCT GAGATGAACA TGATTCAACA ATCTCAGGAC
 151  CTGACAAATC CCGCAGCAGC AACACGCACG AAAAAAAAGG AAGAGAAGTT
 201  TCAAACTCTA GAATCTCGGA AAAAAGGAGA AGCTGGAAAG GCTGAGAAAA
 251  AATCTGAATC TACAGAAGAG AAGCCTGACA CAGATCTTGC TGATAAGTAT
 301  GCTTCTGGGA ATTCTGAAAT CTCTGGTCAA GAACTTCGCG GCCTGCGTGA
 351  TGCAATAGGA GACGATGCTT CTCCAGAAGA CATTCTTGCT CTTGTACAAG
```

401 AGAAAATTAA AGACCCAGCT CTGCAATCCA CAGCTTTGGA CTACCTGGTT
451 CAAACGACTC CACCCTCCCA AGGTAAATTA AAAGAAGCGC TTATCCAAGC
501 AAGGAATACT CATACGGAGC AATTCGGACG AACTGCTATT GGTGCGAAAA
551 ACATCTTATT TGCCTCTCAA GAATATGCAG ACCAACTGAA TGTTTCTCCT
601 TCAGGGCTTC GCTCTTTGTA CTTAGAAGTG ACTGGAGACA CACATACCTG
651 TGATCAGCTA CTTTCTATGC TTCAAGACCG CTATACCTAC CAAGATATGG
701 CTATTGTCAG CTCCTTTCTA ATGAAAGGAA TGGCAACAGA ATTAAAAAGG
751 CAGGGTCCCT ACGTACCCAG TGCGCAACTA CAAGTTCTCA TGACAGAAAC
801 TCGTAACCTG CAAGCAGTTC TTACCTCGTA CGATTACTTT GAAAGTCGCG
851 TTCCTATTTT ACTCGATAGC TTAAAAGCTG AGGGAATCCA AACTCCTTCT
901 GATCTAAACT TTGTGAAGGT AGCTGAGTCC TACCATAAAA TCATTAACGA
951 TAAGTTCCCA ACAGCATCTA AAGTAGAACG AGAAGTCCGC AATCTCATAG
1001 GAGACGATGT TGATTCTGTG ACCGGTGTCT TGAACTTATT CTTTTCTGCT
1051 TTACGTCAAA CGTCGTCACG CCTTTTCTCT TCAGCAGACA AACGTCAGCA
1101 ATTAGGAGCT ATGATTGCTA ATGCTTTAGA TGCTGTAAAT ATAAACAATG
1151 AAGATTATCC CAAAGCATCA GACTTCCCTA AACCCTATCC TTGGTCATGA

The PSORT algorithm predicts a cytoplasmic location (0.080).

The protein was expressed in *E.coli* and purified as both a His-tag and a GST-fusion product, as shown in Figure 15A. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 15B) and for FACS analysis (Figure 15C).

The cp6602 protein was also identified in the 2D-PAGE experiment (Cpn0324).

These experiments show that cp6602 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 16

The following *C.pneumoniae* protein (PID 4376727) was expressed <SEQ ID 31; cp6727>:

1 **MKYSLPWLLT SSALVF**SLHP LMAANTDLSS SDNYENGSSG SAAFTAKETS
51 DASGTTYTLT SDVSITNVSA ITPADKSCFT NTGGALSFVG ADHSLVLQTI
101 ALTHDGAAIN NTNTALSFSG FSSLLIDSAP ATGTSGGKGA ICVTNTEGGT
151 ATFTDNASVT LQKNTSEKDG AAVSAYSIDL AKTTTAALLD QNTSTKNGGA
201 LCSTANTTVQ GNSGTVTFSS NTATDKGGGI YSKEKDSTLD ANTGVVTFKS
251 NTAKTGGAWS SDDNLALTGN TQVLFQENKT TGSAAQANNP EGCGGAICCY
301 LATATDKTGL AISQNQEMSF TSNTTTANGG AIYATKCTLD GNTTLTFDQN
351 TATAGCGGAI YTETEDFSLK GSTGTVTFST NTAKTGGALY SKGNSSLTGN
401 TNLLFSGNKA TGPSNSSANQ EGCGGAILAF IDSGSVSDKT GLSIANNQEV
451 SLTSNAATVS GGAIYATKCT LTGNGSLTFD GNTAGTSGGA IYTETEDFTL
501 TGSTGTVTFS TNTAKTGGAL YSKGNNSLSG NTNLLFSGNK ATGPSNSSAN
551 QEGCGGAILS FLESASVSTK KGLWIEDNEN VSLSGNTATV SGGAIYATKC
601 ALHGNTTLTF DGNTAETAGG AIYTETEDFT LTGSTGTVTF STNTAKTAGA
651 LHTKGNTSFT KNKALVFSGN SATATATTTT DQEGCGGAIL CNISESDIAT
701 KSLTLTENES LSFINNTAKR SGGGIYAPKC VISGSESINF DGNTAETSGG
751 AIYSKNLSIT ANGPVSFTNN SGGKGGAIYI ADSGELSLEA IDGDITFSGN
801 RATEGTSTPN SIHLGAGAKI TKLAAAPGHT IYFYDPITME APASGGTIEE
851 LVINPVVKAI VPPPQPKNGP IASVPVVPVA PANPNTGTIV FSSGKLPSQD
901 ASIPANTTTI LNQKINLAGG NVVLKEGATL QVYSFTQQPD STVFMDAGTT
951 LETTTTNNTD GSIDLKNLSV NLDALDGKRM ITIAVNSTSG GLKISGDLKF
1001 HNNEGSFYDN PGLKANLNLP FLDLSSTSGT VNLDDFNPIP SSMAAPDYGY
1051 QGSWTLVPKV GAGGKVTLVA EWQALGYTPK PELRATLVPN SLWNAYVNIH
1101 SIQQEIATAM SDAPSHPGIW IGGIGNAFHQ DKQKENAGFR LISRGYIVGG
1151 SMTTPQEYTF AVAFSQLFGK SKDYVVSDIK SQVYAGSLCA QSSYVIPLHS
1201 SLRRHVLSKV LPELPGETPL VLHGQVSYGR NHHNMTTKLA NNTQGKSDWD
1251 SHSFAVEVGG SLPVDLNYRY LTSYSPYVKL QVVSVNQKGF QEVAADPRIF
1301 DASHLVNVSI PMGLTFKHES AKPPSALLLT LGYAVDAYRD HPHCLTSLTN
1351 GTSWSTFATN LSRQAFFAEA SGHLKLLHGL DCFASGSCEL RSSSRSYNAN
1401 CGTRYSF*

A predicted signal peptide is highlighted.

The cp6727 nucleotide sequence <SEQ ID 32> is:

```
   1 ATGAAATATT CTTTACCTTG GCTACTTACC TCTTCGGCTT TAGTTTTCTC
  51 CCTACATCCA CTAATGGCTG CTAACACGGA TCTCTCATCA TCCGATAACT
 101 ATGAAAATGG TAGTAGTGGT AGCGCAGCAT TCACTGCCAA GGAAACTTCG
 151 GATGCTTCAG GAACTACCTA CACTCTCACT AGCGATGTTT CTATTACGAA
 201 TGTATCTGCA ATTACTCCTG CAGATAAAAG CTGTTTTACA AACACAGGAG
 251 GAGCATTGAG TTTTGTTGGA GCTGATCACT CATTGGTTCT GCAAACCATA
 301 GCGCTTACGC ATGATGGTGC TGCAATTAAC AATACCAACA CAGCTCTTTC
 351 TTTCTCAGGA TTCTCGTCAC TCTTAATCGA CTCAGCTCCA GCAACAGGAA
 401 CTTCGGGCGG CAAGGGTGCT ATTTGTGTGA CAAATACAGA GGGAGGTACT
 451 GCGACTTTTA CTGACAATGC CAGTGTCACC CTCCAAAAAA ATACTTCAGA
 501 AAAAGATGGA GCTGCAGTTT CTGCCTACAG CATCGATCTT GCTAAGACTA
 551 CGACAGCAGC TCTCTTAGAT CAAAATACTA GCACAAAAAA TGGCGGGGCC
 601 CTCTGTAGTA CAGCAAACAC TACAGTCCAA GGAAACTCAG GAACGGTGAC
 651 CTTCTCCTCA AATACTGCTA CAGATAAAGG TGGGGGGATC TACTCAAAAG
 701 AAAAGGATAG CACGCTAGAT GCCAATACAG GAGTCGTTAC CTTCAAATCT
 751 AATACTGCAA AGACGGGGGG TGCTTGGAGC TCTGATGACA ATCTTGCTCT
 801 TACCGGCAAC ACTCAAGTAC TTTTTCAGGA AAATAAAACA ACCGGCTCAG
 851 CAGCACAGGC AAATAACCCG GAAGGTTGTG GTGGGGCAAT CTGTTGTTAT
 901 CTTGCTACAG CAACAGACAA AACTGGATTA GCCATTTCTC AGAATCAAGA
 951 AATGAGCTTC ACTAGTAATA CAACAACTGC GAATGGTGGA GCGATCTACG
1001 CTACTAAATG TACTCTGGAT GGAAACACAA CTCTTACCTT CGATCAGAAT
1051 ACTGCGACAG CAGGATGTGG CGGAGCTATC TATACAGAAA CTGAAGATTT
1101 TTCTCTTAAG GGAAGTACGG GAACCGTGAC CTTCAGCACA AATACAGCAA
1151 AGACAGGCGG CGCCTTATAT TCTAAAGGAA ACAGCTCGCT GACTGGAAAT
1201 ACCAACCTGC TCTTTTCAGG GAACAAAGCT ACGGGCCCGA GTAATTCTTC
1251 AGCAAATCAA GAGGGTTGCG GTGGGGCAAT CCTAGCCTTT ATTGATTCAG
1301 GATCCGTAAG CGATAAAACA GGACTATCGA TTGCAAACAA CCAAGAAGTC
1351 AGCCTCACTA GTAATGCTGC AACAGTAAGT GGTGGTGCGA TCTATGCTAC
1401 CAAATGTACT CTAACTGGAA ACGGCTCCCT GACCTTTGAC GGCAATACTG
1451 CTGGAACTTC AGGAGGGGCG ATCTATACAG AAACTGAAGA TTTTACTCTT
1501 ACAGGAAGTA CAGGAACCGT GACCTTCAGC ACAAATACAG CAAAGACAGG
1551 CGGCGCCTTA TATTCTAAAG GCAACAACTC TCTGTCTGGT AATACCAACC
1601 TGCTCTTTTC AGGGAACAAA GCTACGGGCC CGAGTAATTC TTCAGCAAAT
1651 CAAGAGGGTT GCGGTGGGGC AATCCTATCG TTTCTTGAGT CAGCATCTGT
1701 AAGTACTAAA AAAGGACTCT GGATTGAAGA TAACGAAAAC GTGAGTCTCT
1751 CTGGTAATAC TGCAACAGTA AGTGGCGGTG CGATCTATGC GACCAAGTGT
1801 GCTCTGCATG GAAACACGAC TCTTACCTTT GATGGCAATA CTGCCGAAAC
1851 TGCAGGAGGA GCGATCTATA CAGAAACCGA AGATTTTACT CTTACGGGAA
1901 GTACGGGAAC CGTGACCTTC AGCACAAATA CAGCAAAGAC AGCAGGGGCT
1951 CTACATACTA AAGGAAATAC TTCCTTTACC AAAAATAAGG CTCTTGTATT
2001 TTCTGGAAAT TCAGCAACAG CAACAGCAAC AACAACTACA GATCAAGAAG
2051 GTTGTGGTGG AGCGATCCTC TGTAATATCT CAGAGTCTGA CATAGCTACA
2101 AAAAGCTTAA CTCTTACTGA AAATGAGAGT TTAAGTTTCA TTAACAATAC
2151 GGCAAAAAGA AGTGGTGGTG GTATTTATGC TCCTAAGTGT GTAATCTCAG
2201 GCAGTGAATC CATAAACTTT GATGGCAATA CTGCTGAAAC TTCGGGAGGA
2251 GCGATTTATT CGAAAAACCT TTCGATTACA GCTAACGGTC CTGTCTCCTT
2301 TACCAATAAT TCTGGAGGCA AGGGAGGCGC CATTTATATA GCCGATAGCG
2351 GAGAACTTTC CTTAGAGGCT ATTGATGGGG ATATTACTTT CTCAGGGAAC
2401 CGAGCGACTG AGGGAACTTC AACTCCCAAC TCGATCCATT TAGGTGCAGG
2451 GGCTAAGATC ACTAAGCTTG CAGCAGCTCC TGGTCATACG ATTTATTTTT
2501 ATGATCCTAT TACGATGGAA GCTCCTGCAT CTGGAGGAAC AATAGAGGAG
2551 TTAGTCATCA ATCCTGTTGT CAAAGCTATT GTTCCTCCTC CCCAACCAAA
2601 AAATGGTCCT ATAGCTTCAG TGCCTGTAGT CCCTGTAGCA CCTGCAAACC
2651 CAAACACGGG AACTATAGTA TTTTCTTCTG GAAAACTCCC CAGTCAAGAT
2701 GCCTCGATTC CTGCAAATAC TACCACCATA CTGAACCAGA AGATCAACTT
2751 AGCAGGAGGA AATGTCGTTT TAAAAGAAGG AGCCACCCTA CAAGTATATT
2801 CCTTCACACA GCAGCCTGAT TCTACAGTAT TCATGGATGC AGGAACGACC
2851 TTAGAGACCA CGACAACTAA CAATACAGAT GGCAGCATCG ATCTAAAGAA
2901 TCTCTCTGTA AATCTGGATG CTTTAGATGG CAAGCGTATG ATAACGATTG
2951 CCGTAAACAG CACAAGTGGG GGATTAAAAA TCTCAGGGGA TCTGAAATTC
3001 CATAACAATG AAGGAAGTTT CTATGACAAT CCTGGGTTGA AAGCAAACTT
3051 AAATCTTCCT TTCTTAGATC TTTCTTCTAC TTCAGGAACT GTAAATTTAG
3101 ACGACTTCAA TCCGATTCCT TCTAGCATGG CTGCTCCGGA TTATGGGTAT
3151 CAAGGGAGTT GGACTCTGGT TCCTAAAGTA GGAGCTGGAG GGAAGGTGAC
3201 TTTGGTCGCG GAATGGCAAG CGTTAGGATA CACTCCTAAA CCAGAGCTTC
3251 GTGCGACTTT AGTTCCTAAT AGCCTTTGGA ATGCTTATGT AAACATCCAT
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3301  TCTATACAGC AGGAGATCGC CACTGCGATG TCGGACGCTC CCTCACATCC
3351  AGGGATTTGG ATTGGAGGTA TTGGCAACGC CTTCCATCAA GACAAGCAAA
3401  AGGAAAATGC AGGATTCCGT TTGATTTCCA GAGGTTATAT TGTTGGTGGC
3451  AGCATGACCA CCCCTCAAGA ATATACCTTT GCTGTTGCAT TCAGCCAACT
3501  CTTTGGCAAA TCTAAGGATT ACGTAGTCTC GGATATTAAA TCTCAAGTCT
3551  ATGCAGGATC TCTCTGTGCT CAGAGCTCTT ATGTCATTCC CCTGCATAGC
3601  TCATTACGTC GCCACGTCCT CTCTAAGGTC CTTCCAGAGC TCCCAGGAGA
3651  AACTCCCCTT GTTCTCCATG GTCAAGTTTC CTATGGAAGA AACCACCATA
3701  ATATGACGAC AAAGCTTGCG AACAACACAC AAGGGAAATC AGACTGGGAC
3751  AGCCATAGCT TCGCTGTTGA AGTCGGTGGT TCTCTTCCTG TAGATCTAAA
3801  CTACAGATAC CTTACCAGCT ACTCTCCCTA TGTGAAACTC CAAGTTGTGA
3851  GTGTAAATCA AAAAGGATTC CAAGAGGTTG CTGCTGATCC ACGTATCTTT
3901  GACGCTAGCC ATCTGGTCAA CGTGTCTATC CCTATGGGAC TCACCTTCAA
3951  ACACGAATCA GCAAAGCCCC CCAGTGCTTT GCTTCTTACT TTAGGTTACG
4001  CTGTAGATGC TTACCGGGAT CACCCTCACT GCCTGACCTC CTTAACAAAT
4051  GGCACCTCGT GGTCTACGTT TGCTACAAAC TTATCACGAC AAGCTTTCTT
4101  TGCTGAGGCT TCTGGACATC TGAAGTTACT TCATGGTCTT GACTGCTTCG
4151  CTTCTGGAAG TTGTGAACTG CGCAGCTCCT CAAGAAGCTA TAATGCAAAC
4201  TGTGGAACTC GTTATTCTTT CTAA
```

The PSORT algorithm predicts an outer membrane location (0.915).

The protein was expressed in *E.coli* and purified as a his-tag product, as shown in Figure 16A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 16B) and for FACS analysis (Figure 16C). A GST-fusion protein was also expressed.

The cp6727 protein was also identified in the 2D-PAGE experiment (Cpn0444).

These experiments show that cp6727 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 17

The following *C.pneumoniae* protein (`PID 4376731`) was expressed <SEQ ID 33; cp6731>:

```
  1  MKSSLHWFLI SSSLALPLSL NFSAFAAVVE INLGPTNSFS GPGTYTPPAQ
 51  TTNADGTIYN LTGDVSITNA GSPTALTASC FKETTGNLSF QGHGYQFLLQ
101  NIDAGANCTF TNTAANKLLS FSGFSYLSLI QTTNATTGTG AIKSTGACSI
151  QSNYSCYFGQ NFSNDNGGAL QGSSISLSLN PNLTFAKNKA TQKGGALYST
201  GGITINNTLN SASFSENTAA NNGGAIYTEA SSFISSNKAI SFINNSVTAT
251  SATGGAIYCS STSAPKPVLT LSDNGELNFI GNTAITSGGA IYTDNLVLSS
301  GGPTLFKNNS AIDTAAPLGG AIAIADSGSL SLSALGGDIT FEGNTVVKGA
351  SSSQTTTRNS INIGNTNAKI VQLRASQGNT IYFYDPITTS ITAALSDALN
401  LNGPDLAGNP AYQGTIVFSG EKLSEAEAAE ADNLKSTIQQ PLTLAGGQLS
451  LKSGVTLVAK SFSQSPGSTL LMDAGTTLET ADGITINNLV LNVDSLKETK
501  KATLKATQAS QTVTLSGSLS LVDPSGNVYE DVSWNNPQVF SCLTLTADDP
551  ANIHITDLAA DPLEKNPIHW GYQGNWALSW QEDTATKSKA ATLTWTKTGY
601  NPNPERRGTL VANTLWGSFV DVRSIQQLVA TKVRQSQETR GIWCEGISNF
651  FHKDSTKINK GFRHISAGYV VGATTTLASD NLITAAFCQL FGKDRDHFIN
701  KNRASAYAAS LHLQHLATLS SPSLLRYLPG SESEQPVLFD AQISYIYSKN
751  TMKTYYTQAP KGESSWYNDG CALELASSLP HTALSHEGLF HAYFPFIKVE
801  ASYIHQDSFK ERNTTLVRSF DSGDLINVSV PIGITFERFS RNERASYEAT
851  VIYVADVYRK NPDCTTALLI NNTSWKTTGT NLSRQAGIGR AGIFYAFSPN
901  LEVTSNLSME IRGSSRSYNA DLGGKFQF*
```

A predicted signal peptide is highlighted.

The cp6731 nucleotide sequence <SEQ ID 34> is:

```
  1  ATGAAATCCT CTCTTCATTG GTTTTTAATC TCGTCATCTT TAGCACTTCC
 51  CTTGTCACTA AATTTCTCTG CGTTTGCTGC TGTTGTTGAA ATCAATCTAG
101  GACCTACCAA TAGCTTCTCT GGACCAGGAA CCTACACTCC TCCAGCCCAA
151  ACAACAAATG CAGATGGAAC TATCTATAAT CTAACAGGGG ATGTCTCAAT
201  CACCAATGCA GGATCTCCGA CAGCTCTAAC CGCTTCCTGC TTTAAAGAAA
```

```
 251  CTACTGGGAA TCTTTCTTTC CAAGGCCACG GCTACCAATT TCTCCTACAA
 301  AATATCGATG CGGGAGCGAA CTGTACCTTT ACCAATACAG CTGCAAATAA
 351  GCTTCTCTCC TTTTCAGGAT TCTCCTATTT GTCACTAATA CAAACCACGA
 401  ATGCTACCAC AGGAACAGGA GCCATCAAGT CCACAGGAGC TTGTTCTATT
 451  CAGTCGAACT ATAGTTGCTA CTTTGGCCAA AACTTTTCTA ATGACAATGG
 501  AGGCGCCCTC CAAGGCAGCT CTATCAGTCT ATCGCTAAAC CCCAACCTAA
 551  CGTTTGCCAA AAACAAAGCA ACGCAAAAAG GGGGTGCCCT CTATTCCACG
 601  GGAGGGATTA CAATTAACAA TACGTTAAAC TCAGCATCAT TTTCTGAAAA
 651  TACCGCGGCG AACAATGGCG GAGCCATTTA CACGGAAGCT AGCAGTTTTA
 701  TTAGCAGCAA CAAAGCAATT AGCTTTATAA ACAATAGTGT GACCGCAACC
 751  TCAGCTACAG GGGGAGCCAT TTACTGTAGT AGTACATCAG CCCCCAAACC
 801  AGTCTTAACT CTATCAGACA ACGGGGAACT GAACTTTATA GGAAATACAG
 851  CAATTACTAG TGGTGGGGCG ATTTATACTG ACAATCTAGT TCTTTCTTCT
 901  GGAGGACCTA CGCTTTTTAA AAACAACTCT GCTATAGATA CTGCAGCTCC
 951  CTTAGGAGGA GCAATTGCGA TTGCTGACTC TGGATCTTTG AGTCTTTCGG
1001  CTCTTGGTGG AGACATCACT TTTGAAGGAA ACACAGTAGT CAAAGGAGCT
1051  TCTTCGAGTC AGACCACTAC CAGAAATTCT ATTAACATCG GAAACACCAA
1101  TGCTAAGATT GTACAGCTGC GAGCCTCTCA AGGCAATACT ATCTACTTCT
1151  ATGATCCTAT AACAACTAGC ATCACTGCAG CTCTCTCAGA TGCTCTAAAC
1201  TTAAATGGTC CTGACCTTGC AGGGAATCCT GCATATCAAG GAACCATCGT
1251  ATTTTCTGGA GAGAAGCTCT CGGAAGCAGA AGCTGCAGAA GCTGATAATC
1301  TCAAATCTAC AATTCAGCAA CCTCTAACTC TTGCGGGAGG GCAACTCTCT
1351  CTTAAATCAG GAGTCACTCT AGTTGCTAAG TCCTTTTCGC AATCTCCGGG
1401  CTCTACCCTC CTCATGGATG CAGGGACCAC ATTAGAAACC GCTGATGGGA
1451  TCACTATCAA TAATCTTGTT CTCAATGTAG ATTCCTTAAA AGAGACCAAG
1501  AAGGCTACGC TAAAAGCAAC ACAAGCAAGT CAGACAGTCA CTTTATCTGG
1551  ATCGCTCTCT CTTGTAGATC CTTCTGGAAA TGTCTACGAA GATGTCTCTT
1601  GGAATAACCC TCAAGTCTTT TCTTGTCTCA CTCTTACTGC TGACGACCCC
1651  GCGAATATTC ACATCACAGA CTTAGCTGCT GATCCCCTAG AAAAAAATCC
1701  TATCCATTGG GGATACCAAG GGAATTGGGC ATTATCTTGG CAAGAGGATA
1751  CTGCGACTAA ATCCAAAGCA GCGACTCTTA CCTGGACAAA AACAGGATAC
1801  AATCCGAATC CTGAGCGTCG TGGAACCTTA GTTGCTAACA CGCTATGGGG
1851  ATCCTTTGTT GATGTGCGCT CCATACAACA GCTTGTAGCC ACTAAAGTAC
1901  GCCAATCTCA AGAAACTCGC GGCATCTGGT GTGAAGGGAT CTCGAACTTC
1951  TTCCATAAAG ATAGCACGAA GATAAATAAA GGTTTTCGCC ACATAAGTGC
2001  AGGTTATGTT GTAGGAGCGA CTACAACATT AGCTTCTGAT AATCTTATCA
2051  CTGCAGCCTT CTGCCAATTA TTCGGGAAAG ATAGAGATCA CTTTATAAAT
2101  AAAAATAGAG CTTCTGCCTA TGCAGCTTCT CTCCATCTCC AGCATCTAGC
2151  GACCTTGTCT TCTCCAAGCT TGTTACGCTA CCTTCCTGGA TCTGAAAGTG
2201  AGCAGCCTGT CCTCTTTGAT GCTCAGATCA GCTATATCTA TAGTAAAAAT
2251  ACTATGAAAA CCTATTACAC CCAAGCACCA AAGGGAGAGA GCTCGTGGTA
2301  TAATGACGGT TGCGCTCTGG AACTTGCGAG CTCCCTACCA CACACTGCTT
2351  TAAGCCATGA GGGTCTCTTC CACGCGTATT TTCCTTTCAT CAAAGTAGAA
2401  GCTTCGTACA TACACCAAGA TAGCTTCAAA GAACGTAATA CTACCTTGGT
2451  ACGATCTTTC GATAGCGGTG ATTTAATTAA CGTCTCTGTG CCTATTGGAA
2501  TTACCTTCGA GAGATTCTCG AGAAACGAGC GTGCGTCTTA CGAAGCTACT
2551  GTCATCTACG TTGCCGATGT CTATCGTAAG AATCCTGACT GCACGACAGC
2601  TCTCCTAATC AACAATACCT CGTGGAAAAC TACAGGAACG AATCTCTCAA
2651  GACAAGCTGG TATCGGAAGA GCAGGGATCT TTTATGCCTT CTCTCCAAAT
2701  CTTGAGGTCA CAAGTAACCT ATCTATGGAA ATTCGTGGAT CTTCACGCAG
2751  CTACAATGCA GATCTTGGAG GTAAGTTCCA GTTCTAA
```

The PSORT algorithm predicts an outer membrane location (0.926).

The protein was expressed in *E.coli* and purified as a his-tag product, as shown in Figure 17A. A GST-fusion protein was also expressed. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 17B; his-tag) and for FACS analysis (Figure 17C; his-tag and GST-fusion).

The GST-fusion protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis. Less cross-reactivity was seen with the his-fusion.

These experiments show that cp6731 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 18

The following *C.pneumoniae* protein (PID 4376737) was expressed <SEQ ID 35; cp6737>:

```
  1 MPLSFKSSSF CLLACLCSAS CAFAETRLGG NFVPPITNQG EEILLTSDFV
 51 CSNFLGASFS SSFINSSSNL SLLGKGLSLT FTSCQAPTNS NYALLSAAET
101 LTFKNFSSIN FTGNQSTGLG GLIYGKDIVF QSIKDLIFTT NRVAYSPASV
151 TTSATPAITT VTTGASALQP TDSLTVENIS QSIKFFGNLA NFGSAISSSP
201 TAVVKFINNT ATMSFSHNFT SSGGGVIYGG SSLLFENNSG CIIFTANSCV
251 NSLKGVTPSS GTYALGSGGA ICIPTGTFEL KNNQGKCTFS YNGTPNDAGA
301 IYAETCNIVG NQGALLLDSN TAARNGGAIC AKVLNIQGRG PIEFSRNRAE
351 KGGAIFIGPS VGDPAKQTST LTILASEGDI AFQGNMLNTK PGIRNAITVE
401 AGGEIVSLSA QGGSRLVFYD PITHSLPTTS PSNKDITINA NGASGSVVFT
451 SKGLSSTELL LPANTTTILL GTVKIASGEL KITDNAVVNV LGFATQGSGQ
501 LTLGSGGTLG LATPTGAPAA VDFTIGKLAF DPFSFLKRDF VSASVNAGTK
551 NVTLTGALVL DEHDVTDLYD MVSLQTPVAI PIAVFKGATV TKTGFPDGEI
601 ATPSHYGYQG KWSYTWSRPL LIPAPDGGFP GGPSPSANTL YAVWNSDTLV
651 RSTYILDPER YGEIVSNSLW ISFLGNQAFS DILQDVLLID HPGLSITAKA
701 LGAYVEHTPR QGHEGFSGRY GGYQAALSMN YTDHTTLGLS FGQLYGKTNA
751 NPYDSRCSEQ MYLLSFFGQF PIVTQKSEAL ISWKAAYGYS KNHLNTTYLR
801 PDKAPKSQGQ WHNNSYYVLI SAEHPFLNWC LLTRPLAQAW DLSGFISAEF
851 LGGWQSKFTE TGDLQRSFSR GKGYNVSLPI GCSSQWFTPF KKAPSTLTIK
901 LAYKPDIYRV NPHNIVTVVS NQESTSISGA NLRRHGLFVQ IHDVVDLTED
951 TQAFLNYTFD GKNGFTNHRV STGLKSTF*
```

A predicted signal peptide is highlighted.

The cp6737 nucleotide sequence <SEQ ID 36> is:

```
   1 ATGCCTCTTT CTTTCAAATC TTCATCTTTT TGTCTACTTG CCTGTTTATG
  51 TAGTGCAAGT TGCGCGTTTG CTGAGACTAG ACTCGGAGGG AACTTTGTTC
 101 CTCCAATTAC GAATCAGGGT GAAGAGATCT TACTCACTTC AGATTTTGTT
 151 TGTTCAAACT TCTTGGGGGC GAGTTTTTCA AGTTCCTTTA TCAATAGTTC
 201 CAGCAATCTC TCCTTATTAG GGAAGGGCCT TTCCTTAACG TTTACCTCTT
 251 GTCAAGCTCC TACAAATAGT AACTATGCGC TACTTTCTGC CGCAGAGACT
 301 CTGACCTTCA AGAATTTTTC TTCTATAAAC TTTACAGGGA ACCAATCGAC
 351 AGGACTTGGC GGCCTCATCT ACGGAAAAGA TATTGTTTTC CAATCTATCA
 401 AAGATTTGAT CTTCACTACG AACCGTGTTG CCTATTCTCC AGCATCTGTA
 451 ACTACGTCGG CAACTCCCGC AATCACTACA GTAACTACAG GAGCCTCTGC
 501 TCTCCAACCT ACAGACTCAC TCACTGTCGA AAACATATCC CAATCGATCA
 551 AGTTTTTTGG GAACCTTGCC AACTTCGGCT CTGCAATTAG CAGTTCTCCC
 601 ACGGCAGTCG TTAAATTCAT CAATAACACC GCTACCATGA GCTTCTCCCA
 651 TAACTTTACT TCGTCAGGAG GCGGCGTGAT TTATGGAGGA AGCTCTCTCC
 701 TTTTTGAAAA CAATTCTGGA TGCATCATCT TCACCGCCAA CTCCTGTGTG
 751 AACAGCTTAA AAGGCGTCAC CCCTTCATCA GGAACCTATG CTTTAGGAAG
 801 TGGCGGAGCC ATCTGCATCC CTACGGGAAC TTTCGAATTA AAAAACAATC
 851 AGGGGAAGTG CACCTTCTCT TATAATGGTA CACCAAATGA TGCGGGTGCG
 901 ATCTACGCCG AAACCTGCAA CATCGTAGGG AACCAGGGTG CCTTGCTCCT
 951 AGATAGCAAC ACTGCAGCGA GAAATGGCGG AGCCATCTGT GCTAAAGTGC
1001 TCAATATTCA AGGACGCGGT CCTATTGAAT TCTCTAGAAA CCGCGCGGAG
1051 AAGGGTGGAG CTATTTTCAT AGGCCCCTCT GTTGGAGACC CTGCGAAGCA
1101 AACATCGACA CTTACGATTT TGGCTTCCGA AGGTGATATT GCGTTCCAAG
1151 GAAACATGCT CAATACAAAA CCTGGAATCC GCAATGCCAT CACTGTAGAA
1201 GCAGGGGGAG AGATTGTGTC TCTATCTGCA CAAGGAGGCT CACGTCTTGT
1251 ATTTTATGAT CCCATTACAC ATAGCCTCCC AACCACAAGT CCGTCTAATA
1301 AAGACATTAC AATCAACGCT AATGGCGCTT CAGGATCTGT AGTCTTTACA
1351 AGTAAGGGAC TCTCCTCTAC AGAACTCCTG TTGCCTGCCA ACACGACAAC
1401 TATACTTCTA GGAACAGTCA AGATCGCTAG TGGAGAACTG AAGATTACTG
1451 ACAATGCGGT TGTCAATGTT CTTGGCTTCG CTACTCAGGG CTCAGGTCAG
1501 CTTACCCTGG GCTCTGGAGG AACCTTAGGG CTGGCAACAC CCACGGGAGC
1551 ACCTGCCGCT GTAGACTTTA CGATTGGAAA GTTAGCATTC GATCCTTTTT
1601 CCTTCCTAAA AAGAGATTTT GTTTCAGCAT CAGTAAATGC AGGCACAAAA
1651 AACGTCACTT TAACAGGAGC TCTGGTTCTT GATGAACATG ACGTTACAGA
```

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1701  TCTTTATGAT ATGGTGTCAT TACAAACTCC AGTAGCAATT CCTATCGCTG
1751  TTTTCAAAGG AGCAACCGTT ACTAAGACAG GATTTCCTGA TGGGGAGATT
1801  GCGACTCCAA GCCACTACGG CTACCAAGGA AAGTGGTCCT ACACATGGTC
1851  CCGTCCCCTG TTAATTCCAG CTCCTGATGG AGGATTTCCT GGAGGTCCCT
1901  CTCCTAGCGC AAATACTCTC TATGCTGTAT GGAATTCAGA CACTCTCGTG
1951  CGTTCTACCT ATATCTTAGA TCCCGAGCGT TACGGAGAAA TTGTCAGCAA
2001  CAGCTTATGG ATTTCCTTCT TAGGAAATCA GGCATTCTCT GATATTCTCC
2051  AAGATGTTCT TTTGATAGAT CATCCCGGGT TGTCCATAAC CGCGAAAGCT
2101  TTAGGAGCCT ATGTCGAACA CACACCAAGA CAAGGACATG AGGGCTTTTC
2151  AGGTCGCTAT GGAGGCTACC AAGCTGCGCT ATCTATGAAC TACACGGACC
2201  ACACTACGTT AGGACTTTCT TTCGGGCAGC TTTATGGAAA AACTAACGCC
2251  AACCCCTACG ATTCACGTTG CTCAGAACAA ATGTATTTAC TCTCGTTCTT
2301  TGGTCAATTC CCTATCGTGA CTCAAAAGAG CGAGGCCTTA ATTTCCTGGA
2351  AAGCAGCTTA TGGTTATTCC AAAAATCACC TAAATACCAC CTACCTCAGA
2401  CCTGACAAAG CTCCAAAATC TCAAGGGCAA TGGCATAACA ATAGTTACTA
2451  TGTTCTTATT TCTGCAGAAC ATCCTTTCCT AAACTGGTGT CTTCTTACAA
2501  GACCTCTGGC TCAAGCTTGG GATCTTTCAG GTTTTATTTC CGCAGAATTC
2551  CTAGGTGGTT GGCAAAGTAA GTTCACAGAA ACTGGAGATC TGCAACGTAG
2601  CTTTAGTAGA GGTAAAGGGT ACAATGTTTC CCTACCGATA GGATGTTCTT
2651  CTCAATGGTT CACACCATTT AAGAAGGCTC CTTCTACACT GACCATCAAA
2701  CTTGCCTACA AGCCTGATAT CTATCGTGTC AACCCTCACA ATATTGTGAC
2751  TGTCGTCTCA AACCAAGAGA GCACTTCGAT CTCAGGAGCA AATCTACGCC
2801  GCCACGGTTT GTTTGTACAA ATCCATGATG TAGTAGATCT CACCGAGGAC
2851  ACTCAGGCCT TTCTAAACTA TACCTTTGAC GGGAAAAATG GATTTACAAA
2901  CCACCGAGTG TCTACAGGAC TAAAATCCAC ATTTTAA
```

The PSORT algorithm predicts an outer membrane location (0.940).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 18A. The recombinant protein was used to immunise mice, whose sera were used in an immunoblot analysis blot (Figure 18B) and for FACS analysis (Figure 18C). A his-tagged protein was also expressed.

The cp6737 protein was also identified in the 2D-PAGE experiment (Cpn0454) and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6737 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 19

The following *C.pneumoniae* protein (PID 4377090) was expressed <SEQ ID 37; cp7090>:

```
  1  MNIHSLWKLC TLLALLALPA CSLSPNYGWE DSCNTCHHTR RKKPSSFGFV
 51  PLYTEEDFNP NFTFGEYDSK EEKQYKSSQV AAFRNITFAT DSYTIKGEEN
101  LAILTNLVHY MKKNPKATLY IEGHTDERGA ASYNLALGAR RANAIKEHLR
151  KQGISADRLS TISYGKEHPL NSGHNELAWQ QNRRTEFKIH AR*
```

A predicted signal peptide is highlighted.

The cp7090 nucleotide sequence <SEQ ID 38> is:

```
  1  ATGAATATAC ATTCCCTATG GAAACTTTGT ACTTTATTGG CTTTACTTGC
 51  ATTGCCAGCA TGTAGCCTTT CCCCTAATTA TGGCTGGGAG GATTCCTGTA
101  ATACATGCCA TCATACAAGA CGAAAAAAGC CTTCTTCTTT TGGCTTTGTT
151  CCTCTCTATA CCGAAGAGGA CTTTAACCCT AATTTTACCT TCGGTGAGTA
201  TGATTCCAAA GAAGAAAAAC AATACAAGTC AAGCCAAGTT GCAGCATTTC
251  GTAATATCAC CTTTGCTACA GACAGCTATA CAATTAAAGG TGAAGAGAAC
301  CTTGCGATTC TCACGAACTT GGTTCACTAC ATGAAGAAAA ACCCGAAAGC
351  TACACTGTAC ATTGAAGGGC ATACTGACGA GCGTGGAGCT GCATCCTATA
401  ACCTTGCTTT AGGAGCACGA CGAGCCAATG CGATTAAAGA GCATCTCCGA
451  AAGCAGGGAA TCTCTGCAGA TCGTCTATCT ACTATTTCCT ACGGAAAAGA
```

```
501  ACATCCTTTA AATTCGGGAC ACAACGAACT AGCATGGCAA CAAAATCGCC
551  GTACAGAGTT TAAGATTCAT GCACGCTAA
```

The PSORT algorithm predicts an outer membrane location (0.790).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 19A. A his-tagged protein was also expressed. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 19B) and for FACS analysis.

These experiments show that cp7090 is useful immunogen. These properties are not evident from the sequence alone.

Example 20

The following *C.pneumoniae* protein (PID 4377091) was expressed <SEQ ID 39; cp7091>:

```
  1  MLRQLCFQVF FFCFASLVYA EELEVVVRSE HITLPIEVSC QTDTKDPKIQ
 51  KYLSSLTEIF CKDIALGDCL QPTAASKESS SPLAISLRLH VPQLSVVLLQ
101  SSKTPQTLCS FTISQNLSVD RQKIHHAADT VHYALTGIPG ISAGKIVFAL
151  SSLGKDQKLK QGELWTTDYD GKNLAPLTTE CSLSITPKWV GVGSNFPYLY
201  VSYKYGVPKI FLGSLENTEG KKVLPLKGNQ LMPTFSPRKK LLAFVADTYG
251  NPDLFIQPFS LTSGPMGRPR RLLNENFGTQ GNPSFNPEGS QLVFISNKDG
301  RPRLYIMSLD PEPQAPRLLT KKYRNSSCPA WSPDGKKIAF CSVIKGVRQI
351  CIYDLSSGED YQLTTSPTNK ESPSWAIDSR HLVFSAGNAE ESELYLISLV
401  TKKTNKIAIG VGEKRFPSWG AFPQQPIKRT L*
```

A predicted signal peptide is highlighted.

The cp7091 nucleotide sequence <SEQ ID 40> is:

```
   1  ATGTTACGGC AACTATGCTT CCAAGTTTTT TTCTTTTGCT TCGCATCGCT
  51  AGTCTATGCT GAAGAATTAG AAGTTGTTGT CCGTTCCGAA CATATCACGC
 101  TCCCTATTGA GGTCTCTTGC CAGACCGATA CGAAAGATCC AAAAATACAG
 151  AAATACCTCA GCTCGCTAAC GGAGATATTT TGCAAGGACA TTGCCCTAGG
 201  AGATTGTCTA CAACCCACAG CGGCTTCTAA AGAATCGTCA TCTCCTTTAG
 251  CAATATCTTT ACGGTTGCAT GTACCTCAGC TATCTGTAGT GCTTTTACAG
 301  TCTTCAAAAA CTCCTCAAAC CTTATGTTCT TTTACTATTT CTCAAAATCT
 351  TTCTGTAGAT CGTCAAAAAA TCCATCACGC TGCTGATACA GTTCATTACG
 401  CCCTCACAGG GATTCCTGGA ATCAGTGCTG GGAAAATTGT TTTTGCTCTA
 451  AGTTCTTTAG GAAAAGATCA AAAGCTCAAG CAAGGAGAAT TATGGACTAC
 501  AGATTACGAT GGGAAAAACC TCGCCCCTTT AACCACAGAA TGTTCGCTCT
 551  CTATAACTCC AAAATGGGTG GGTGTGGGAT CAAATTTTCC CTATCTCTAT
 601  GTTTCGTATA AGTATGGTGT GCCTAAAATT TTTCTTGGTT CCCTAGAGAA
 651  CACTGAAGGT AAAAAAGTCC TTCCGTTAAA AGGCAACCAA CTCATGCCTA
 701  CGTTTTCTCC AAGAAAAAAG CTTTTAGCTT TCGTTGCTGA TACGTATGGA
 751  AATCCTGATT TATTTATTCA ACCGTTCTCA CTAACTTCAG GACCTATGGG
 801  TCGCCCACGT CGCCTCCTTA ATGAGAATTT CGGGACTCAA GGGAATCCCT
 851  CCTTCAACCC TGAAGGATCC CAGCTTGTCT TTATATCGAA CAAAGACGGC
 901  CGTCCGCGTC TTTATATTAT GTCCCTCGAT CCTGAACCCC AAGCACCTCG
 951  CTTGCTGACA AAAAAATACA GAAATAGCAG TTGCCCTGCA TGGTCTCCAG
1001  ATGGTAAAAA AATAGCCTTC TGCTCTGTAA TTAAAGGGGT GCGACAAATT
1051  TGTATTTACG ATCTCTCCTC TGGAGAGGAT TACCAACTCA CTACGTCTCC
1101  CACAAATAAA GAGAGTCCTT CTTGGGCTAT AGACAGCCGT CATCTTGTCT
1151  TTAGTGCGGG GAATGCTGAA GAATCAGAGT TATATTTAAT CAGTCTAGTC
1201  ACCAAAAAAA CTAACAAAAT TGCTATAGGA GTAGGAGAAA AACGGTTCCC
1251  CTCCTGGGGT GCTTTCCCTC AGCAACCGAT AAAGAGAACA CTATGA
```

The PSORT algorithm predicts an inner membrane location (0.109).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 20A. A his-tagged protein was also expressed. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figurc 20B) and for FACS analysis.

These experiments show that cp7091 is a useful immunogen. These properties are not evident from the sequence alone.

Example 21

The following *C.pneumoniae* protein (PID 4376260) was expressed <SEQ ID 41; cp6260>:

```
  1 MRFSLCGFPL VFSFTLLSVF DTSLSATTIS LTPEDSFHGD SQNAERSYNV
 51 QAGDVYSLTG DVSISNVDNS ALNKACFNVT SGSVTFAGNH HGLYFNNISS
101 GTTKEGAVLC CQDPQATARF SGFSTLSFIQ SPGDIKEQGC LYSKNALMLL
151 NNYVVRFEQN QSKTKGGAIS GANVTIVGNY DSVSFYQNAA TFGGAIHSSG
201 PLQIAVNQAE IRFAQNTAKN GSGGALYSDG DIDIDQNAYV LFRENEALTT
251 AIGKGGAVCC LPTSGSSTPV PIVTFSDNKQ LVFERNHSIM GGGAIYARKL
301 SISSGGPTLF INNISYANSQ NLGGAIAIDT GGEISLSAEK GTITFQGNRT
351 SLPFLNGIHL LQNAKFLKLQ ARNGYSIEFY DPITSEADGS TQLNINGDPK
401 NKEYTGTILF SGEKSLANDP RDFKSTIPQN VNLSAGYLVI KEGAEVTVSK
451 FTQSPGSHLV LDLGTKLIAS KEDIAITGLA IDIDSLSSSS TAAVIKANTA
501 NKQISVTDSI ELISPTGNAY EDLRMRNSQT FPLLSLEPGA GGSVTVTAGD
551 FLPVSPHYGF QGNWKLAWTG TGNKVGEFFW DKINYKPRPE KEGNLVPNIL
601 WGNAVDVRSL MQVQETHASS LQTDRGLWID GIGNFFHVSA SEDNIRYRHN
651 SGGYVLSVNN EITPKHYTSM AFSQLFSRDK DYAVSNNEYR MYLGSYLYQY
701 TTSLGNIFRY ASRNPNVNVG ILSRRFLQNP LMIFHFLCAY GHATNDMKTD
751 YANFPMVKNS WRNNCWAIEC GGSMPLLVFE NGRLFQGAIP FMKLQLVYAY
801 QGDFKETTAD GRRFSNGSLT SISVPLGIRF EKLALSQDVL YDFSFSYIPD
851 IFRKDPSCEA ALVISGDSWL VPAAHVSRHA FVGSGTGRYH FNDYTELLCR
901 GSIECRPHAR NYNINCGSKF RF*
```

A predicted signal peptide is highlighted.

The cp6260 nucleotide sequence <SEQ ID 42> is:

```
   1 ATGCGATTTT CGCTCTGCGG ATTTCCTCTA GTTTTTTCTT TTACATTGCT
  51 CTCAGTCTTC GACACTTCTT TGAGTGCTAC TACGATTTCT TTAACCCCAG
 101 AAGATAGTTT TCATGGAGAT AGTCAGAATG CAGAACGTTC TTATAATGTT
 151 CAAGCTGGGG ATGTCTATAG CCTTACTGGT GATGTCTCAA TATCTAACGT
 201 CGATAACTCT GCATTAAATA AAGCCTGCTT CAATGTGACC TCAGGAAGTG
 251 TGACGTTCGC AGGAAATCAT CATGGGTTAT ATTTTAATAA TATTTCCTCA
 301 GGAACTACAA AGGAAGGGGC TGTACTTTGT TGCCAAGATC CTCAAGCAAC
 351 GGCACGTTTT TCTGGGTTCT CCACGCTCTC TTTTATTCAG AGCCCCGGAG
 401 ATATTAAAGA ACAGGGATGT CTCTATTCAA AAAATGCACT TATGCTCTTA
 451 AACAATTATG TAGTGCGTTT TGAACAAAAC CAAAGTAAGA CTAAAGGCGG
 501 AGCTATTAGT GGGGCGAATG TTACTATAGT AGGCAACTAC GATTCCGTCT
 551 CTTTCTATCA GAATGCAGCC ACTTTTGGAG GTGCTATCCA TTCTTCAGGT
 601 CCCCTACAGA TTGCAGTAAA TCAGGCAGAG ATAAGATTTG CACAAAATAC
 651 TGCCAAGAAT GGTTCTGGAG GGGCTTTGTA CTCCGATGGT GATATTGATA
 701 TTGATCAGAA TGCTTATGTT CTATTTCGAG AAAATGAGGC ATTGACTACT
 751 GCTATAGGTA AGGGAGGGGC TGTCTGTTGT CTTCCCACTT CAGGAAGTAG
 801 TACTCCAGTT CCTATTGTGA CTTTCTCTGA CAATAAACAG TTAGTCTTTG
 851 AAAGAAACCA TTCCATAATG GGTGGCGGAG CCATTTATGC TAGGAAACTT
 901 AGCATCTCTT CAGGAGGTCC TACTCTATTT ATCAATAATA TATCATATGC
 951 AAATTCGCAA AATTTAGGTG GAGCTATTGC CATTGATACT GGAGGGGAGA
1001 TCAGTTTATC AGCAGAGAAA GGAACAATTA CATTCCAAGG AAACCGGACG
1051 AGCTTACCGT TTTTGAATGG CATCCATCTT TTACAAAATG CTAAATTCCT
1101 GAAATTACAG GCGAGAAATG GATACTCTAT AGAATTTTAT GATCCTATTA
1151 CTTCTGAAGC AGATGGGTCT ACCCAATTGA ATATCAACGG AGATCCTAAA
1201 AATAAAGAGT ACACAGGGAC CATACTCTTT TCTGGAGAAA AGAGTCTAGC
1251 AAACGATCCT AGGGATTTTA AATCTACAAT CCCTCAGAAC GTCAACCTGT
1301 CTGCAGGATA CTTAGTTATT AAAGAGGGGG CCGAAGTCAC AGTTTCAAAA
1351 TTCACGCAGT CTCCAGGATC GCATTTAGTT TTAGATTTAG GAACCAAACT
1401 GATAGCCTCT AAGGAAGACA TTGCCATCAC AGGCCTCGCG ATAGATATAG
1451 ATAGCTTAAG CTCATCCTCA ACAGCAGCTG TTATTAAAGC AAACACCGCA
1501 AATAAACAGA TATCCGTGAC GGACTCTATA GAACTTATCT CGCCTACTGG
1551 CAATGCCTAT GAAGATCTCA GAATGAGAAA TTCACAGACG TTCCCTCTGC
1601 TCTCTTTAGA GCCTGGAGCC GGGGGTAGTG TGACTGTAAC TGCTGGAGAT
1651 TTCCTACCGG TAAGTCCCCA TTATGGTTTT CAAGGCAATT GGAAATTAGC
1701 TTGGACAGGA ACTGGAAACA AAGTTGGAGA ATTCTTCTGG GATAAAATAA
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1751 ATTATAAGCC TAGACCTGAA AAAGAAGGAA ATTTAGTTCC TAATATCTTG
1801 TGGGGGAATG CTGTAGATGT CAGATCCTTA ATGCAGGTTC AAGAGACCCA
1851 TGCATCGAGC TTACAGACAG ATCGAGGGCT GTGGATCGAT GGAATTGGGA
1901 ATTTCTTCCA TGTATCTGCC TCCGAAGACA ATATAAGGTA CCGTCATAAC
1951 AGCGGTGGAT ATGTTCTATC TGTAAATAAT GAGATCACAC CTAAGCACTA
2001 TACTTCGATG GCATTTTCCC AACTCTTTAG TAGAGACAAG GACTATGCGG
2051 TTTCCAACAA CGAATACAGA ATGTATTTAG GATCGTATCT CTATCAATAT
2101 ACAACCTCCC TAGGGAATAT TTTCCGTTAT GCTTCGCGTA ACCCTAATGT
2151 AAACGTCGGG ATTCTCTCAA GAAGGTTTCT TCAAAATCCT CTTATGATTT
2201 TTCATTTTTT GTGTGCTTAT GGTCATGCCA CCAATGATAT GAAAACAGAC
2251 TACGCAAATT TCCCTATGGT GAAAAACAGC TGGAGAAACA ATTGTTGGGC
2301 TATAGAGTGC GGAGGGAGCA TGCCTCTATT GGTATTTGAG AACGGAAGAC
2351 TTTTCCAAGG TGCCATCCCA TTTATGAAAC TACAATTAGT TTATGCTTAT
2401 CAGGGAGATT TCAAAGAGAC GACTGCAGAT GGCCGTAGAT TTAGTAATGG
2451 GAGTTTAACA TCGATTTCTG TACCTCTAGG CATACGCTTT GAGAAGCTGG
2501 CACTTTCTCA GGATGTACTC TATGACTTTA GTTTCTCCTA TATTCCTGAT
2551 ATTTTCCGTA AGGATCCCTC ATGTGAAGCT GCTCTGGTGA TTAGCGGAGA
2601 CTCCTGGCTT GTTCCGGCAG CACACGTATC AAGACATGCT TTTGTAGGGA
2651 GTGGAACGGG TCGGTATCAC TTTAACGACT ATACTGAGCT CTTATGTCGA
2701 GGAAGTATAG AATGCCGCCC CCATGCTAGG AATTATAATA TAAACTGTGG
2751 AAGCAAATTT CGTTTTTAG
```

The PSORT algorithm predicts an outer membrane location (0.921).

The protein was expressed in *E.coli* and purified both as a his-tag and GST-fusion product. The GST-fusion is shown in Figure 21A. This recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 21B) and for FACS analysis (Figure 21C).

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6260 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 22

The following *C.pneumoniae* protein (PID 4376456) was expressed <SEQ ID 43; cp6456>:

```
  1 MSSPVNNTPS APNIPIPAPT TPGIPTTKPR SSFIEKVIIV AKYILFAIAA
 51 TSGALGTILG LSGALTPGIG IALLVIFFVS MVLLGLILKD SISGGEERRL
101 REEVSRFTSE NQRLTVITTT LETEVKDLKA AKDQLTLEIE AFRNENGNLK
151 TTAEDLEEQV SKLSEQLEAL ERINQLIQAN AGDAQEISSE LKKLISGWDS
201 KVVEQINTSI QALKVLLGQE WVQEAQTHVK AMQEQIQALQ AEILGMHNQS
251 TALQKSVENL LVQDQALTRV VGELLESENK LSQACSALRQ EIEKLAQHET
301 SLQQRIDAML AQEQNLAEQV TALEKMKQEA QKAESEFIAC VRDRTFGRRE
351 TPPPTTPVVE GDESQEEDEG GTPPVSQPSS PVDRATGDGQ *
```

The cp6456 nucleotide sequence <SEQ ID 44> is:

```
  1 ATGTCATCTC CTGTAAATAA CACACCCTCA GCACCAAACA TTCCAATACC
 51 AGCGCCCACG ACTCCAGGTA TTCCTACAAC AAAACCTCGT TCTAGTTTCA
101 TTGAAAAGGT TATCATTGTA GCTAAGTACA TACTATTTGC AATTGCAGCC
151 ACATCAGGAG CACTCGGAAC AATTCTAGGT CTATCTGGAG CGCTAACCCC
201 AGGAATAGGT ATTGCCCTTC TTGTTATCTT CTTTGTTTCT ATGGTGCTTT
251 TAGGTTTAAT CCTTAAAGAT TCTATAAGTG GAGGAGAAGA ACGCAGGCTC
301 AGAGAAGAGG TCTCTCGATT TACAAGTGAG AATCAACGGT TGACAGTCAT
351 AACCACAACA CTTGAGACTG AAGTAAAGGA TTTAAAAGCA GCTAAAGATC
401 AACTTACACT TGAAATCGAA GCATTTAGAA ATGAAAACGG TAATTTAAAA
451 ACAACTGCTG AGGACTTAGA AGAGCAGGTT TCTAAACTTA GCGAACAATT
501 AGAAGCACTA GAGCGAATTA ATCAACTTAT CCAAGCAAAC GCTGGAGATG
551 CTCAAGAAAT TTCGTCTGAA CTAAAGAAAT TAATAAGCGG TTGGGATTCC
601 AAAGTTGTTG AACAGATAAA TACTTCTATT CAAGCATTGA AAGTGTTATT
651 GGGTCAAGAG TGGGTGCAAG AGGCTCAAAC ACACGTTAAA GCAATGCAAG
701 AGCAAATTCA AGCATTGCAA GCTGAAATTC TAGGAATGCA CAATCAATCT
```

```
 751  ACAGCATTGC AAAAGTCAGT TGAGAATCTA TTAGTACAAG ATCAAGCTCT
 801  AACAAGAGTA GTAGGTGAGT TGTTAGAGTC TGAGAACAAG CTAAGCCAAG
 851  CTTGTTCTGC GCTACGTCAA GAAATAGAAA AGTTGGCCCA ACATGAAACA
 901  TCTTTGCAAC AACGTATTGA TGCGATGCTA GCCCAAGAGC AAAATTTGGC
 951  AGAGCAGGTC ACAGCCCTTG AAAAAATGAA ACAAGAAGCT CAGAAGGCTG
1001  AGTCCGAGTT CATTGCTTGT GTACGTGATC GAACTTTCGG ACGTCGTGAA
1051  ACACCTCCAC CAACAACACC TGTAGTTGAA GGTGATGAAA GTCAAGAAGA
1101  AGACGAAGGA GGTACTCCCC CAGTATCACA ACCATCTTCA CCCGTAGATA
1151  GAGCAACAGG AGATGGTCAG TAA
```

The PSORT algorithm predicts inner membrane (0.127).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 22A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 22B) and for FACS analysis (Figure 22C). A his-tag protein was also expressed.

These experiments show that cp6456 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 23

The following *C.pneumoniae* protein (PID 4376729) was expressed <SEQ ID 45; cp6729>:

```
  1  MKIPLHKLLI SSTLVTPILL SIATYGADAS LSPTDSFDGA GGSTFTPKST
 51  ADANGTNYVL SGNVYINDAG KGTALTGCCF TETTGDLTFT GKGYSFSFNT
101  VDAGSNAGAA ASTTADKALT FTGFSNLSFI AAPGTTVASG KSTLSSAGAL
151  NLTDNGTILF SQNVSNEANN NGGAITTKTL SISGNTSSIT FTSNSAKKLG
201  GAIYSSAAAS ISGNTGQLVF MNNKGETGGG ALGFEASSSI TQNSSLFFSG
251  NTATDAAGKG GAIYCEKTGE TPTLTISGNK SLTFAENSSV TQGGAICAHG
301  LDLSAAGPTL FSNNRCGNTA AGKGGAIAIA DSGSLSLSAN QGDITFLGNT
351  LTSTSAPTST RNAIYLGSSA KITNLRAAQG QSIYFYDPIA SNTTGASDVL
401  TINQPDSNSP LDYSGTIVFS GEKLSADEAK AADNFTSILK QPLALASGTL
451  ALKGNVELDV NGFTQTEGST LLMQPGTKLK ADTEAISLTK LVVDLSALEG
501  NKSVSIETAG ANKTITLTSP LVFQDSSGNF YESHTINQAF TQPLVVFTAA
551  TAASDIYIDA LLTSPVQTPE PHYGYQGHWE ATWADTSTAK SGTMTWVTTG
601  YNPNPERRAS VVPDSLWASF TDIRTLQQIM TSQANSIYQQ RGLWASGTAN
651  FFHKDKSGTN QAFRHKSYGY IVGGSAEDFS ENIFSVAFCQ LFGKDKDLFI
701  VENTSHNYLA SLYLQHRAFL GGLPMPSFGS ITDMLKDIPL ILNAQLSYSY
751  TKNDMDTRYT SYPEAQGSWT NNSGALELGG SLALYLPKEA PFFQGYFPFL
801  KFQAVYSRQQ NFKESGAEAR AFDDGDLVNC SIPVGIRLEK ISEDEKNNFE
851  ISLAYIGDVY RKNPRSRTSL MVSGASWTSL CKNLARQAFL ASAGSHLTLS
901  PHVELSGEAA YELRGSAHIY NVDCGLRYSF *
```

A predicted signal peptide is highlighted.

The cp6729 nucleotide sequence <SEQ ID 46> is:

```
  1  ATGAAAATAC CCTTGCACAA ACTCCTGATC TCTTCGACTC TTGTCACTCC
 51  CATTCTATTG AGCATTGCAA CTTACGGAGC AGATGCTTCT TTATCCCCTA
101  CAGATAGCTT TGATGGAGCG GGCGGCTCTA CATTTACTCC AAAATCTACA
151  GCAGATGCCA ATGGAACGAA CTATGTCTTA TCAGGAAATG TCTATATAAA
201  CGATGCTGGG AAAGGCACAG CATTAACAGG CTGCTGCTTT ACAGAAACTA
251  CGGGTGATCT GACATTTACT GGAAAGGGAT ACTCATTTTC ATTCAACACG
301  GTAGATGCGG GTTCGAATGC AGGAGCTGCG GCAAGCACAA CTGCTGATAA
351  AGCCCTAACA TTCACAGGAT TTTCTAACCT TTCCTTCATT GCAGCTCCTG
401  GAACTACAGT TGCTTCAGGA AAAAGTACTT TAAGTTCTGC AGGAGCCTTA
451  AATCTTACCG ATAATGGAAC GATTCTCTTT AGCCAAAACG TCTCCAATGA
501  AGCTAATAAC AATGGCGGAG CGATCACCAC AAAAACTCTT TCTATTTCTG
551  GGAATACCTC TTCTATAACC TTCACTAGTA ATAGCGCAAA AAAATTAGGT
601  GGAGCGATCT ATAGCTCTGC GGCTGCAAGT ATTTCAGGAA ACACCGGCCA
651  GTTAGTCTTT ATGAATAATA AAGGAGAAAC TGGGGGTGGG GCTCTGGGCT
701  TTGAAGCCAG CTCCTCGATT ACTCAAAATA GCTCCCTTTT CTTCTCTGGA
751  AACACTGCAA CAGATGCTGC AGGCAAGGGC GGGGCCATTT ATTGTGAAAA
801  AACAGGAGAG ACTCCTACTC TTACTATCTC TGGAAATAAA AGTCTGACCT
851  TCGCCGAGAA CTCTTCAGTA ACTCAAGGCG GAGCAATCTG TGCCCATGGT
```

```
 901  CTAGATCTTT CCGCTGCTGG CCCTACCCTA TTTTCAAATA ATAGATGCGG
 951  GAACACAGCT GCAGGCAAGG GCGGCGCTAT TGCAATTGCC GACTCTGGAT
1001  CTTTAAGTCT CTCTGCAAAT CAAGGAGACA TCACGTTCCT TGGCAACACT
1051  CTAACCTCAA CCTCCGCGCC AACATCGACA CGGAATGCTA TCTACCTGGG
1101  ATCGTCAGCA AAAATTACGA ACTTAAGGGC AGCCCAAGGC CAATCTATCT
1151  ATTTCTATGA TCCGATTGCA TCTAACACCA CAGGAGCTTC AGACGTTCTG
1201  ACCATCAACC AACCGGATAG CAACTCGCCT TTAGATTATT CAGGAACGAT
1251  TGTATTTTCT GGGGAAAAGC TCTCTGCAGA TGAAGCGAAA GCTGCTGATA
1301  ACTTCACATC TATATTAAAG CAACCATTGG CTCTAGCCTC TGGAACCTTA
1351  GCACTCAAAG GAAATGTCGA GTTAGATGTC AATGGTTTCA CACAGACTGA
1401  AGGCTCTACA CTCCTCATGC AACCAGGAAC AAAGCTCAAA GCAGATACTG
1451  AAGCTATCAG TCTTACCAAA CTTGTCGTTG ATCTTTCTGC CTTAGAGGGA
1501  AATAAGAGTG TGTCCATTGA AACAGCAGGA GCCAACAAAA CTATAACTCT
1551  AACCTCTCCT CTTGTTTTCC AAGATAGTAG CGGCAATTTT TATGAAAGCC
1601  ATACGATAAA CCAAGCCTTC ACGCAGCCTT TGGTGGTATT CACTGCTGCT
1651  ACTGCTGCTA GCGATATTTA TATCGATGCG CTTCTCACTT CTCCAGTACA
1701  AACTCCAGAA CCTCATTACG GGTATCAGGG ACATTGGGAA GCCACTTGGG
1751  CAGACACATC AACTGCAAAA TCAGGAACTA TGACTTGGGT AACTACGGGC
1801  TACAACCCTA ATCCTGAGCG TAGAGCTTCC GTAGTTCCCG ATTCATTATG
1851  GGCATCCTTT ACTGACATTC GCACTCTACA GCAGATCATG ACATCTCAAG
1901  CGAATAGTAT CTATCAGCAA CGAGGACTCT GGGCATCAGG AACTGCGAAT
1951  TTCTTCCATA AGGATAAATC AGGAACTAAC CAAGCATTCC GACATAAAAG
2001  CTACGGCTAT ATTGTTGGAG GAAGTGCTGA AGATTTTTCT GAAAATATCT
2051  TCAGTGTAGC TTTCTGCCAG CTCTTCGGTA AAGATAAAGA CCTGTTTATA
2101  GTTGAAAATA CCTCTCATAA CTATTTAGCG TCGCTATACC TGCAACATCG
2151  AGCATTCCTA GGAGGACTTC CCATGCCCTC ATTTGGAAGT ATCACCGACA
2201  TGCTGAAAGA TATTCCTCTC ATTTTGAATG CCCAGCTAAG CTACAGCTAC
2251  ACTAAAAATG ATATGGATAC TCGCTATACT TCCTATCCTG AAGCTCAAGG
2301  CTCTTGGACC AATAACTCTG GGGCTCTAGA GCTCGGAGGA TCTCTGGCTC
2351  TATATCTCCC TAAAGAAGCA CCGTTCTTCC AGGGATATTT CCCCTTCTTA
2401  AAGTTCCAGG CAGTCTACAG CCGCCAACAA AACTTTAAAG AGAGTGGCGC
2451  TGAAGCCCGT GCTTTTGATG ATGGAGACCT AGTGAACTGC TCTATCCCTG
2501  TCGGCATTCG GTTAGAAAAA ATCTCCGAAG ATGAAAAAAA TAATTTCGAG
2551  ATTTCTCTAG CCTACATTGG TGATGTGTAT CGTAAAAATC CCCGTTCGCG
2601  TACTTCTCTA ATGGTCAGTG GAGCCTCTTG GACTTCGCTA TGTAAAAACC
2651  TCGCACGACA AGCCTTCTTA GCAAGTGCTG GAAGCCATCT GACTCTCTCC
2701  CCTCATGTAG AACTCTCTGG GGAAGCTGCT TATGAGCTTC GTGGCTCAGC
2751  ACACATCTAC AATGTAGATT GTGGGCTAAG ATACTCATTC TAG
```

The PSORT algorithm predicts outer membrane (0.927).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 23A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 23B) and for FACS analysis (Figure 23C). A his-tag protein was also expressed.

The cp6729 protein was also identified in the 2D-PAGE experiment (Cpn0446) and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6729 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 24

The following *C.pneumoniae* protein (PID 4376849) was expressed <SEQ ID 47; cp6849>:

```
  1  MSKLIRRVVT VLALTSMASC FASGGIEAAV AESLITKIVA SAETKPAPVP
 51  MTAKKVRLVR RNKQPVEQKS RGAFCDKEFY PCEEGRCQPV EAQQESCYGR
101  LYSVKVNDDC NVEICQSVPE YATVGSPYPI EILAIGKKDC VDVVITQQLP
151  CEAEFVSSDP ETTPTSDGKL VWKIDRLGAG DKCKITVWVK PLKEGCCFTA
201  ATVCACPELR SYTKCGQPAI CIKQEGPDCA CLRCPVCYKI EVVNTGSAIA
251  RNVTVDNPVP DGYSHASGQR VLSFNLGDMR PGDKKVFTVE FCPQRRGQIT
301  NVATVTYCGG HKCSANVTTV VNEPCVQVNI SGADWSYVCK PVEYSISVSN
351  PGDLVLHDVV IQDTLPSGVT VLEAPGGEIC CNKVVWRIKE MCPGETLQFK
```

```
401  LVVKAQVPGR FTNQVAVTSE SNCGTCTSCA ETTTHWKGLA ATHMCVLDTN
451  DPICVGENTV YRICVTNRGS AEDTNVSLIL KFSKELQPIA SSGPTKGTIS
501  GNTVVFDALP KLGSKESVEF SVTLKGIAPG DARGEAILSS DTLTSPVSDT
551  ENTHVY*
```

A predicted signal peptide is highlighted.

The cp6849 nucleotide sequence <SEQ ID 48> is:

```
   1  ATGTCCAAAC TCATCAGACG AGTAGTTACG GTCCTTGCGC TAACGAGTAT
  51  GGCGAGTTGC TTTGCCAGCG GGGGTATAGA GGCCGCTGTA GCAGAGTCTC
 101  TGATTACTAA GATCGTCGCT AGTGCGGAAA CAAAGCCAGC ACCTGTTCCT
 151  ATGACAGCGA AGAAGGTTAG ACTTGTCCGT AGAAATAAAC AACCAGTTGA
 201  ACAAAAAAGC CGTGGTGCTT TTTGTGATAA AGAATTTTAT CCCTGTGAAG
 251  AGGGACGATG TCAACCTGTA GAGGCTCAGC AAGAGTCTTG CTACGGAAGA
 301  TTGTATTCTG TAAAAGTAAA CGATGATTGC AACGTAGAAA TTTGCCAGTC
 351  CGTTCCAGAA TACGCTACTG TAGGATCTCC TTACCCTATT GAAATCCTTG
 401  CTATAGGCAA AAAAGATTGT GTTGATGTTG TGATTACACA ACAGCTACCT
 451  TGCGAAGCTG AATTCGTAAG CAGTGATCCA GAAACAACTC CTACAAGTGA
 501  TGGGAAATTA GTCTGGAAAA TCGATCGCCT GGGTGCAGGA GATAAATGCA
 551  AAATTACTGT ATGGGTAAAA CCTCTTAAAG AAGGTTGCTG CTTCACAGCT
 601  GCTACTGTAT GTGCTTGCCC AGAGCTCCGT TCTTATACTA AATGCGGTCA
 651  ACCAGCCATT TGTATTAAGC AAGAAGGACC TGACTGTGCT TGCCTAAGAT
 701  GCCCTGTATG CTACAAAATC GAAGTAGTGA ACACAGGATC TGCTATTGCC
 751  CGTAACGTAA CTGTAGATAA TCCTGTTCCC GATGGCTATT CTCATGCATC
 801  TGGTCAAAGA GTTCTCTCTT TTAACTTAGG AGACATGAGA CCTGGCGATA
 851  AAAAGGTATT TACAGTTGAG TTCTGCCCTC AAAGAAGAGG TCAAATCACT
 901  AACGTTGCTA CTGTAACTTA CTGCGGTGGA CACAAATGTT CTGCAAATGT
 951  AACTACAGTT GTTAATGAGC CTTGTGTACA AGTAAATATC TCTGGTGCTG
1001  ATTGGTCTTA CGTATGTAAA CCTGTGGAGT ACTCTATCTC AGTATCGAAT
1051  CCTGGAGACT TGGTTCTTCA TGATGTCGTG ATCCAAGATA CACTCCCTTC
1101  TGGTGTTACA GTACTCGAAG CTCCTGGTGG AGAGATCTGC TGTAATAAAG
1151  TTGTTTGGCG TATTAAAGAA ATGTGCCCAG GAGAAACCCT CCAGTTTAAA
1201  CTTGTAGTGA AAGCTCAAGT TCCTGGAAGA TTCACAAATC AAGTTGCAGT
1251  AACTAGTGAG TCTAACTGCG GAACATGTAC ATCTTGCGCA GAAACAACAA
1301  CACATTGGAA AGGTCTTGCA GCTACCCATA TGTGCGTATT AGACACAAAT
1351  GATCCTATCT GTGTAGGAGA AAATACTGTC TATCGTATCT GTGTAACTAA
1401  CCGTGGTTCT GCTGAAGATA CTAACGTATC TTTAATCTTG AAGTTCTCAA
1451  AAGAACTTCA GCCAATAGCT TCTTCAGGTC CAACTAAAGG AACGATTTCA
1501  GGTAATACCG TTGTTTTCGA CGCTTTACCT AAACTCGGTT CTAAGGAATC
1551  TGTAGAGTTT TCTGTTACCT TGAAAGGTAT TGCTCCCGGA GATGCTCGCG
1601  GCGAAGCTAT TCTTTCTTCT GATACACTGA CTTCACCAGT ATCAGACACA
1651  GAAAATACCC ACGTGTATTA A
```

The PSORT algorithm predicts periplasmic space (0.93).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 24A, and also as a his-tag protein. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 24B) and for FACS analysis (Figure 24C).

The cp6849 protein was also identified in the 2D-PAGE experiment (Cpn0557).

These experiments show that cp6849 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 25

The following *C.pneumoniae* protein (PID 4376273) was expressed <SEQ ID 49; cp6273>:

```
  1  MGLFHLTLFG LLLCSLPISL VAKFPESVGH KILYISTQST QQALATYLEA
 51  LDAYGDHDFF VLRKIGEDYL KQSIHSSDPQ TRKSTIIGAG LAGSSEALDV
101  LSQAMETADP LQQLLVLSAV SGHLGKTSDD LLFKALASPY PVIRLEAAYR
151  LANLKNTKVI DHLHSFIHKL PEEIQCLSAA IFLRLETEES DAYIRDLLAA
201  KKSAIRSATA LQIGEYQQKR FLPTLRNLLT SASPQDQEAI LYALGKLKDG
```

```
251  QSYYNIKKQL QKPDVDVTLA AAQALIALGK EEDALPVIKK QALEERPRAL
301  YALRHLPSEI GIPIALPIFL KTKNSEAKLN VALALLELGC DTPKLLEYIT
351  ERLVQPHYNE TLALSFSKGR TLQNWKRVNI IVPQDPQERE RLLSTTRGLE
401  EQILTFLFRL PKEAYLPCIY KLLASQKTQL ATTAISFLSH TSHQEALDLL
451  FQAAKLPGEP IIRAYADLAI YNLTKDPEKK RSLHDYAKKL IQETLLFVDT
501  ENQRPHPSMP YLRYQVTPES RTKLMLDILE TLATSKSSED IRLLIQLMTE
551  GDAKNFPVLA GLLIKIVE*
```

A predicted signal peptide is highlighted.

The cp6273 nucleotide sequence <SEQ ID 50> is:

```
   1  ATGGGACTAT TCCATCTAAC TCTCTTTGGA CTTTTATTGT GTAGTCTTCC
  51  CATTTCTCTT GTTGCTAAAT TCCCTGAGTC TGTAGGTCAT AAGATCCTTT
 101  ATATAAGTAC GCAATCTACA CAGCAGGCCT TAGCAACATA TCTGGAAGCT
 151  CTAGATGCCT ACGGTGATCA TGACTTCTTC GTTTTAAGAA AAATCGGAGA
 201  AGACTATCTC AAGCAAAGCA TCCACTCCTC AGATCCGCAA ACTAGAAAAA
 251  GCACCATCAT TGGAGCAGGC CTGGCGGGAT CTTCAGAAGC CTTGGACGTG
 301  CTCTCCCAAG CTATGGAAAC TGCAGACCCC CTGCAGCAGC TACTGGTTTT
 351  ATCGGCAGTC TCAGGACATC TTGGGAAAAC TTCTGACGAC TTACTGTTTA
 401  AAGCTTTAGC ATCTCCCTAT CCTGTCATCC GCTTAGAAGC CGCCTATAGA
 451  CTTGCTAATT TGAAGAACAC TAAAGTCATT GATCATCTAC ATTCTTTCAT
 501  TCATAAGCTT CCCGAAGAAA TCCAATGCCT ATCTGCGGCA ATATTCCTAC
 551  GCTTGGAGAC TGAAGAATCT GATGCTTATA TTCGGGATCT CTTAGCTGCC
 601  AAGAAAAGCG CGATTCGGAG TGCCACAGCT TTGCAGATCG GAGAATACCA
 651  ACAAAAACGC TTTCTTCCGA CACTTAGGAA TTTGCTAACG AGTGCGTCTC
 701  CTCAAGATCA AGAAGCTATT CTTTATGCTT TAGGGAAGCT TAAGGATGGT
 751  CAGAGCTACT ACAATATAAA AAAGCAATTG CAGAAGCCTG ATGTGGATGT
 801  CACTTTAGCA GCAGCTCAAG CTTTAATTGC TTTGGGGAAA GAAGAGGACG
 851  CTCTTCCCGT GATAAAAAAG CAAGCACTTG AGGAGCGGCC TCGAGCCCTG
 901  TATGCCTTAC GGCATCTACC CTCTGAGATA GGGATTCCGA TTGCCCTGCC
 951  GATATTCCTA AAAACTAAGA ACAGCGAAGC CAAGTTGAAT GTAGCTTTAG
1001  CTCTCTTAGA GTTAGGGTGT GACACCCCTA AACTACTGGA ATACATTACC
1051  GAAAGGCTTG TCCAACCACA TTATAATGAG ACTCTAGCCT TGAGTTTCTC
1101  TAAGGGGCGT ACTTTACAAA ATTGGAAGCG GGTGAACATC ATAGTCCCTC
1151  AAGATCCCCA GGAGAGGGAA AGGTTGCTCT CCACAACCCG AGGTCTTGAA
1201  GAGCAGATCC TTACGTTTCT CTTCCGCCTA CCTAAAGAAG CTTACCTCCC
1251  CTGTATTTAT AAGCTTTTGG CGAGTCAGAA AACTCAGCTT GCCACTACTG
1301  CGATTTCTTT TTTAAGTCAC ACCTCACATC AGGAAGCCTT AGATCTACTT
1351  TTCCAAGCTG CGAAGCTTCC TGGAGAACCT ATCATCCGCG CCTATGCAGA
1401  TCTTGCTATT TATAATCTCA CCAAAGATCC TGAAAAAAAA CGTTCTCTCC
1451  ATGATTATGC AAAAAAGCTA ATTCAGGAAA CCTTGTTATT TGTGGACACG
1501  GAAAACCAAA GACCCCATCC CAGCATGCCC TATCTACGTT ATCAGGTCAC
1551  CCCAGAAAGC CGTACGAAGC TCATGTTGGA TATTCTAGAG ACACTAGCCA
1601  CCTCGAAGTC TTCCGAAGAT ATCCGTTTAT TGATACAACT GATGACGGAA
1651  GGAGATGCAA AAAATTTCCC AGTCCTTGCA GGCTTACTCA TAAAAATTGT
1701  GGAGTAA
```

The PSORT algorithm predicts a periplasmic location (0.922).

The protein was expressed in *E.coli* and purified as a his-tag product and as a GST-fusion product, as shown in Figure 25A. The recombinant GST-fusion was used to immunise mice, whose sera were used in a Western blot (Figure 25B) and for FACS analysis (Figure 25C).

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6273 is a surfaee-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 26

The following *C.pneumoniae* protein (PID 4376735) was expressed <SEQ ID 51; cp6735>:

1 **MTILRNFLTC SALFLALPA**A AQVVYLHESD GYNGAINNKS LEPKITCYPE
51 GTSYIFLDDV RISNVKHDQE DAGVFINRSG NLFFMGNRCN FTFHNLMTEG
101 FGAAISNRVG DTTLTLSNFS YLAFTSAPLL PQGQGAIYSL GSVMIENSEE
151 VTFCGNYSSW SGAAIYTPYL LGSKASRPSV NLSGNRYLVF RDNVSQGYGG
201 AISTHNLTLT TRGPSCFENN HAYHDVNSNG GAIAIAPGGS ISISVKSGDL
251 IFKGNTASQD GNTIHNSIHL QSGAQFKNLR AVSESGVYFY DPISHSESHK
301 ITDLVINAPE GKETYEGTIS FSGLCLDDHE VCAENLTSTI LQDVTLAGGT
351 LSLSDGVTLQ LHSFKQEASS TLTMSPGTTL LCSGDARVQN LHILIEDTDN
401 FVPVRIRAED KDALVSLEKL KVAFEAYWSV YDFPQFKEAF TIPLLELLGP
451 SFDSLLLGET TLERTQVTTE NDAVRGFWSL SWEEYPPSLD KDRRITPTKK
501 TVFLTWNPEI TSTP*

A predicted signal peptide is highlighted.

The cp6735 nucleotide sequence <SEQ ID 52> is:

```
   1 ATGACCATAC TTCGAAATTT TCTTACCTGC TCGGCTTTAT TCCTCGCTCT
  51 CCCTGCAGCA GCACAAGTTG TATATCTTCA TGAAAGTGAT GGTTATAACG
 101 GTGCTATCAA TAATAAAAGC TTAGAACCTA AAATTACCTG TTATCCAGAA
 151 GGAACTTCTT ACATCTTTCT AGATGACGTG AGGATTTCCA ACGTTAAGCA
 201 TGATCAAGAA GATGCTGGGG TTTTTATAAA TCGATCTGGG AATCTTTTTT
 251 TCATGGGCAA CCGTTGCAAC TTCACTTTTC ACAACCTTAT GACCGAGGGT
 301 TTTGGCGCTG CCATTTCGAA CCGCGTTGGA GACACCACTC TCACTCTCTC
 351 TAATTTTTCT TACTTAGCGT TCACCTCAGC ACCTCTACTA CCTCAAGGAC
 401 AAGGAGCGAT TTATAGTCTT GGTTCCGTGA TGATCGAAAA TAGTGAGGAA
 451 GTGACTTTCT GTGGGAACTA CTCTTCGTGG AGTGGAGCTG CGATTTATAC
 501 TCCCTACCTT TTAGGTTCTA AGGCGAGTCG TCCTTCAGTA AATCTCAGCG
 551 GGAACCGCTA CCTGGTGTTT AGAGACAATG TGAGCCAAGG TTATGGCGGC
 601 GCCATATCTA CCCACAATCT CACACTCACG ACTCGAGGAC CTTCGTGTTT
 651 TGAAAATAAT CATGCTTATC ATGACGTGAA TAGTAATGGA GGAGCCATTG
 701 CCATTGCTCC TGGAGGATCG ATCTCTATAT CCGTGAAAAG CGGAGATCTC
 751 ATCTTCAAAG GAAATACAGC ATCACAAGAC GGAAATACAA TACACAACTC
 801 CATCCATCTG CAATCTGGAG CACAGTTTAA GAACCTACGT GCTGTTTCAG
 851 AATCCGGAGT TTATTTCTAT GATCCTATAA GCCATAGCGA GTCGCATAAA
 901 ATTACAGATC TTGTAATCAA TGCTCCTGAA GGAAAGGAAA CTTATGAAGG
 951 AACAATTAGC TTCTCAGGAC TATGCCTGGA TGATCATGAA GTTTGTGCGG
1001 AAAATCTTAC TTCCACAATC CTACAAGATG TCACATTAGC AGGAGGAACT
1051 CTCTCTCTAT CGGATGGGGT TACCTTGCAA CTGCATTCTT TTAAGCAGGA
1101 AGCAAGCTCT ACGCTTACTA TGTCTCCAGG AACCACTCTG CTCTGCTCAG
1151 GAGATGCTCG GGTTCAGAAT CTGCACATCC TGATTGAAGA TACCGACAAC
1201 TTTGTTCCTG TAAGGATTCG CGCCGAGGAC AAGGATGCTC TTGTCTCATT
1251 AGAAAAACTT AAAGTTGCCT TTGAGGCTTA TTGGTCCGTC TATGACTTTC
1301 CTCAATTTAA GGAAGCCTTT ACGATTCCTC TTCTTGAACT TCTAGGGCCT
1351 TCTTTTGACA GTCTTCTCCT AGGGGAGACC ACTTTGGAGA GAACCCAAGT
1401 CACAACAGAG AATGACGCCG TTCGAGGTTT CTGGTCCCTA AGCTGGGAAG
1451 AGTACCCCCC TTCTCTGGAT AAAGACAGAA GGATCACACC AACTAAGAAA
1501 ACTGTTTTCC TCACTTGGAA TCCTGAGATC ACTTCTACGC CATAA
```

The PSORT algorithm predicts an outer membrane location (0.922).

The protein was expressed in *E.coli* and purified as a as a his-tag product and as a GST-fusion product, as shown in Figure 26A. The recombinant GST-fusion protein was used to immunise mice, whose sera were used in a Western blot (Figure 26B).

These experiments show that cp6735 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 27

The following *C.pneumoniae* protein (PID 4376784) was expressed <SEQ ID 53; cp6784>:

1 **MNRRKARWVV ALFAMTALIS VGCCPWSQA**K SRCSIDKYIP VVNRLLEVCG
51 LPEAENVEDL IESSSAWVLT PEERFSGELV SICQVKDEHA FYNDLSLLHM
101 TQAVPSYSAT YDCAVVFGGP LPALRQRLDF LVREWQRGVR FKKIVFLCGE
151 RGRYQSIEEQ EHFFDSRYNP FPTEENWESG NRVTPSSEEE IAKFVWMQML

```
201  LPRAWRDSTS GVRVTFLLAK PEENRVVANR KDTLLLFRSY QEAFPGRVLF
251  VSSQPFIGLD ACRVGQFFKG ESYDLAGPGF AQGVLKYHWA PRICLHTLAE
301  WLKETNGCLN ISEGCFG*
```

A predicted signal peptide is highlighted.

The cp6784 nucleotide sequence <SEQ ID 54> is:

```
  1  ATGAATAGAA GAAAAGCAAG ATGGGTAGTG GCATTGTTCG CAATGACGGC
 51  GCTCATTTCT GTTGGGTGTT GTCCTTGGTC ACAAGCGAAA TCAAGATGTT
101  CTATTGATAA GTATATTCCT GTAGTCAATC GTTTACTAGA AGTTTGTGGA
151  CTTCCTGAAG CTGAGAATGT TGAGGATTTA ATCGAGTCCT CGTCTGCTTG
201  GGTACTGACT CCTGAAGAAC GTTTTTCTGG AGAGTTAGTC TCTATCTGTC
251  AGGTTAAAGA TGAGCATGCT TTCTATAACG ATTTGTCTTT ATTACATATG
301  ACTCAGGCTG TGCCTTCGTA TTCTGCAACG TATGATTGTG CTGTAGTTTT
351  TGGCGGGCCT TTGCCAGCGC TACGTCAGCG CTTAGATTTT TTGGTGCGAG
401  AGTGGCAGCG TGGCGTGCGC TTTAAGAAAA TCGTTTTTCT ATGTGGAGAG
451  CGAGGGCGCT ATCAGTCTAT TGAAGAACAA GAGCATTTCT TTGATTCTCG
501  GTACAATCCT TTCCCTACTG AAGAGAACTG GGAATCTGGT AACCGAGTTA
551  CTCCCTCTTC TGAAGAAGAG ATTGCCAAAT TTGTTTGGAT GCAAATGCTT
601  TTACCTAGAG CATGGCGAGA TAGTACTTCA GGAGTCAGAG TGACATTTCT
651  TCTAGCAAAG CCAGAGGAAA ATCGTGTGGT TGCGAATCGT AAGGACACCT
701  TACTTTTATT CCGTTCTTAT CAAGAAGCGT TTCCGGGACG CGTGTTATTT
751  GTAAGTAGTC AACCCTTTAT CGGTTTAGAT GCTTGCAGGG TCGGGCAGTT
801  TTTCAAAGGG GAAAGCTATG ATCTTGCTGG ACCTGGATTT GCTCAAGGAG
851  TCTTGAAGTA TCATTGGGCT CCAAGGATTT GTCTACATAC TTTAGCGGAA
901  TGGTTAAAGG AAACGAACGG CTGCTTAAAT ATTTCAGAGG GTTGTTTTGG
951  ATGA
```

The PSORT algorithm predicts a periplasmic location (0.894).

The protein was expressed in *E.coli* and purified as a his-tag product and as a GST-fusion product, as shown in Figure 27A. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 27B). The GST-fusion product was used for FACS analysis (Figure 27C).

The cp6784 protein was also identified in the 2D-PAGE experiment (Cpn0498).

These experiments show that cp6784 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 28

The following *C.pneumoniae* protein (PID 4376960) was expressed <SEQ ID 55; cp6960>:

```
  1  MNRRWNLVLA TVALALSVAS CDVRSKDKDK DQGSLVEYKD NKDTNDIELS
 51  DNQKLSRTFG HLLARQLRKS EDMFFDIAEV AKGLQAELVC KSAPLTETEY
101  EEKMAEVQKL VFEKKSKENL SLAEKFLKEN SKNAGVVEVQ PSKLQYKIIK
151  EGAGKAISGK PSALLHYKGS FINGQVFSSS EGNNEPILLP LGQTIPGFAL
201  GMQGMKEGET RVLYIHPDLA YGTAGQLPPN SLLIFEINLI QASADEVAAV
251  PQEGNQGE*
```

A predicted signal peptide is highlighted.

The cp6960 nucleotide sequence <SEQ ID 56> is:

```
  1  ATGAACAGAC GGTGGAATTT AGTTTTAGCA ACAGTAGCTC TGGCACTCTC
 51  CGTCGCTTCT TGTGACGTAC GGTCTAAGGA TAAAGACAAG GATCAGGGGT
101  CGTTAGTGGA ATATAAAGAT AACAAAGATA CCAATGACAT AGAATTATCC
151  GATAATCAAA AGTTATCCAG AACATTTGGT CATTTATTAG CACGCCAATT
201  ACGCAAGTCA GAAGATATGT TTTTTGATAT TGCAGAAGTG GCTAAGGGGT
251  TGCAGGCGGA ATTGGTTTGT AAAAGTGCTC CTTTAACAGA AACAGAGTAT
301  GAAGAAAAAA TGGCTGAAGT ACAGAAGTTG GTTTTTGAAA AAAAATCAAA
351  AGAAAATCTT TCATTGGCAG AAAAATTCTT AAAAGAAAAT AGCAAGAACG
401  CTGGTGTTGT TGAAGTGCAA CCAAGTAAAT TGCAATACAA AATTATTAAA
```

```
451  GAAGGTGCAG GGAAAGCAAT TTCAGGTAAA CCTTCAGCTC TATTGCACTA
501  CAAGGGTTCC TTCATCAATG GCCAAGTATT TAGCAGTTCA GAAGGCAACA
551  ATGAGCCTAT CTTGCTTCCT CTAGGCCAAA CAATTCCTGG TTTTGCTTTA
601  GGTATGCAGG GCATGAAAGA AGGAGAAACT CGAGTTCTCT ACATCCATCC
651  TGATCTTGCT TACGGAACCG CAGGACAACT TCCTCCAAAC TCTTTATTAA
701  TTTTTGAAAT TAACTTGATT CAGGCTTCAG CAGATGAAGT TGCTGCTGTA
751  CCCCAAGAAG GAAATCAAGG TGAATGA
```

The PSORT algorithm predicts periplasmic space location (0.930).

The protein was expressed in *E.coli* and purified as a his-tag product and as a GST-fusion product, as shown in Figure 28A. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 28B) and for FACS analysis (Figure 28C).

The cp6960 protein was also identified in the 2D-PAGE experiment.

These experiments show that cp6960 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 29

The following *C.pneumoniae* protein (PID 4376968) was expressed <SEQ ID 57; cp6968>:

1 **MKFLLYVPLL LVLVSTG**CDA KPVSFEPFSG KLSTQRFEPQ HSAEEYFSQG
51 QEFLKKGNFR KALLCFGIIT HHFPRDILRN QAQYLIGVCY FTQDHPDLAD
101 KAFASYLQLP DAEYSEELFQ MKYAIAQRFA QGKRKRICRL EGFPKLMNAD
151 EDALRIYDEI LTAFPSKDLG AQALYSKAAL LIVKNDLTEA TKTLKKLTLQ
201 FPLHILSSEA FVRLSEIYLQ QAKKEPHNLQ YLHFAKLNEE AMKKQHPNHP
251 LNEVVSANVG AMREHYARGL YATGRFYEKK KKAEAANIYY RTAITNYPDT
301 LLVAKCQKRL DRISKHTS*

A predicted signal peptide is highlighted.

The cp6968 nucleotide sequence <SEQ ID 58> is:

```
  1  ATGAAATTTC TATTATACGT TCCACTTCTT CTTGTTCTCG TATCTACGGG
 51  GTGCGATGCA AAACCTGTTT CTTTTGAGCC CTTTTCAGGA AAGCTTTCCA
101  CCCAGCGTTT TGAGCCTCAG CACTCTGCTG AAGAATATTT TTCTCAGGGA
151  CAGGAATTCT TAAAAAAAGG AAATTTCAGA AAAGCTTTAC TATGCTTTGG
201  AATCATTACG CATCACTTCC CTAGGGACAT CTTGCGTAAT CAAGCACAGT
251  ATCTTATAGG AGTCTGTTAC TTCACGCAGG ATCACCCAGA TTTAGCAGAC
301  AAGGCATTTG CATCTTACTT ACAACTTCCT GATGCGGAGT ACTCTGAAGA
351  GTTGTTCCAG ATGAAATATG CGATTGCTCA AAGATTTGCT CAAGGCAAGC
401  GTAAACGGAT TTGTCGATTA GAGGGCTTCC CAAAACTAAT GAATGCTGAT
451  GAAGATGCGC TACGCATTTA TGACGAGATT CTAACAGCGT TTCCTAGTAA
501  AGACTTAGGA GCTCAGGCCC TCTATAGTAA AGCTGCGTTA CTTATTGTAA
551  AAAACGATCT TACAGAAGCC ACCAAAACCT TAAAAAAACT CACGTTACAA
601  TTTCCTCTAC ATATTTTATC TTCAGAGGCC TTTGTACGTT TATCGGAAAT
651  CTATTTACAG CAAGCTAAGA AAGAGCCTCA CAATCTTCAA TATCTTCATT
701  TTGCAAAGCT TAATGAAGAG GCAATGAAAA AGCAGCATCC TAACCATCCT
751  CTGAATGAGG TTGTTTCTGC TAATGTTGGA GCTATGCGGG AACATTATGC
801  TCGAGGTTTG TATGCCACAG GTCGTTTCTA TGAGAAGAAG AAAAAAGCCG
851  AGGCTGCGAA TATCTATTAC CGCACTGCGA TTACAAACTA CCCAGACACT
901  TTATTAGTGG CTAAATGTCA AAAGCGTCTA GATAGAATAT CTAAGCATAC
951  TTCCTAA
```

The PSORT algorithm predicts an inner membrane location (0.790).

The protein was expressed in *E.coli* and purified as a his-tag product and as a GST-fusion product, as shown in Figure 29A. The recombinant GST-fusion was used to immunise mice, whose sera were used in a Western blot (Figure 29B) and for FACS analysis (Figure 29C).

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6968 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 30

The following *C.pneumoniae* protein (PID 4376998) was expressed <SEQ ID 59; cp6998>:

```
  1  MKKLLKSALL SAAFAGSVGS LQALPVGNPS DPSLLIDGTI WEGAAGDPCD
 51  PCATWCDAIS LRAGFYGDYV FDRILKVDAP KTFSMGAKPT GSAAANYTTA
101  VDRPNPAYNK HLHDAEWFTN AGFIALNIWD RFDVFCTLGA SNGYIRGNST
151  AFNLVGLFGV KGTTVNANEL PNVSLSNGVV ELYTDTSFSW SVGARGALWE
201  CGCATLGAEF QYAQSKPKVE ELNVICNVSQ FSVNKPKGYK GVAFPLPTDA
251  GVATATGTKS ATINYHEWQV GASLSYRLNS LVPYIGVQWS RATFDADNIR
301  IAQPKLPTAV LNLTAWNPSL LGNATALSTT DSFSDFMQIV SCQINKFKSR
351  KACGVTVGAT LVDADKWSLT AEARLINERA AHVSGQFRF*
```

A predicted signal peptide is highlighted.

The cp6998 nucleotide sequence <SEQ ID 60> is:

```
   1  ATGAAAAAAC TCTTAAAGTC GGCGTTATTA TCCGCCGCAT TTGCTGGTTC
  51  TGTTGGCTCC TTACAAGCCT TGCCTGTAGG GAACCCTTCT GATCCAAGCT
 101  TATTAATTGA TGGTACAATA TGGGAAGGTG CTGCAGGAGA TCCTTGCGAT
 151  CCTTGCGCTA CTTGGTGCGA CGCTATTAGC TTACGTGCTG GATTTTACGG
 201  AGACTATGTT TTCGACCGTA TCTTAAAAGT AGATGCACCT AAAACATTTT
 251  CTATGGGAGC CAAGCCTACT GGATCCGCTG CTGCAAACTA TACTACTGCC
 301  GTAGATAGAC CTAACCCGGC CTACAATAAG CATTTACACG ATGCAGAGTG
 351  GTTCACTAAT GCAGGCTTCA TTGCCTTAAA CATTTGGGAT CGCTTTGATG
 401  TTTTCTGTAC TTTAGGAGCT TCTAATGGTT ACATTAGAGG AAACTCTACA
 451  GCGTTCAATC TCGTTGGTTT ATTCGGAGTT AAAGGTACTA CTGTAAATGC
 501  AAATGAACTA CCAAACGTTT CTTTAAGTAA CGGAGTTGTT GAACTTTACA
 551  CAGACACCTC TTTCTCTTGG AGCGTAGGCG CTCGTGGAGC CTTATGGGAA
 601  TGCGGTTGTG CAACTTTGGG AGCTGAATTC CAATATGCAC AGTCCAAACC
 651  TAAAGTTGAA GAACTTAATG TGATCTGTAA CGTATCGCAA TTCTCTGTAA
 701  ACAAACCCAA GGGCTATAAA GGCGTTGCTT TCCCCTTGCC AACAGACGCT
 751  GGCGTAGCAA CAGCTACTGG AACAAAGTCT GCGACCATCA ATTATCATGA
 801  ATGGCAAGTA GGAGCCTCTC TATCTTACAG ACTAAACTCT TTAGTGCCAT
 851  ACATTGGAGT ACAATGGTCT CGAGCAACTT TTGATGCTGA TAACATCCGC
 901  ATTGCTCAGC CAAAACTACC TACAGCTGTT TTAAACTTAA CTGCATGGAA
 951  CCCTTCTTTA CTAGGAAATG CCACAGCATT GTCTACTACT GATTCGTTCT
1001  CAGACTTCAT GCAAATTGTT TCCTGTCAGA TCAACAAGTT TAAATCTAGA
1051  AAAGCTTGTG GAGTTACTGT AGGAGCTACT TTAGTTGATG CTGATAAATG
1101  GTCACTTACT GCAGAAGCTC GTTTAATTAA CGAGAGAGCT GCTCACGTAT
1151  CTGGTCAGTT CAGATTCTAA
```

The PSORT algorithm predicts an outer membrane location (0.707).

The protein was expressed in *E.coli* and purified as a GST-fusion (Figure 30A) and as a his-tag product. The recombinant GST-fusion protein was used to immunise mice, whose sera were used in a Western blot (Figure 30B) and for FACS analysis (Figure 30C).

The cp6998 protein was also identified in the 2D-PAGE experiment (Cpn0695) and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6998 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 31

The following *C.pneumoniae* protein (PID 4377102) was expressed <SEQ ID 61; cp7102>:

```
  1  MKHTFTKRVL FFFFLVIPIP LLLNLMVVGF FSFSAAKANL VQVLHTRATN
 51  LSIEFEKKLT IHKLFLDRLA NTLALKSYAS PSAEPYAQAY NEMMALSNTD
101  FSLCLIDPFD GSVRTKNPGD PFIRYLKQHP EMKKKLSAAV GKAFLLTIPG
151  KPLLHYLILV EDVASWDSTT TSGLLVSFYP MSFLQKDLFQ SLHITKGNIC
201  LVNKYGEVLF CAQDSESSFV FSLDLPNLPQ FQARSPSAIE IEKASGILGG
251  ENLITVSINK KRYLGLVLNK IPIQGTYTLS LVPVSDLIQS ALKVPLNICF
301  FYVLAFLLMW WIFSKINTKL NKPLQELTFC MEAAWRGNHN VRFEPQPYGY
351  EFNELGNIFN CTLLLLLNSI EKADIDYHSG EKLQKELGIL SSLQSALLSP
401  DFPTFPKVTF SSQHLRRRQL SGHFNGWTVQ DGGDTLLGII GLAGDIGLPS
451  YLYALSARSL FLAYASSDVS LQKISKDTAD SFSKTTEGNE AVVAMTFIKY
501  VEKDRSLELL SLSEGAPTMF LQRGESFVRL PLETHQALQP GDRLICLTGG
551  EDILKYFSQL PIEELLKDPL NPLNTENLID SLTMMLNNET EHSADGTLTI
601  LSFS*
```

A predicted signal peptide is highlighted.

The cp7102 nucleotide sequence <SEQ ID 62> is:

```
   1  ATGAAACATA CCTTTACCAA GCGTGTTCTA TTTTTTTTCT TTTTAGTGAT
  51  TCCCATTCCC CTACTCCTCA ATCTTATGGT CGTAGGTTTT TTCTCATTTT
 101  CTGCCGCTAA AGCAAATTTA GTACAGGTCC TCCATACCCG TGCTACGAAC
 151  TTAAGTATAG AATTCGAAAA AAAACTGACG ATACACAAGC TTTTCCTCGA
 201  TAGACTTGCC AACACATTAG CCTTAAAATC CTATGCATCT CCTTCTGCAG
 251  AGCCCTATGC ACAGGCATAC AATGAGATGA TGGCACTCTC CAATACAGAC
 301  TTTTCCTTAT GCCTTATAGA TCCCTTTGAT GGATCTGTAA GGACGAAAAA
 351  TCCTGGAGAC CCTTTCATTC GCTATCTAAA ACAGCATCCT GAAATGAAGA
 401  AAAAGCTATC CGCAGCTGTA GGGAAAGCCT TTTTATTGAC CATTCCAGGT
 451  AAACCACTTT TACATTATCT TATTCTAGTT GAAGATGTCG CATCTTGGGA
 501  TTCTACAACG ACTTCAGGAC TGCTTGTAAG TTTCTATCCC ATGTCTTTTT
 551  TACAGAAAGA TTTATTCCAA TCCTTACACA TCACCAAAGG AAATATCTGC
 601  CTTGTAAATA AGTATGGCGA GGTCCTCTTC TGTGCTCAGG ACAGTGAATC
 651  TTCTTTTGTA TTTTCTCTAG ATCTCCCTAA TTTACCGCAA TTCCAAGCAA
 701  GAAGCCCCTC TGCCATAGAA ATTGAGAAAG CTTCTGGAAT TCTTGGTGGG
 751  GAGAACCTAA TCACAGTGAG TATCAACAAG AAACGCTACC TAGGATTGGT
 801  ACTGAATAAA ATTCCTATCC AAGGGACCTA CACTCTATCT TTAGTTCCAG
 851  TTTCTGATCT CATCCAATCC GCCTTGAAAG TTCCTCTCAA TATTTGTTTT
 901  TTCTATGTAC TTGCTTTCCT CCTCATGTGG TGGATTTTCT CTAAGATCAA
 951  CACCAAACTT AACAAGCCTC TTCAAGAACT GACCTTCTGT ATGGAAGCTG
1001  CCTGGCGAGG AAACCATAAC GTGAGGTTTG AACCCCAGCC TTACGGTTAT
1051  GAATTCAATG AACTAGGAAA TATTTTCAAT TGCACTCTCC TACTCTTATT
1101  GAATTCCATT GAGAAAGCAG ATATCGATTA CCATTCAGGC GAAAAATTAC
1151  AAAAAGAATT AGGGATTTTA TCTTCACTAC AAAGTGCGTT ACTAAGTCCG
1201  GATTTCCCTA CGTTCCCTAA AGTTACCTTT AGTTCCCAAC ATCTCCGGAG
1251  AAGGCAACTT TCCGGTCATT TTAATGGTTG GACAGTTCAA GATGGTGGCG
1301  ATACCCTTTT AGGGATCATA GGGCTCGCTG GCGATATTGG TCTTCCTTCC
1351  TATCTCTATG CTTTATCCGC ACGGAGTCTT TTTCTTGCCT ATGCTTCCTC
1401  GGACGTTTCG TTACAAAAAA TCAGCAAGGA TACTGCCGAC AGCTTCTCAA
1451  AAACAACAGA AGGCAATGAG GCTGTAGTTG CTATGACTTT CATTAAATAT
1501  GTAGAAAAAG ATCGATCTCT AGAGCTCCTC TCGTTAAGCG AGGGAGCTCC
1551  TACCATGTTT CTACAACGAG GAGAATCTTT CGTACGTCTC CCCTTAGAGA
1601  CTCACCAAGC TCTACAGCCT GGAGATCGGT TGATCTGCCT CACTGGAGGA
1651  GAAGACATCC TCAAGTACTT TTCTCAGCTT CCTATTGAAG AGCTCTTAAA
1701  AGATCCTTTA AACCCTCTAA ATACAGAGAA TCTTATTGAT TCTCTAACCA
1751  TGATGTTAAA CAACGAAACC GAACATTCTG CAGATGGAAC TCTGACCATC
1801  CTTTCATTTT CATAA
```

The PSORT algorithm predicts an inner membrane location (0.338).

The protein was expressed in *E.coli* and purified as a his-tag product and as a GST-fusion product. The purified GST-fusion product is shown in Figure 31A. The recombinant GST-fusion protein was used to immunise mice, whose sera were used in a Western blot and for FACS analysis (Figure 31B).

These experiments show that cp7102 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 32

The following *C.pneumoniae* protein (PID 4377106) was expressed <SEQ ID 63; cp7106>:

```
  1 MKDLGTLGGT SSTAKTVSPD GKVIMGRSQI ADGSWHAFMC HTDFSSNNVL
 51 FDLDNTYKTL RENGRQLNSI FNLQNMMLQR ASDHEFTEFG RSNIALGAGL
101 YVNALQNLPS NLAAQYFGIA YKIRPKYRLG VFLDHNFSSH VPNNFNVSHN
151 RLWMGAFIGW QDSDALGSSV KVSFGYGKQK ATITREQLEN TEAGSGESHF
201 EGVAAQIEGR YGKSLGGHVR VQPFLGLQFV HITRKEYTEN AVQFPVHYDP
251 IDYSTGVVYL GIGSHIALVD SLHVGTRMGM EQNFAAHTDR FSGSIASIGN
301 FVFEKLDVTH TRAFAEMRVN YELPYLQSLN LILRVNQQPL QGVMGFSSDL
351 RYALGF*
```

The cp7106 nucleotide sequence <SEQ ID 64> is:

```
   1 ATGAAAGATT TGGGGACTCT TGGGGGTACC TCTTCTACAG CAAAAACAGT
  51 GTCCCCAGAT GGTAAAGTGA TCATGGGTAG ATCACAAATT GCTGATGGCA
 101 GTTGGCACGC ATTTATGTGT CATACGGATT TCTCCTCTAA TAATGTACTC
 151 TTTGATCTCG ATAATACGTA TAAAACTCTA AGAGAAAATG GCCGTCAGCT
 201 AAATTCCATA TTCAACCTAC AAAATATGAT GTTACAGAGA GCCTCAGATC
 251 ATGAGTTCAC AGAGTTTGGA AGGAGTAACA TCGCTCTTGG TGCCGGGCTT
 301 TATGTGAATG CCTTGCAGAA TCTCCCTAGC AATTTAGCAG CACAATATTT
 351 TGGAATCGCA TACAAAATAC GTCCTAAATA TCGTTTGGGG GTGTTTTTGG
 401 ACCATAATTT CAGCTCCCAC GTTCCTAATA ATTTTAACGT AAGCCACAAT
 451 AGACTCTGGA TGGGAGCCTT TATTGGATGG CAGGATTCTG ATGCTCTAGG
 501 ATCTAGTGTC AAGGTGTCTT TCGGATATGG AAAACAAAAA GCCACGATTA
 551 CAAGAGAGCA ATTAGAGAAT ACAGAAGCCG GGAGTGGGGA GAGCCATTTT
 601 GAAGGGGTCG CTGCTCAGAT AGAAGGGCGG TATGGTAAGA GCCTCGGAGG
 651 ACATGTCAGG GTCCAGCCTT TCCTAGGACT GCAGTTTGTC CACATTACAA
 701 GGAAAGAATA TACCGAAAAT GCAGTGCAAT TTCCTGTACA CTATGATCCT
 751 ATAGACTATT CTACAGGTGT AGTGTATTTA GGAATTGGAT CTCATATTGC
 801 ACTTGTAGAT TCTTTACATG TAGGCACACG CATGGGAATG GAGCAAAACT
 851 TTGCAGCCCA TACGGACAGG TTCTCAGGAT CTATAGCGTC TATTGGAAAC
 901 TTTGTGTTTG AAAAGCTTGA TGTGACTCAC ACAAGGGCAT TTGCGGAAAT
 951 GCGTGTCAAC TATGAGCTTC CCTATCTACA GTCTCTGAAT CTTATTCTAC
1001 GAGTTAATCA ACAGCCTCTA CAAGGGGTTA TGGGATTTTC CAGTGATCTT
1051 AGGTATGCCT TAGGATTCTA A
```

The PSORT algorithm predicts a cytoplasmic location (0.224).

The protein was expressed in *E.coli* and purified as a his-tag product and as a GST-fusion product. The purified GST-fusion product is shown in Figure 32A. The recombinant GST-fusion protein was used to immunise mice, whose sera were used in a Western blot (Figure 32B) and for FACS analysis (Figure 32C).

This protein also showed very good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp7106 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 33

The following *C.pneumoniae* protein (PID 4377228) was expressed <SEQ ID 65; cp7228>:

```
  1 MTAVLILTSF PSEESARSLA RHLITERLAS CVHVFPKGTS TYLWEGKLCE
 51 SEEHHIQIKS IDIRFSEICL AIQEFSGYEV PEVLLFPIEN GDPRYLNWLT
101 ILSYPEKPPL SD*
```

The cp7228 nucleotide sequence <SEQ ID 66> is:

```
   1  ATGACTGCTG TTCTTATTCT TACATCTTTC CCTTCGGAGG AAAGTGCTCG
  51  CTCCTTAGCT AGACATCTGA TTACAGAGCG TCTTGCTTCC TGTGTGCATG
 101  TATTCCCTAA AGGCACATCG ACATATCTAT GGGAAGGCAA GCTATGTGAG
 151  TCTGAAGAAC ATCATATACA AATCAAATCG ATAGACATAC GCTTCTCGGA
 201  AATTTGTCTT GCTATTCAGG AGTTCTCTGG CTATGAGGTT CCTGAAGTCT
 251  TACTATTTCC TATTGAAAAT GGGGATCCGA GGTACTTGAA TTGGTTAACG
 301  ATTCTCAGCT ATCCAGAGAA GCCTCCGCTT TCAGATTAG
```

The PSORT algorithm predicts an inner membrane location (0.040).

The protein was expressed in *E.coli* and purified as a his-tag product and as a GST-fusion product, as shown in Figure 33A (his-tag = left-hand arrow, GST = right-hand arrow). The proteins were used to immunise mice, whose sera were used in a Western blot (Figure 33B) and FACS analysis.

These experiments show that cp7228 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 34

The following *C.pneumoniae* protein (`PID 4377170`) was expressed <SEQ ID 67; cp7170>:

```
   1  MNSKMLKHLR LATLSFSMFF GIVSSPAVYA LGAGNPAAPV LPGVNPEQTG
  51  WCAFQLCNSY DLFAALAGSL KFGFYGDYVF SESAHITNVP VITSVTTSGT
 101  GTTPTITSTT KNVDFDLNNS SISSSCVFAT IALQETSPAA IPLLDIAFTA
 151  RVGGLKQYYR LPLNAYRDFT SNPLNAESEV TDGLIEVQSD YGIVWGLSLQ
 201  KVLWKDGVSF VGVSADYRHG SSPINYIIVY NKANPEIYFD ATDGNLSYKE
 251  WSASIGISTY LNDYVLPYAS VSIGNTSRKA PSDSFTELEK QFTNFKFKIR
 301  KITNFDRVNF CFGTTCCISN NFYYSVEGRW GYQRAINITS GLQF*
```

A predicted signal peptide is highlighted.

The cp7170 nucleotide sequence <SEQ ID 68> is:

```
   1  ATGAATAGCA AGATGCTAAA ACATTTACGT TTAGCAACCC TTTCCTTCTC
  51  TATGTTCTTC GGGATTGTAT CTTCTCCCGC AGTATATGCC CTAGGGGCTG
 101  GAAACCCTGC AGCTCCAGTA CTCCCAGGTG TGAATCCTGA GCAAACGGGA
 151  TGGTGTGCCT TCCAACTTTG TAATAGTTAC GATCTTTTTG CTGCTCTTGC
 201  AGGAAGCCTC AAATTTGGGT TCTATGGAGA TTATGTCTTC TCAGAAAGTG
 251  CCCATATTAC CAATGTCCCT GTCATTACCT CCGTTACGAC TTCAGGCACA
 301  GGAACAACGC CAACCATTAC CTCTACAACT AAAAACGTAG ACTTTGATCT
 351  TAACAACAGC TCCATCAGCT CGAGCTGTGT TTTTGCAACC ATAGCTCTAC
 401  AGGAAACATC CCCAGCTGCC ATTCCCCTTT TAGATATAGC CTTCACTGCA
 451  CGTGTCGGAG GACTTAAGCA GTACTACCGC CTCCCTCTCA ATGCTTACAG
 501  AGACTTCACT TCAAATCCTT TAAATGCAGA ATCTGAAGTT ACAGATGGTC
 551  TCATTGAAGT CCAGTCAGAC TATGGAATTG TCTGGGGTCT GAGTTTACAA
 601  AAAGTATTGT GGAAAGATGG AGTGTCTTTT GTAGGGGTGA GCGCTGACTA
 651  CCGTCACGGT TCCAGTCCCA TCAACTATAT CATCGTTTAC AACAAGGCCA
 701  ACCCCGAGAT CTATTTCGAT GCTACTGATG GAAACCTAAG CTATAAAGAA
 751  TGGTCTGCAA GCATCGGCAT CTCTACGTAT CTTAATGACT ATGTGCTTCC
 801  CTATGCATCC GTATCTATAG GAAATACTTC AAGAAAAGCT CCTTCTGATA
 851  GCTTCACAGA ACTCGAAAAG CAATTTACGA ATTTTAAATT TAAAATTCGT
 901  AAAATCACAA ACTTCGACAG AGTAAACTTC TGCTTCGGAA CTACCTGCTG
 951  CATCTCAAAT AACTTCTACT ATAGTGTAGA AGGCCGTTGG GGATATCAGC
1001  GTGCTATCAA CATTACGTCA GGTCTGCAGT TTTAG
```

The PSORT algorithm predicts a bacterial outer membrane location (0.936).

The protein was expressed in *E.coli* and purified as a his-tag product and as a GST-fusion product. The purified GST-fusion product is shown in Figure 34A. The GST-fusion protein was used to immunise mice, whose sera were used in a Western blot (34B) and for FACS analysis (34C).

The cp7170 protein was also identified in the 2D-PAGE experiment (Cpn0854).

These experiments show that cp7170 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 35

The following *C.pneumoniae* protein (`PID 4377072`) was expressed <SEQ ID 69; cp7072>:

```
  1  MDIKKLFCLF LCSSLIAMSP IYGKTGDYEK LTLTGINIID RNGLSETICS
 51  KEKLKKYTKV DFLAPQPYQK VMRMYKNKRG DNVSCLTAYH TNGQIKQYLE
101  CLNNRAYGRY REWHVNGNIK IQAEVIGGIA DLHPSAESGW LFDQTTFAYN
151  DEGILEAAIV YEKGLLEGSS VYYHTNGNIW KECPYHKGVP QGKFLTYTSS
201  GKLLKEQNYQ QGKRHGLSIR YSEDSEEDVL AWEEYHEGRL LKAEYLDPQT
251  HEIYATIHEG NGIQAIYGKY AVIETRAFYR GEPYGKVTRF DNSGTQIVQT
301  YNLLQGAKHG EEFFFYPETG KPKLLLNWHE GILNGIVKTW YPGGTLESCK
351  ELVNNKKSGL LTIYYPEGQI MATEEYDNDL LIKGEYFRPG DRHPYSKIDR
401  GCGTAVFFSS AGTITKKIPY QDGKPLLN*
```

A predicted signal peptide is highlighted.

The cp7072 nucleotide sequence <SEQ ID 70> is:

```
   1  ATGGATATAA AAAAACTCTT TTGCTTATTT CTATGTTCTT CTCTAATTGC
  51  CATGAGTCCC ATTTATGGGA AAACAGGTGA CTATGAGAAA CTCACCCTTA
 101  CAGGGATCAA TATCATTGAT AGAAACGGCC TGTCAGAAAC TATTTGCTCT
 151  AAAGAGAAGC TAAAGAAATA CACCAAGGTA GACTTTCTTG CTCCCCAGCC
 201  CTATCAAAAG GTCATGAGGA TGTATAAAAA CAAACGCGGA GATAACGTTT
 251  CTTGTTTAAC AGCCTATCAC ACTAACGGGC AAATTAAGCA GTACCTGGAG
 301  TGTCTCAATA ATCGTGCTTA TGGAAGATAT CGTGAATGGC ACGTCAACGG
 351  GAATATCAAA ATCCAAGCTG AGGTTATCGG AGGTATTGCG GATCTTCATC
 401  CCTCAGCAGA GTCTGGCTGG CTATTTGATC AAACTACATT TGCCTATAAT
 451  GATGAAGGTA TCTTAGAAGC CGCTATCGTC TATGAAAAAG GGCTGCTCGA
 501  AGGATCTTCG GTGTATTACC ATACTAATGG GAATATTTGG AAAGAGTGTC
 551  CCTATCATAA GGGAGTTCCT CAAGGTAAAT TCCTGACATA CACATCTTCG
 601  GGGAAACTGC TCAAAGAACA GAATTACCAA CAAGGCAAAA GACACGGTCT
 651  TTCGATTCGC TACAGCGAAG ATTCCGAAGA AGATGTTTTA GCCTGGGAAG
 701  AATATCATGA GGGACGACTC CTAAAAGCAG AGTACTTAGA TCCTCAAACT
 751  CACGAAATCT ATGCGACTAT ACACGAAGGG AACGGCATTC AAGCAATCTA
 801  CGGCAAGTAT GCCGTTATAG AAACTAGGGC ATTTTACCGA GGGGAACCTT
 851  ATGGAAAAGT TACCAGATTC GACAACTCCG GAACACAGAT TGTCCAAACG
 901  TATAACCTTT TGCAAGGCGC GAAGCACGGA GAAGAATTTT TCTTTTATCC
 951  TGAGACAGGG AAACCCAAGC TGCTTCTTAA TTGGCATGAA GGAATTTTAA
1001  ATGGGATAGT AAAAACTTGG TATCCCGGAG GAACCTTAGA AAGTTGTAAA
1051  GAACTCGTAA ATAACAAAAA ATCCGGGTTA CTGACCATTT ACTACCCTGA
1101  AGGACAGATC ATGGCGACCG AAGAGTATGA TAATGATCTT CTAATTAAAG
1151  GAGAGTACTT CCGCCCTGGA GACCGTCATC CCTACTCTAA AATAGATCGT
1201  GGTTGTGGGA CTGCAGTATT TTTCTCGTCG GCGGGAACTA TTACTAAAAA
1251  AATCCCCTAT CAGGACGGCA AACCTTTGCT CAACTAG
```

The PSORT algorithm predicts a periplasmic location (0.688).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 35A) and as a GST-fusion product (Figure35B). The recombinant his-tag protein was used to immunise mi ce, whose sera were used in a Western blot (Figure 35C) and for FACS analysis.

These experiments show that cp7072 is a useful immunogen. These properties are not evident from the sequence alone.

Example 36

The following *C.pneumoniae* protein (`PID 4376879`) was expressed <SEQ ID 71; cp6879>:

```
  1  MATPAQKSPT FQDPSFVREL GSNHPVFSPL TLEERGEMAI ARVQQCGWNH
 51  TIVKVSLIIL ALLTILGGGL LVGLLPAVPM FIGTGLIALG AVIFALALIL
101  CLYDSQGLPE ELPPVPEPQQ IQIEDLRNET REVLEGTLLE VLLKDRDAKD
151  PAVPQVVVDC EKRLGMLDRK LRREEEILYR STAHLKDEER YEFLLELLEM
201  RSLVADRLEF NRRSYERFVQ GIMTVRSEEG EKEISRLQDL ISLQQQTVQD
251  LRSRIDDEQK RCWTALQRIN QSQKDIQRAH DREASQRACE GTEMDCAERQ
301  QLEKDLRRQL KSMQEWIEMR GTIHQQEKAW RKQNAKLERL QEDLRLTGIA
351  FDEQSLFYRE YKEKYLSQKL DMQKILQEVN AEKSEKACLE SLVHDYEKQL
401  EQKDANLKKA AAVWEEELGK QQQEDYEQTQ EIRRLSTFIL EYQDSLREAE
451  KVEKDFQELQ QRYSRLQEEK QVKEKILEES MNHFADLFEK AQKENMAYKK
501  KLADLEGAAA PTEIGEDDDW VLTDSASLSQ KKIRELVEEN QELLKALAFK
551  SNELTQLVAD AVEAEKEISK LREHIEEQKE GLRALDKMHA QAIKDCEAAQ
601  RKCCDLESLL SPVREDAGMR FELEVELQRL QEENAQLRAE VERLEQEQFQ
651  G*
```

The cp6879 nucleotide sequence <SEQ ID 72> is:

```
   1  ATGGCAACAC CCGCTCAAAA ATCCCCTACA TTTCAAGATC CTAGTTTTGT
  51  AAGAGAGCTA GGCAGTAACC ACCCTGTCTT TTCCCCGCTA ACGCTTGAGG
 101  AAAGAGGGGA GATGGCAATA GCTCGAGTCC AGCAGTGTGG ATGGAATCAT
 151  ACAATTGTTA AGGTAAGTCT TATTATTCTT GCTCTTCTTA CTATTTTAGG
 201  GGGAGGATTA CTCGTAGGAT TGCTGCCAGC AGTTCCTATG TTTATTGGAA
 251  CAGGTCTGAT TGCTTTGGGA GCCGTTATAT TTGCTTTGGC TTTGATTTTA
 301  TGTCTTTATG ATTCTCAGGG CCTTCCTGAG GAACTCCCTC CGGTTCCTGA
 351  ACCACAACAA ATTCAGATTG AAGATTTAAG AAACGAGACC AGAGAAGTTC
 401  TTGAAGGGAC TCTTTTAGAG GTTCTCTTAA AGGATAGAGA CGCTAAGGAC
 451  CCTGCGGTGC CCCAGGTGGT TGTAGACTGT GAAAAGCGTC TTGGAATGTT
 501  GGATCGTAAG CTGCGACGTG AAGAGGAGAT TCTGTATCGC TCGACGGCCC
 551  ATCTTAAAGA CGAGGAAAGG TATGAGTTCT TGCTGGAGCT CTTGGAAATG
 601  CGTAGTCTGG TTGCCGATCG GCTAGAATTT AACCGTAGAA GTTATGAGCG
 651  ATTTGTTCAA GGAATTATGA CAGTTAGATC AGAGGAGGGG GAAAAAGAGA
 701  TTTCTCGTCT ACAAGATCTA ATCAGTTTGC AGCAGCAGAC GGTGCAAGAT
 751  TTAAGGAGTC GGATCGATGA CGAGCAGAAG AGATGCTGGA CGGCTTTACA
 801  ACGTATTAAC CAATCTCAGA AGGATATACA ACGGGCTCAT GATCGCGAGG
 851  CTTCGCAGCG TGCCTGTGAG GGCACAGAGA TGGATTGTGC AGAACGCCAG
 901  CAACTGGAGA AGGATTTAAG GAGACAGCTG AAATCTATGC AGGAGTGGAT
 951  TGAGATGAGG GGCACAATCC ATCAACAAGA GAAGGCTTGG CGTAAGCAGA
1001  ATGCCAAATT AGAAAGATTA CAAGAGGATC TGAGACTTAC TGGGATTGCT
1051  TTTGACGAAC AATCTCTGTT CTATCGCGAA TATAAAGAGA AATATCTGAG
1101  TCAGAAACTA GATATGCAAA AGATTTTACA GGAAGTCAAC GCAGAGAAAA
1151  GTGAGAAGGC TTGCTTAGAG AGTCTGGTCC ATGACTATGA GAAGCAGCTC
1201  GAACAAAAAG ATGCTAATCT GAAGAAAGCA GCAGCTGTTT GGGAAGAAGA
1251  ATTAGGGAAG CAGCAACAGG AAGACTACGA ACAAACCCAA GAAATTAGAC
1301  GTCTGAGTAC ATTCATTCTT GAGTACCAGG ACAGTCTGCG TGAGGCAGAA
1351  AAAGTTGAGA AAGATTTCCA AGAGCTACAA CAAAGGTATA GCCGTCTTCA
1401  AGAGGAGAAA CAGGTAAAAG AAAAAATCTT AGAAGAAAGT ATGAATCATT
1451  TTGCCGATCT CTTTGAGAAG GCTCAAAAGG AAAACATGGC CTACAAGAAG
1501  AAGTTAGCGG ATTTAGAGGG TGCCGCTGCT CCTACTGAGA TCGGTGAGGA
1551  CGATGACTGG GTACTCACAG ATTCTGCTTC TCTCAGCCAG AAGAAGATCC
1601  GCGAACTCGT GGAAGAGAAT CAAGAACTCC TGAAAGCACT TGCATTTAAA
1651  TCTAACGAAT TGACTCAACT GGTTGCCGAT GCTGTAGAAG CTGAAAAAGA
1701  AATCAGCAAG CTTCGAGAAC ACATAGAAGA GCAGAAAGAA GGATTACGAG
1751  CTCTTGATAA GATGCATGCA CAAGCGATCA AAGATTGCGA AGCTGCTCAG
1801  AGAAAATGCT GTGACCTTGA GAGCCTTCTC TCTCCTGTTC GAGAAGATGC
1851  TGGAATGAGA TTTGAGCTAG AGGTCGAGCT TCAAAGATTG CAAGAAGAAA
1901  ATGCACAGCT TAGAGCGGAG GTTGAAAGAC TAGAGCAAGA GCAATTTCAA
1951  GGATAA
```

The PSORT algorithm predicts an inner membrane location (0.646).

The protein was expressed in *E.coli* and purified as a his-tag product and as a GST-fusion product. The purified GST-fusion product is shown in Figure 36A. The recombinant GST-fusion protein was used to immunise mice, whose sera were used in a Western blot (Figure 36B) and for FACS analysis.

These experiments show that cp6879 is useful immunogen. These properties are not evident from the sequence alone.

Example 37

The following *C.pneumoniae* protein (PID 4376767) was expressed <SEQ ID 73; cp6767>:

```
  1  MIKQIGRFFR AFIFIMPLSL TSCESKIDRN RIWIVGTNAT YPPFEYVDAQ
 51  GEVVGFDIDL AKAISEKLGK QLEVREFAFD ALILNLKKHR IDAILAGMSI
101  TPSRQKEIAL LPYYGDEVQE LMVVSKRSLE TPVLPLTQYS SVAVQTGTFQ
151  EHYLLSQPGI CVRSFDSTLE VIMEVRYGKS PVAVLEPSVG RVVLKDFPNL
201  VATRLELPPE CWVLGCGLGV AKDRPEEIQT IQQAITDLKS EGVIQSLTKK
251  WQLSEVAYE*
```

The cp6767 nucleotide sequence <SEQ ID 74> is:

```
  1  ATGATAAAAC AAATAGGCCG TTTTTTTAGA GCATTTATTT TTATAATGCC
 51  TTTATCTTTA ACAAGTTGTG AGTCTAAAAT CGATCGAAAT CGCATCTGGA
101  TTGTAGGTAC GAATGCTACA TATCCTCCTT TTGAGTATGT GGATGCTCAG
151  GGGGAAGTTG TAGGTTTCGA TATAGATTTG GCAAAGGCAA TTAGTGAAAA
201  ACTTGGCAAG CAATTGGAAG TTAGAGAATT CGCTTTCGAT GCTTTAATTT
251  TAAATTTAAA AAAACATCGT ATCGATGCAA TTTTAGCAGG AATGTCCATT
301  ACTCCTTCGC GTCAGAAGGA AATCGCCCTG CTTCCCTATT ATGGCGATGA
351  GGTTCAAGAG CTGATGGTGG TTTCTAAGCG GTCTTTAGAG ACCCCTGTGC
401  TTCCCCTAAC ACAGTATTCT TCTGTTGCTG TTCAGACAGG AACGTTTCAG
451  GAGCATTATC TTTTATCTCA GCCCGGAATT TGTGTCCGTT CTTTTGATAG
501  CACCTTGGAG GTGATTATGG AAGTTCGTTA TGGGAAATCT CCGGTTGCCG
551  TTCTAGAACC CTCGGTAGGA CGTGTCGTTC TTAAAGACTT CCCTAATCTT
601  GTTGCAACAA GATTAGAGCT CCCTCCTGAA TGTTGGGTGT TGGGCTGTGG
651  TCTCGGCGTA GCTAAAGATC GTCCTGAAGA AATACAAACG ATTCAACAAG
701  CGATTACAGA TTTAAAGAGC GAAGGGGTGA TTCAATCTTT AACCAAGAAA
751  TGGCAACTTT CTGAAGTTGC TTACGAATAG
```

The PSORT algorithm predicts an inner membrane location (0.083).

The protein was expressed in *E.coli* and purified as a his-tag product and as a GST-fusion product. The purified his-tag product is shown in Figure 37A. The recombinant his-tag protein was used to immunise mice, whose sera were used in a Western blot (Figure 37B) and for FACS analysis (Figure 37C). The GST-fusion was also used in a Western blot (Figure 37D).

The cp6767 protein was also identified in the 2D-PAGE experiment and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6767 is a useful immunogen. These properties are not evident from the sequence alone.

Example 38

The following *C.pneumoniae* protein (PID 4376717) was expressed <SEQ ID 75; cp6717>:

```
  1  MMSRLRFRLA ALGIFFILLV PNSVSAKTIV ASDKEKVGVL VYDNSVEAFQ
 51  QILDCIDHAN FYVELCPCMT GGRTLKEMVD HLEARMDLVP ELCSYIIIQP
101  TFTDAEDQKL LKALKERHPN RFFYVFTGCP PSTSILAPNV IEMHIKLSII
151  DGKYCILGGT NFEEFMCTPG DEVPEKVDNP RLFVSGVRRP LAFRDQDIML
201  RSTAFGLQLR EEYHKQFAMW DYYAHHMWFI DNPEQFAGAC PPLTLEQAEE
251  TVFPGFDKHE DLVLVDSSKI RIVLGGPHDK QPNPVTQEYL KLIQGARSSV
301  KLAHMYFIPK DELLNALVDV SHNHGVHLSL ITNGCHELSP AITGPYAWGN
351  RINYFALLYG KRYPLWKKWF CEKLKPYERV SIYEFAIWET QLHKKCMIID
401  DEIFVIGSYN FGKKSDAFDY ESIVVIESPE VAAKANKVFN KDIGLSIPVS
451  HGDIFSWYFH SVHHTLGHLQ LTYMPA*
```

A predicted signal peptide is highlighted.

The cp6717 nucleotide sequence <SEQ ID 76> is:

```
   1  ATGATGAGTC GGTTGCGTTT TCGCTTGGCA GCTCTTGGAA TATTTTTTAT
  51  TTTGCTGGTT CCTAATTCTG TTTCAGCAAA GACAATCGTA GCTTCAGACA
 101  AGGAGAAGGT TGGAGTTCTT GTTTATGACA ATAGTGTAGA GGCCTTTCAA
 151  CAGATATTGG ATTGCATAGA TCATGCAAAT TTTTATGTAG AACTGTGTCC
 201  CTGCATGACA GGAGGCCGAA CGCTTAAAGA GATGGTAGAT CACCTCGAGG
 251  CTCGTATGGA TCTGGTTCCA GAGCTCTGTA GCTATATCAT TATCCAACCC
 301  ACGTTTACCG ATGCTGAAGA CCAAAAATTA CTCAAAGCTC TCAAAGAACG
 351  TCATCCCAAC CGGTTTTTCT ACGTTTTTAC AGGGTGCCCA CCCTCAACAA
 401  GCATCCTCGC TCCTAATGTC ATTGAAATGC ATATCAAACT TTCTATCATC
 451  GATGGGAAAT ATTGTATTTT AGGTGGTACC AATTTTGAAG AGTTTATGTG
 501  CACTCCAGGG GATGAGGTTC CTGAGAAAGT GGATAACCCA CGTTTATTTG
 551  TCAGTGGAGT GCGTCGGCCC CTAGCATTTC GTGATCAGGA TATCATGTTG
 601  CGTTCTACAG CATTCGGTTT GCAGCTCAGA GAAGAATATC ATAAGCAATT
 651  TGCTATGTGG GACTACTATG CACATCATAT GTGGTTCATT GATAATCCTG
 701  AACAGTTTGC AGGCGCCTGT CCTCCACTGA CTTTAGAACA AGCCGAGGAG
 751  ACAGTATTTC CTGGATTTGA CAAACATGAA GATCTTGTTC TTGTCGACTC
 801  TTCCAAGATC AGGATAGTTT TAGGTGGTCC CCACGATAAG CAACCCAATC
 851  CTGTGACTCA AGAATATTTG AAACTTATCC AGGGAGCTAG ATCTTCTGTG
 901  AAGCTTGCTC ACATGTATTT CATCCCTAAG GACGAGCTTT TAAATGCTCT
 951  TGTCGACGTT TCTCATAATC ACGGTGTTCA TCTGAGTTTA ATTACGAACG
1001  GCTGTCATGA ATTAAGTCCT GCAATTACAG GACCCTATGC TTGGGGAAAC
1051  CGTATTAACT ATTTCGCCTT GCTCTATGGG AAACGGTATC CTCTTTGGAA
1101  AAAATGGTTT TGCGAAAAGC TAAAACCTTA TGAGCGGGTT TCTATTTATG
1151  AGTTTGCTAT TTGGGAAACG CAGTTGCACA AGAAGTGTAT GATTATCGAT
1201  GATGAAATTT TTGTGATCGG AAGTTATAAT TTTGGAAAGA AAAGTGATGC
1251  CTTTGATTAC GAAAGTATTG TAGTTATCGA ATCTCCAGAA GTCGCTGCAA
1301  AAGCTAACAA AGTCTTCAAT AAAGATATCG GATTGTCGAT TCCTGTAAGT
1351  CATGGCGACA TTTTCTCTTG GTATTTCCAT TCCGTACACC ACACTTTGGG
1401  ACATTTGCAG CTGACCTATA TGCCAGCCTA G
```

The PSORT algorithm predicts a periplasmic location (0.939).

The protein was expressed in *E.coli* and purified as a GST-fusion (Figure 38A), as a his-tagged protein, and as a GST/his fusion product. The proteins were used to immunise mice, whose sera were used in a Western blot (Figure 38B) and for FACS analysis.

These experiments show that cp6717 is a useful immunogen. These properties are not evident from the sequence alone.

Example 39

The following *C.pneumoniae* protein (PID 4376577) was expressed <SEQ ID 77; cp6577>:

```
  1  MKKLLFSTFL LVLGSTSAAH ANLGYVNLKR CLEESDLGKK ETEELEAMKQ
 51  QFVKNAEKIE EELTSIYNKL QDEDYMESLS DSASEELRKK FEDLSGEYNA
101  YQSQYYQSIN QSNVKRIQKL IQEVKIAAES VRSKEKLEAI LNEEAVLAIA
151  PGTDKTTEII AILNESFKKQ N*
```

A predieted signal peptide is highlighted.

The cp6577 nucleotide sequence <SEQ ID 78> is:

```
  1  ATGAAAAAAT TATTATTTTC TACATTTCTT CTTGTTTTAG GATCAACAAG
 51  CGCAGCTCAT GCAAATTTAG GCTATGTTAA TTTAAAGCGA TGTCTTGAAG
101  AATCCGATCT AGGTAAAAAG GAAACTGAAG AATTGGAAGC TATGAAACAG
151  CAGTTTGTAA AAAATGCTGA GAAAATAGAA GAAGAACTCA CTTCTATTTA
201  TAATAAGTTG CAAGATGAAG ATTACATGGA AAGCCTATCG GATTCTGCCT
251  CTGAAGAGTT GCGAAAGAAA TTCGAAGATC TTTCAGGAGA GTACAATGCG
301  TACCAGTCTC AGTACTATCA ATCTATCAAT CAAAGTAATG TAAAACGCAT
351  TCAAAAACTC ATTCAAGAAG TAAAAATAGC TGCAGAATCA GTGCGGTCCA
401  AAGAAAAACT AGAAGCTATC CTTAATGAAG AAGCTGTCTT AGCAATAGCA
451  CCTGGGACTG ATAAAACAAC CGAAATTATT GCTATTCTTA ACGAATCTTT
501  CAAAAAACAA AACTAG
```

The PSORT algorithm predicts a periplasmic space location (0.932).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 39A) and as a GST-fusion produet (Figure 39B). The recombinant GST-fusion protein was used to immunise mice, whose sera were used in a Western blot (Figure 39C) and for FACS analysis.

The cp6577 protein was also identified in the 2D-PAGE experiment.

These experiments show that cp6577 is a useful immunogen. These properties are not evident from the sequence alone.

Example 40

The following *C.pneumoniae* protein (PID 4376446) was expressed <SEQ ID 79; cp6446>:

```
  1 MKQPMSLIFS SVCLGLGLGS LSSCNQKPSW NYHNTSTSEE FFVHGNKSVS
 51 QLPHYPSAFR TTQIFSEEHN DPYVVAKTDE ESRKIWREIH KNLKIKGSYI
101 PISTYGSLMH PKSAALTLKT YRPHPIWING YERSFNIDTG KYLKNGSRRR
151 TSHDGPKNRA VLNLIKSSGR RCNAIGLEMT EEDFVIARRR EGVYSLYPVE
201 VCSYPQGNPF VIAYAWIADE SACSKEVLPV KGYYSLVWES VSSSDSLNAF
251 GDSFAEDYLR STFLANGTSI LCVHESYKKV PPQP*
```

A predicted signal peptide is highlighted.

The cp6446 nucleotide sequence <SEQ ID 80> is:

```
  1 ATGAAACAGC CCATGTCTCT TATCTTTTCA AGTGTATGTT TAGGATTAGG
 51 TCTTGGATCT CTTTCCTCCT GTAATCAAAA GCCCTCTTGG AATTATCACA
101 ACACTTCAAC GAGCGAAGAA TTCTTTGTTC ATGGAAATAA GAGTGTTTCG
151 CAACTGCCTC ATTATCCTTC TGCATTTCGT ACGACTCAAA TCTTTTCTGA
201 AGAGCACAAT GATCCTTATG TCGTAGCTAA GACTGATGAA GAGTCTCGTA
251 AAATTTGGAG AGAAATCCAT AAAAATCTCA AAATCAAAGG TTCTTACATT
301 CCCATATCGA CTTATGGAAG TCTGATGCAC CCAAAATCAG CAGCTCTTAC
351 ATTAAAAACG TATCGTCCAC ATCCTATTTG GATAAATGGA TACGAGCGTT
401 CTTTTAATAT AGACACAGGA AAGTACTTAA AAAACGGAAG TCGCCGTAGA
451 ACTTCTCACG ATGGTCCGAA AAATCGAGCT GTACTGAATC TCATTAAATC
501 TTCGGGACGA CGCTGTAATG CTATAGGCCT TGAGATGACA GAAGAAGACT
551 TTGTAATAGC TAGAAGGCGA GAAGGTGTTT ATAGCCTGTA TCCCGTTGAA
601 GTGTGCTCGT ATCCTCAGGG GAATCCTTTT GTCATTGCTT ATGCCTGGAT
651 TGCAGATGAG AGTGCTTGCT CAAAAGAGGT CCTACCTGTA AAAGGGTACT
701 ATTCTTTAGT CTGGGAAAGC GTTTCTTCCT CTGATTCTCT GAATGCTTTT
751 GGAGATTCCT TTGCAGAGGA CTACCTCAGA AGCACGTTTT TAGCAAACGG
801 AACTTCTATA CTCTGTGTTC ATGAAAGCTA TAAGAAAGTT CCTCCTCAGC
851 CCTAA
```

The PSORT algorithm predicts an inner membrane loeation (0.177).

The protein was expressed in *E.coli* and purified as a his-tag product and a GST-fusion produet. The GST-fusion product is shown in Figure 40A. The recombinant his-tag protein was used to immunise mice, whose sera were used in a Western blot (Figure 40B) and for FACS analysis.

These experiments show that cp6446 is a useful immunogen. These properties are not evident from the sequence alone.

Example 41

The following *C.pneumoniae* protein (PID 4377108) was expressed <SEQ ID 81; cp7108>:

```
  1 MSKKIKVLGH LTLCTLFRGV LCAAALSNIG YASTSQESPY QKSIEDWKGY
 51 TFTDLELLSK EGWSEAHAVS GNGSRIVGAS GAGQGSVTAV IWESHLIKHL
101 GTLGGEASSA EGISKDGEVV VGWSDTREGY THAFVFDGRD MKDLGTLGAT
151 YSVARGVSGD GSIIVGVSAT ARGEDYGWQV GVKWEKGKIK QLKLLPQGLW
```

```
201  SEANAISEDG TVIVGRGEIS RNHIVAVKWN KNAVYSLGTL GGSVASAEAI
251  SANGKVIVGW STTNNGETHA FMHKDETMHD LGTLGGGFSV ATGVSADGRA
301  IVGFSAVKTG EIHAFYYAEG EMEDLTTLGG EEARVFDISS EGNDIIGSIK
351  TDAGAERAYL FHIHK*
```

A predicted signal peptide is highlighted.

The cp7108 nucleotide sequence <SEQ ID 82> is:

```
   1  ATGAGTAAGA AGATAAAGGT TCTAGGTCAT TTGACGCTCT GCACTCTGTT
  51  TAGAGGAGTG CTGTGTGCAG CGGCCCTTTC CAACATAGGA TATGCGAGTA
 101  CTTCTCAGGA ATCACCATAT CAGAAGTCTA TAGAAGACTG GAAAGGGTAT
 151  ACCTTTACAG ATCTTGAGTT ACTGAGTAAG GAAGGGTGGT CTGAAGCTCA
 201  TGCAGTTTCT GGAAATGGCA GTAGAATTGT AGGAGCTTCG GGAGCTGGCC
 251  AAGGTAGTGT GACTGCTGTC ATATGGGAAA GTCACCTGAT AAAACATCTC
 301  GGCACTTTAG GTGGCGAGGC TTCATCTGCA GAGGGAATTT CAAAGGATGG
 351  AGAGGTGGTC GTTGGGTGGT CAGATACTAG AGAGGGATAT ACTCATGCCT
 401  TTGTCTTCGA CGGTAGAGAT ATGAAAGATC TCGGTACTCT AGGAGCTACC
 451  TATTCTGTAG CAAGGGGTGT TTCTGGAGAT GGTAGTATCA TCGTAGGAGT
 501  CTCTGCAACT GCTCGTGGAG AGGATTACGG ATGGCAAGTT GGTGTCAAGT
 551  GGGAAAAAGG GAAAATCAAA CAATTGAAGT TGTTGCCTCA AGGTCTCTGG
 601  TCTGAGGCGA ATGCAATCTC TGAGGATGGT ACGGTGATTG TCGGGAGAGG
 651  GGAAATCTCT CGCAATCACA TCGTTGCTGT AAAATGGAAT AAAAATGCTG
 701  TGTATAGTTT GGGGACTCTC GGAGGTAGTG TCGCTTCAGC AGAGGCTATA
 751  TCGGCAAATG GGAAAGTAAT TGTAGGATGG TCCACGACTA ATAATGGTGA
 801  GACTCATGCC TTTATGCACA AAGATGAGAC AATGCACGAT CTCGGCACTC
 851  TAGGAGGAGG TTTTTCTGTC GCAACTGGAG TTTCTGCTGA TGGGAGAGCC
 901  ATCGTAGGAT TTTCAGCAGT GAAGACCGGA GAAATTCATG CTTTTTACTA
 951  TGCAGAAGGA GAAATGGAGG ATTTAACAAC TTTGGGAGGG GAAGAAGCTC
1001  GAGTGTTCGA CATATCTAGC GAAGGAAACG ATATCATTGG CTCTATAAAA
1051  ACTGACGCTG GAGCTGAACG CGCCTATCTG TTCCATATAC ATAAATAA
```

The PSORT algorithm predicts an outer membrane location (0.921).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 41A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 41B) and for FACS analysis (Figure 41C). A his-tagged protein was also expressed.

The cp7108 protein was also identified in the 2D-PAGE experiment.

These experiments show that cp7108 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 42

The following *C.pneumoniae* protein (PID 4377287) was expressed <SEQ ID 83; cp7287>:

1 **MVAKKTVRSY RSSFSHSVIV AILSAGIAFE AHS**LHSSELD LGVFNKQFEE

```
 51  HSAHVEEAQT SVLKGSDPVN PSQKESEKVL YTQVPLTQGS SGESLDLADA
101  NFLEHFQHLF EETTVFGIDQ KLVWSDLDTR NFSQPTQEPD TSNAVSEKIS
151  SDTKENRKDL ETEDPSKKSG LKEVSSDLPK SPETAVAAIS EDLEISENIS
201  ARDPLQGLAF FYKNTSSQSI SEKDSSFQGI IFSGSGANSG LGFENLKAPK
251  SGAAVYSDRD IVFENLVKGL SFISCESLED GSAAGVNIVV THCGDVTLTD
301  CATGLDLEAL RLVKDFSRGG AVFTARNHEV QNNLAGGILS VVGNKGAIVV
351  EKNSAEKSNG GAFACGSFVY SNNENTALWK ENQALSGGAI SSASDIDIQG
401  NCSAIEFSGN QSLIALGEHI GLTDFVGGGA LAAQGTLTLR NNAVVQCVKN
451  TSKTHGGAIL AGTVDLNETI SEVAFKQNTA ALTGGALSAN DKVIIANNFG
501  EILFEQNEVR NHGGAIYCGC RSNPKLEQKD SGENINIIGN SGAITFLKNK
551  ASVLEVMTQA EDYAGGGALW GHNVLLDSNS GNIQFIGNIG GSTFWIGEYV
601  GGGAILSTDR VTISNNSGDV VFKGNKGQCL AQKYVAPQET APVESDASST
651  NKDEKSLNAC SHGDHYPPKT VEEEVPPSLL EEHPVVSSTD IRGGGAILAQ
701  HIFITDNTGN LRFSGNLGGG EESSTVGDLA IVGGGALLST NEVNVCSNQN
751  VVFSDNVTSN GCDSGGAILA KKVDISANHS VEFVSNGSGK FGGAVCALNE
801  SVNITDNGSA VSFSKNRTRL GGAGVAAPQG SVTICGNQGN IAFKENFVFG
```

```
 851  SENQRSGGGA IIANSSVNIQ DNAGDILFVS NSTGSYGGAI FVGSLVASEG
 901  SNPRTLTITG NSGDILFAKN STQTAASLSE KDSFGGGAIY TQNLKIVKNA
 951  GNVSFYGNRA PSGAGVQIAD GGTVCLEAFG GDILFEGNIN FDGSFNAIHL
1001  CGNDSKIVEL SAVQDKNIIF QDAITYEENT IRGLPDKDVS PLSAPSLIFN
1051  SKPQDDSAQH HEGTIRFSRG VSKIPQIAAI QEGTLALSQN AELWLAGLKQ
1101  ETGSSIVLSA GSILRIFDSQ VDSSAPLPTE NKEETLVSAG VQINMSSPTP
1151  NKDKAVDTPV LADIISITVD LSSFVPEQDG TLPLPPEIII PKGTKLHSNA
1201  IDLKIIDPTN VGYENHALLS SHKDIPLISL KTAEGMTGTP TADASLSNIK
1251  IDVSLPSITP ATYGHTGVWS ESKMEDGRLV VGWQPTGYKL NPEKQGALVL
1301  NNLWSHYTDL RALKQEIFAH HTIAQRMELD FSTNVWGSGL GVVEDCQNIG
1351  EFDGFKHHLT GYALGLDTQL VEDFLIGGCF SQFFGKTESQ SYKAKNDVKS
1401  YMGAAYAGIL AGPWLIKGAF VYGNINNDLT TDYGTLGIST GSWIGKGFIA
1451  GTSIDYRYIV NPRRFISAIV STVVPFVEAE YVRIDLPEIS EQGKEVRTFQ
1501  KTRFENVAIP FGFALEHAYS RGSRAEVNSV QLAYVFDVYR KGPVSLITLK
1551  DAAYSWKSYG VDIPCKAWKA RLSNNTEWNS YLSTYLAFNY EWREDLIAYD
1601  FNGGIRIIF*
```

A predicted signal peptide is highlighted.

The cp7287 nucleotide sequence <SEQ ID 84> is:

```
   1  ATGGTAGCGA AAAAAACAGT ACGATCTTAT AGGTCTTCAT TTTCTCATTC
  51  CGTAATAGTA GCAATATTGT CAGCAGGCAT TGCTTTTGAA GCACATTCCT
 101  TACACAGCTC AGAACTAGAT TTAGGTGTAT TCAATAAACA GTTTGAGGAA
 151  CATTCTGCTC ATGTTGAAGA GGCTCAAACA TCTGTTTTAA AGGGATCAGA
 201  TCCTGTAAAT CCCTCTCAGA AAGAATCCGA GAAGGTTTTG TACACTCAAG
 251  TGCCTCTTAC CCAAGGAAGC TCTGGAGAGA GTTTGGATCT CGCCGATGCT
 301  AATTTCTTAG AGCATTTTCA GCATCTTTTT GAAGAGACTA CAGTATTTGG
 351  TATCGATCAA AAGCTGGTTT GGTCAGATTT AGATACTAGG AATTTTTCCC
 401  AACCCACTCA AGAACCTGAT ACAAGTAATG CTGTAAGTGA GAAAATCTCC
 451  TCAGATACCA AAGAGAATAG AAAAGACCTA GAGACTGAAG ATCCTTCAAA
 501  AAAAAGTGGC CTTAAAGAAG TTTCATCAGA TCTCCCTAAA AGTCCTGAAA
 551  CTGCAGTAGC AGCTATTTCT GAAGATCTTG AAATCTCAGA AAACATTTCA
 601  GCAAGAGATC CTCTTCAGGG TTTAGCATTT TTTTATAAAA ATACATCTTC
 651  TCAGTCTATC TCTGAAAAGG ATTCTTCATT TCAAGGAATT ATCTTTTCTG
 701  GTTCAGGAGC TAATTCAGGG CTAGGTTTTG AAAATCTTAA GGCGCCGAAA
 751  TCTGGGGCTG CAGTTTATTC TGATCGAGAT ATTGTTTTTG AAAATCTTGT
 801  TAAAGGATTG AGTTTTATAT CTTGTGAATC TTTAGAAGAT GGCTCTGCCG
 851  CAGGTGTAAA CATTGTTGTG ACCCATTGTG GTGATGTAAC TCTCACTGAT
 901  TGTGCCACTG GTTTAGACCT TGAAGCTTTA CGTCTGGTTA AAGATTTTTC
 951  TCGTGGAGGA GCTGTTTTCA CTGCTCGCAA CCATGAAGTG CAAAATAACC
1001  TTGCAGGTGG AATTCTATCC GTTGTAGGCA ATAAAGGAGC TATTGTTGTA
1051  GAGAAAAATA GTGCTGAGAA GTCCAATGGA GGAGCTTTTG CTTGCGGAAG
1101  TTTTGTTTAC AGTAACAACG AAAACACCGC CTTGTGGAAA GAAAATCAAG
1151  CATTATCAGG AGGAGCCATA TCCTCAGCAA GTGATATTGA TATTCAAGGG
1201  AACTGTAGCG CTATTGAATT TTCAGGAAAC CAGTCTCTAA TTGCTCTTGG
1251  AGAGCATATA GGGCTTACAG ATTTTGTAGG TGGAGGAGCT TTAGCTGCTC
1301  AAGGGACGCT TACCTTAAGA AATAATGCAG TAGTGCAATG TGTTAAAAAC
1351  ACTTCTAAAA CACATGGTGG AGCTATTTTA GCAGGTACTG TTGATCTCAA
1401  CGAAACAATT AGCGAAGTTG CCTTTAAGCA GAATACAGCA GCTCTAACTG
1451  GAGGTGCTTT AAGTGCAAAT GATAAGGTTA TAATTGCAAA TAACTTTGGA
1501  GAAATTCTTT TTGAGCAAAA CGAAGTGAGG AATCACGGAG GAGCCATTTA
1551  TTGTGGATGT CGATCTAATC CTAAGTTAGA ACAAAAGGAT TCTGGAGAGA
1601  ACATCAATAT TATTGGAAAC TCCGGAGCTA TCACTTTTTT AAAAAATAAG
1651  GCTTCTGTTT TAGAAGTGAT GACACAAGCT GAAGATTATG CTGGTGGAGG
1701  CGCTTTATGG GGGCATAATG TTCTTCTAGA TTCCAATAGT GGGAATATTC
1751  AATTTATAGG AAATATAGGT GGAAGTACCT TCTGGATAGG AGAATATGTC
1801  GGTGGTGGTG CGATTCTCTC TACTGATAGA GTGACAATTT CTAATAACTC
1851  TGGAGATGTT GTTTTTAAAG GAAACAAAGG CCAATGTCTT GCTCAAAAAT
1901  ATGTAGCTCC TCAAGAAACA GCTCCCGTGG AATCAGATGC TTCATCTACA
1951  AATAAAGACG AGAAGAGCCT TAATGCTTGT AGTCATGGAG ATCATTATCC
2001  TCCTAAAACT GTAGAAGAGG AAGTGCCACC TTCATTGTTA GAAGAACATC
2051  CTGTTGTTTC TTCGACAGAT ATTCGTGGTG GTGGGGCCAT TCTAGCTCAA
2101  CATATCTTTA TTACAGATAA TACAGGAAAT CTGAGATTCT CTGGGAACCT
2151  TGGTGGTGGT GAAGAGTCTT CTACTGTCGG TGATTTAGCT ATCGTAGGAG
2201  GAGGTGCTTT GCTTTCTACT AATGAAGTTA ATGTTTGCAG TAACCAAAAT
2251  GTTGTTTTTT CTGATAACGT GACTTCAAAT GGTTGTGATT CAGGGGGAGC
2301  TATTTTAGCT AAAAAAGTAG ATATCTCCGC GAACCACTCG GTTGAATTTG
```

```
2351  TCTCTAATGG TTCAGGGAAA TTCGGTGGTG CCGTTTGCGC TTTAAACGAA
2401  TCAGTAAACA TTACGGACAA TGGCTCGGCA GTATCATTCT CTAAAAATAG
2451  AACACGTCTT GGCGGTGCTG GAGTTGCAGC TCCTCAAGGC TCTGTAACGA
2501  TTTGTGGAAA TCAGGGAAAC ATAGCATTTA AAGAGAACTT TGTTTTTGGC
2551  TCTGAAAATC AAAGATCAGG TGGAGGAGCT ATCATTGCTA ACTCTTCTGT
2601  AAATATTCAG GATAACGCAG GAGATATCCT ATTTGTAAGT AACTCTACGG
2651  GATCTTATGG AGGTGCTATT TTTGTAGGAT CTTTGGTTGC TTCTGAAGGC
2701  AGCAACCCAC GAACGCTTAC AATTACAGGC AACAGTGGGG ATATCCTATT
2751  TGCTAAAAAT AGCACGCAAA CAGCCGCTTC TTTATCAGAA AAAGATTCCT
2801  TTGGTGGAGG GGCCATCTAT ACACAAAACC TCAAAATTGT AAAGAATGCA
2851  GGGAACGTTT CTTTCTATGG CAACAGAGCT CCTAGTGGTG CTGGTGTCCA
2901  AATTGCAGAC GGAGGAACTG TTTGTTTAGA GGCTTTTGGA GGAGATATCT
2951  TATTTGAAGG GAATATCAAT TTTGATGGGA GTTTCAATGC GATTCACTTA
3001  TGCGGGAATG ACTCAAAAAT CGTAGAGCTT TCTGCTGTTC AAGATAAAAA
3051  TATTATTTTC CAAGATGCAA TTACTTATGA AGAGAACACA ATTCGTGGCT
3101  TGCCAGATAA AGATGTCAGT CCTTTAAGTG CCCCTTCATT AATTTTTAAC
3151  TCCAAGCCAC AAGATGACAG CGCTCAACAT CATGAAGGGA CGATACGGTT
3201  TTCTCGAGGG GTATCTAAAA TTCCTCAGAT TGCTGCTATA CAAGAGGGAA
3251  CCTTAGCTTT ATCACAAAAC GCAGAGCTTT GGTTGGCAGG ACTTAAACAG
3301  GAAACAGGAA GTTCTATCGT ATTGTCTGCG GGATCTATTC TCCGTATTTT
3351  TGATTCCCAG GTTGATAGCA GTGCGCCTCT TCCTACAGAA AATAAAGAGG
3401  AGACTCTTGT TTCTGCCGGA GTTCAAATTA ACATGAGCTC TCCTACACCC
3451  AATAAAGATA AAGCTGTAGA TACTCCAGTA CTTGCAGATA TCATAAGTAT
3501  TACTGTAGAT TTGTCTTCAT TTGTTCCTGA GCAAGACGGA ACTCTTCCTC
3551  TTCCTCCTGA AATTATCATT CCTAAGGGAA CAAAATTACA TTCTAATGCC
3601  ATAGATCTTA AGATTATAGA TCCTACCAAT GTGGGATATG AAAATCATGC
3651  TCTTCTAAGT TCTCATAAAG ATATTCCATT AATTTCTCTT AAGACAGCGG
3701  AAGGAATGAC AGGGACGCCT ACAGCAGATG CTTCTCTATC TAATATAAAA
3751  ATAGATGTAT CTTTACCTTC GATCACACCA GCAACGTATG GTCACACAGG
3801  AGTTTGGTCT GAAAGTAAAA TGGAAGATGG AAGACTTGTA GTCGGTTGGC
3851  AACCTACGGG ATATAAGTTA AATCCTGAGA AGCAAGGGGC TCTAGTTTTG
3901  AATAATCTCT GGAGTCATTA TACAGATCTT AGAGCTCTTA AGCAGGAGAT
3951  CTTTGCTCAT CATACGATAG CTCAAAGAAT GGAGTTAGAT TTCTCGACAA
4001  ATGTCTGGGG ATCAGGATTA GGTGTTGTTG AAGATTGTCA GAACATCGGA
4051  GAGTTTGATG GGTTCAAACA TCATCTCACA GGGTATGCCC TAGGCTTGGA
4101  TACACAACTA GTTGAAGACT TCTTAATTGG AGGATGTTTC TCACAGTTCT
4151  TTGGTAAAAC TGAAAGCCAA TCCTACAAAG CTAAGAACGA TGTGAAGAGT
4201  TATATGGGAG CTGCTTATGC GGGGATTTTA GCAGGTCCTT GGTTAATAAA
4251  AGGAGCTTTT GTTTACGGTA ATATAAACAA CGATTTGACT ACAGATTACG
4301  GTACTTTAGG TATTTCAACA GGTTCATGGA TAGGAAAAGG GTTTATCGCA
4351  GGCACAAGCA TTGATTACCG CTATATTGTA AATCCTCGAC GGTTTATATC
4401  GGCAATCGTA TCCACAGTGG TTCCTTTTGT AGAAGCCGAG TATGTCCGTA
4451  TAGATCTTCC AGAAATTAGC GAACAGGGTA AAGAGGTTAG AACGTTCCAA
4501  AAAACTCGTT TTGAGAATGT CGCCATTCCT TTTGGATTTG CTTTAGAACA
4551  TGCTTATTCG CGTGGCTCAC GTGCTGAAGT GAACAGTGTA CAGCTTGCTT
4601  ACGTCTTTGA TGTATATCGT AAGGGACCTG TCTCTTTGAT TACACTCAAG
4651  GATGCTGCTT ATTCTTGGAA GAGTTATGGG GTAGATATTC CTTGTAAAGC
4701  TTGGAAGGCT CGCTTGAGCA ATAATACGGA ATGGAATTCA TATTTAAGTA
4751  CGTATTTAGC GTTTAATTAT GAATGGAGAG AAGATCTGAT AGCTTATGAC
4801  TTCAATGGTG GTATCCGTAT TATTTTCTAG
```

The PSORT algorithm predicts an inner membrane location (0.106).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 42A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 42B) and for FACS analysis (Figure 42C). A his-tagged protein was also expressed.

The cp7287 protein was also identified in the 2D-PAGE experiment and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp7287 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 43

The following *C.pneumoniae* protein (PID 4377105) was expressed <SEQ ID 85; cp7105>:

```
  1 MSLYQKWWNS QLKKSLCYST VAALIFMIPS QESFADSLID LNLGLDPSVE
 51 CLSGDGAFSV GYFTKAGSTP VEYQPFKYDV SKKTFTILSV ETANQSGYAY
101 GISYDGTITV GTCSLGAGKY NGAKWSADGT LTPLTGITGG TSHTEARAIS
151 KDTQVIEGFS YDASGQPKAV QWASGATTVT QLADISGGSR SSYAYAISDD
201 GTIIVGSMES TITRKTTAVK WVNNVPTYLG TLGGDASTGL YISGDGTVIV
251 GAANTATVTN GNQESHAYMY KDNQMKD*
```

The cp7105 nucleotide sequence <SEQ ID 86> is:

```
  1 GTGAGTCTAT ATCAAAAATG GTGGAACAGT CAGTTAAAGA AGAGCCTCTG
 51 CTATTCGACT GTTGCTGCTC TAATATTTAT GATTCCTTCT CAAGAATCCT
101 TTGCAGATAG TCTTATAGAT TTAAATTTAG GTTTAGATCC TTCGGTCGAA
151 TGTCTGTCAG GAGATGGTGC ATTTTCTGTT GGGTATTTTA CTAAGGCGGG
201 ATCGACTCCC GTAGAATATC AGCCGTTTAA ATACGACGTA TCTAAGAAGA
251 CATTCACAAT CCTTTCCGTA GAAACGGCAA ATCAGAGCGG CTATGCTTAC
301 GGAATCTCCT ACGATGGCAC GATCACTGTA GGAACGTGTA GCCTAGGTGC
351 AGGAAAATAT AACGGCGCAA AATGGAGTGC GGATGGCACT TTAACACCCT
401 TAACTGGAAT CACGGGGGGG ACGTCACATA CGGAAGCGCG TGCGATTTCT
451 AAGGATACTC AGGTGATCGA GGGTTTCTCA TATGATGCTT CAGGGCAACC
501 CAAGGCTGTG CAGTGGGCAA GCGGAGCGAC TACAGTAACA CAATTAGCAG
551 ATATTTCAGG AGGCTCTAGA AGCTCTTATG CGTATGCTAT ATCTGATGAT
601 GGCACGATTA TTGTTGGGTC TATGGAGAGC ACGATAACAA GGAAAACTAC
651 AGCTGTAAAA TGGGTAAATA ATGTTCCTAC GTATCTGGGA ACCTTAGGAG
701 GAGATGCTTC TACAGGTCTT TATATTTCTG GAGACGGCAC CGTGATTGTA
751 GGTGCGGCAA ATACAGCAAC TGTAACCAAT GGGAATCAGG AATCCCACGC
801 CTATATGTAT AAAGATAACC AAATGAAAGA TTGA
```

The PSORT algorithm predicts an inner membrane location (0.100).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 43A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 43B) and for FACS analysis (Figure 43C). A his-tagged protein was also expressed.

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp7105 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 44

The following *C.pneumoniae* protein (PID 4376802) was expressed <SEQ ID 87; cp6802>:

  1 **MSNQLQPCIS LG**CVSYINSF PLSLQLIKRN DIRCVLAPPA DLLNLLIEGK
 51 LDVALTSSLG AISHNLGYVP GFGIAANQRI LSVNLYAAPT FFNSPQPRIA
101 ATLESRSSIG LLKVLCRHLW RIPTPHILRF ITTKVLRQTP ENYDGLLLIG
151 DAALQHPVLP GFVTYDLASG WYDLTKLPFV FALLLHSTSW KEHPLPNLAM
201 EEALQQFESS PEEVLKEAHQ HTGLPPSLLQ EYYALCQYRL GEEHYESFEK
251 FREYYGTLYQ QARL*

A predicted signal peptide is highlighted.

The cp6802 nucleotide sequence <SEQ ID 88> is:

```
  1 ATGTCTAACC AACTCCAGCC ATGTATAAGC TTAGGCTGCG TAAGTTATAT
 51 TAATTCCTTT CCGCTGTCCC TACAACTCAT AAAAAGAAAC GATATTCGCT
101 GTGTTCTTGC TCCCCCTGCA GACCTCCTCA ACTTGCTAAT CGAAGGGAAA
151 CTCGATGTTG CTTTGACCTC ATCCCTAGGA GCTATCTCTC ATAACTTGGG
201 GTATGTCCCC GGCTTTGGAA TTGCAGCAAA CCAACGTATC CTCAGTGTAA
```

```
251  ACCTCTATGC AGCTCCCACT TTCTTTAACT CACCGCAACC TCGGATTGCC
301  GCAACTTTAG AAAGTCGCTC CTCTATAGGA CTCTTAAAAG TGCTTTGTCG
351  TCATCTCTGG CGCATCCCAA CTCCTCATAT CCTAAGATTC ATAACTACAA
401  AAGTACTCAG ACAAACCCCT GAAAATTATG ATGGCCTCCT CCTAATCGGA
451  GATGCAGCGC TACAACATCC TGTACTTCCT GGATTTGTAA CCTATGACCT
501  TGCCTCGGGG TGGTATGATC TTACAAAGCT ACCTTTTGTA TTTGCTCTTC
551  TTCTACACAG CACCTCTTGG AAAGAACATC CCCTACCCAA CCTTGCGATG
601  GAAGAAGCCC TCCAACAGTT CGAATCTTCA CCCGAAGAAG TCCTTAAAGA
651  AGCTCATCAA CATACAGGTC TGCCCCCTTC TCTTCTTCAA GAATACTATG
701  CCCTATGCCA GTACCGTCTA GGAGAAGAAC ACTACGAAAG CTTTGAAAAA
751  TTCCGGGAAT ATTATGGAAC CCTCTACCAA CAAGCCCGAC TGTAA
```

The PSORT algorithm predicts an inner membrane location (0.060).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 44A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 44B) and for FACS analysis (Figure 44C). A his-tagged protein was also expressed.

These experiments show that cp6802 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 45

The following *C.pneumoniae* protein (PID 4376390) was expressed <SEQ ID 89; cp6390>:

```
  1  MVFSYYCMGL FFFSGAISSC GLLVSLGVGL GLSVLGVLLL LLAGLLLFKI
 51  QSMLREVPKA PDLLDLEDAS ERLRVKASRS LASLPKEISQ LESYIRSAAN
101  DLNTIKTWPH KDQRLVETVS RKLERLAAAQ NYMISELCEI SEILEEEEHH
151  LILAQESLEW IGKSLFSTFL DMESFLNLSH LSEVRPYLAV NDPRLLEITE
201  ESWEVVSHFI NVTSAFKKAQ ILFKNNEHSR MKKKLESVQE LLETFIYKSL
251  KRSYRELGCL SEKMRIIHDN PLFPWVQDQQ KYAHAKNEFG EIARCLEEFE
301  KTFFWLDEEC AISYMDCWDF LNESIQNKKS RVDRDYISTK KIALKDRART
351  YAKVLLEENP TTEGKIDLQD AQRAFERQSQ EFYTLEHTET KVRLEALQQC
401  FSDLREATNV RQVRFTNSEN ANDLKESFEK IDKERVRYQK EQRLYWETID
451  RNEQELREEI GESLRLQNRR KGYRAGYDAG RLKGLLRQWK KNLRDVEAHL
501  EDATMDFEHE VSKSELCSVR ARLEVLEEEL MDMSPKVADI EELLSYEERC
551  ILPIRENLER AYLQYNKCSE ILSKAKFFFP EDEQLLVSEA NLREVGAQLK
601  QVQGKCQERA QKFAIFEKHI QEQKSLIKEQ VRSFDLAGVG FLKSELLSIA
651  CNLYIKAVVK ESIPVDVPCM QLYYSYYEDN EAVVRNRLLN MTERYQNFKR
701  SLNSIQFNGD VLLRDPVYQP EGHETRLKER ELQETTLSCK KLKVAQDRLS
751  ELESRLSRR
```

A predieted signal peptide is highlighted.

The ep6390 nucleotide sequence <SEQ ID 90> is:

```
  1  TTGGTATTCT CATACTATTG CATGGGATTA TTTTTTTTCT CTGGAGCTAT
 51  TTCTAGTTGT GGTCTTTTAG TGTCTCTAGG AGTTGGTTTA GGACTTAGTG
101  TTTTAGGAGT ACTTTTACTT CTCTTAGCAG GTCTTTTGCT TTTTAAGATC
151  CAAAGTATGC TTCGAGAGGT GCCTAAGGCT CCTGATCTAT TAGATTTAGA
201  AGATGCAAGT GAACGGCTTA GAGTAAAGGC TAGCCGTTCT TTAGCAAGCC
251  TCCCGAAGGA AATCAGTCAG CTAGAGAGCT ACATTCGTTC TGCAGCTAAT
301  GATCTAAATA CAATTAAGAC TTGGCCGCAT AAAGATCAAA GACTCGTCGA
351  GACCGTGTCA CGAAAATTAG AGCGTCTGGC AGCTGCTCAA AACTATATGA
401  TTTCTGAACT CTGCGAGATT AGTGAGATTC TTGAGGAAGA GGAGCATCAT
451  CTAATTTTGG CTCAGGAATC TCTAGAATGG ATAGGTAAGA GTCTATTTTC
501  TACCTTTCTG GACATGGAAT CTTTTTTAAA TTTGAGCCAT CTATCTGAAG
551  TGCGTCCGTA CTTAGCTGTA AATGATCCTA GATTATTAGA AATTACCGAA
601  GAATCTTGGG AAGTAGTGAG TCATTTCATA AATGTAACGT CTGCTTTTAA
651  GAAAGCTCAG ATTCTTTTTA AGAACAACGA ACATTCTCGG ATGAAGAAGA
701  AGTTAGAAAG TGTTCAAGAG TTACTGGAAA CATTTATTTA TAAGAGTTTA
751  AAGAGAAGTT ATCGAGAATT AGGATGCTTA AGTGAAAAGA TGAGAATCAT
801  TCACGACAAT CCTCTCTTCC CTTGGGTGCA AGATCAGCAG AAGTATGCTC
851  ATGCTAAGAA TGAATTTGGA GAGATTGCGC GGTGTTTAGA GGAGTTTGAA
901  AAGACGTTCT TCTGGTTGGA TGAGGAGTGT GCTATTTCTT ACATGGACTG
```

```
 951  TTGGGATTTT CTAAATGAGT CTATTCAGAA TAAGAAGTCC AGAGTAGATC
1001  GAGATTATAT ATCCACGAAG AAAATTGCAT TAAAGGATAG AGCCCGCACT
1051  TATGCTAAGG TTCTTTTAGA AGAGAATCCG ACTACAGAGG GTAAAATAGA
1101  TTTGCAAGAC GCTCAAAGAG CCTTTGAGCG TCAAAGTCAG GAGTTTTATA
1151  CACTAGAGCA TACGGAAACA AAGGTGAGAC TAGAAGCACT TCAACAGTGC
1201  TTCTCGGATC TTAGGGAGGC GACGAACGTA AGGCAAGTTA GGTTTACAAA
1251  TTCTGAAAAT GCGAATGATT TAAAGGAGAG TTTCGAGAAG ATAGATAAAG
1301  AGCGTGTGCG ATATCAAAAA GAGCAAAGGC TCTATTGGGA AACAATAGAT
1351  CGCAATGAGC AAGAGCTTAG GGAAGAGATT GGGGAGTCGC TTCGTTTACA
1401  AAATCGGAGA AAAGGGTATA GGGCTGGATA TGATGCTGGG CGTTTAAAAG
1451  GTTTGTTGCG TCAGTGGAAG AAAAATCTCC GCGATGTGGA AGCCCACCTT
1501  GAAGATGCAA CTATGGATTT TGAGCATGAA GTAAGCAAGA GCGAATTGTG
1551  CAGTGTTCGG GCGAGGCTCG AGGTTCTAGA AGAAGAGCTG ATGGATATGT
1601  CTCCTAAAGT TGCGGATATA GAAGAGTTGT TGTCCTATGA AGAGCGTTGT
1651  ATTCTTCCTA TTAGGGAAAA TTTAGAAAGG GCATACCTCC AATATAATAA
1701  GTGTTCTGAA ATTTTATCCA AGGCAAAGTT CTTCTTTCCG GAAGACGAGC
1751  AATTGCTAGT TTCGGAAGCG AATCTAAGAG AGGTGGGTGC CCAGTTAAAA
1801  CAAGTACAGG GAAAATGTCA AGAGAGGGCC CAAAAGTTCG CAATATTTGA
1851  AAAGCATATT CAGGAGCAGA AAAGCCTTAT TAAAGAGCAA GTGCGGAGTT
1901  TTGATCTAGC GGGAGTTGGG TTTTTAAAGA GTGAGCTTCT TAGTATTGCT
1951  TGTAACCTTT ATATAAAGGC GGTTGTTAAG GAGTCTATAC CAGTTGATGT
2001  GCCTTGTATG CAGTTATATT ATAGTTATTA CGAAGATAAT GAAGCTGTAG
2051  TGCGAAACCG CCTTTTAAAT ATGACGGAGA GGTATCAAAA TTTTAAAAGG
2101  AGTTTGAATT CCATACAATT TAATGGTGAC GTTCTTTTAC GGGATCCGGT
2151  CTATCAACCT GAAGGTCATG AGACCAGGCT AAAGGAACGG GAGCTACAAG
2201  AAACAACTTT GTCTTGTAAG AAATTAAAAG TGGCTCAAGA TCGTCTTTCT
2251  GAATTAGAGT CAAGGCTGTC TAGGAGATAG
```

The PSORT algorithm predicts a periplasmic location (0.932).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 45A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 45B) and for FACS analysis (Figure 45C). A his-tagged protein was also expressed.

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6390 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 46

The following *C.pneumoniae* protein (`PID 4376272`) was expressed <SEQ ID 91; cp6272>:

```
  1  MKRCFLFLAS FVLMGSSADA LTHQEAVKKK NSYLSHFKSV SGIVTIEDGV
 51  LNIHNNLRIQ ANKVYVENTV GQSLKLVAHG NVMVNYRAKT LVCDYLEYYE
101  DTDSCLLTNG RFAMYPWFLG GSMITLTPET IVIRKGYIST SEGPKKDLCL
151  SGDYLEYSSD SLLSIGKTTL RVCRIPILFL PPFSIMPMEI PKPPINFRGG
201  TGGFLGSYLG MSYSPISRKH FSSTFFLDSF FKHGVGMGFN LHCSQKQVPE
251  NVFNMKSYYA HRLAIDMAEA HDRYRLHGDF CFTHKHVNFS GEYHLSDSWE
301  TVADIFPNNF MLKNTGPTRV DCTWNDNYFE GYLTSSVKVN SFQNANQELP
351  YLTLRQYPIS IYNTGVYLEN IVECGYLNFA FSDHIVGENF SSLRLAARPK
401  LHKTVPLPIG TLSSTLGSSL IYYSDVPEIS SRHSQLSAKL QLDYRFLLHK
451  SYIQRRHIIE PFVTFITETR PLAKNEDHYI FSIQDAFHSL NLLKAGIDTS
501  VLSKTNPRFP RIHAKLWTTH ILSNTESKPT FPKTACELSL PFGKKNTVSL
551  DAEWIWKKHC WDHMNIRWEW IGNDNVAMTL ESLHRSKYSL IKCDRENFIL
601  DVSRPIDQLL DSPLSDHRNL ILGKLFVRPH PCWNYRLSLR YGWHRQDTPN
651  YLEYQMILGT KIFEHWQLYG VYERREADSR FFFFLKLDKP KKPPF*
```

A predicted signal peptide is highlighted.

The cp6272 nucleotide sequence <SEQ ID 92> is:

```
  1  ATGAAACGTT GCTTCTTATT TCTAGCTTCC TTTGTTCTTA TGGGTTCCTC
```

```
  51  AGCTGATGCT TTGACTCATC AAGAGGCTGT GAAAAAGAAA AACTCCTATC
 101  TTAGTCACTT TAAGAGTGTT TCTGGGATTG TGACCATCGA AGATGGGGTA
 151  TTGAATATCC ATAACAACCT GCGGATACAA GCCAATAAAG TGTATGTAGA
 201  AAATACTGTG GGTCAAAGCC TGAAGCTTGT CGCACATGGC AATGTTATGG
 251  TGAACTATAG GGCAAAAACC CTAGTTTGTG ATTACCTAGA GTATTACGAA
 301  GATACAGACT CTTGTCTTCT TACTAATGGA AGATTCGCGA TGTATCCTTG
 351  GTTTCTAGGG GGGTCTATGA TCACTCTAAC CCCAGAAACC ATAGTCATTC
 401  GGAAGGGATA TATCTCTACC TCCGAGGGTC CCAAAAAAGA CCTGTGCCTC
 451  TCCGGAGATT ACCTGGAATA TTCTTCAGAT AGTCTTCTTT CTATAGGGAA
 501  GACAACATTA AGGGTGTGTC GCATTCCGAT ACTTTTCTTA CCTCCATTTT
 551  CTATCATGCC TATGGAGATC CCTAAGCCTC CGATAAACTT TCGAGGAGGA
 601  ACAGGAGGAT TTCTGGGATC CTATTTGGGG ATGAGCTACT CGCCGATTTC
 651  TAGGAAGCAT TTCTCCTCGA CATTTTTCTT GGATAGCTTT TTCAAGCATG
 701  GCGTCGGCAT GGGATTCAAC CTCCATTGTT CTCAGAAGCA GGTTCCTGAG
 751  AATGTCTTCA ATATGAAAAG CTATTATGCC CACCGCCTTG CTATCGATAT
 801  GGCAGAAGCT CATGATCGCT ATCGCCTACA CGGAGATTTC TGCTTCACGC
 851  ATAAGCATGT AAATTTTTCT GGAGAATACC ATCTCAGCGA TAGTTGGGAA
 901  ACTGTTGCTG ACATTTTCCC CAACAACTTC ATGTTGAAAA ATACAGGCCC
 951  CACACGTGTC GATTGCACTT GGAATGACAA CTATTTTGAA GGGTATCTCA
1001  CCTCTTCTGT TAAGGTAAAC TCTTTCCAAA ATGCCAACCA AGAGCTCCCT
1051  TATTTAACAT TAAGGCAGTA CCCGATTTCT ATTTATAATA CGGGAGTGTA
1101  CCTTGAAAAC ATCGTAGAAT GTGGGTATTT AAACTTTGCT TTTAGCGATC
1151  ATATCGTTGG CGAGAATTTC TCTTCACTAC GTCTTGCTGC GCGCCCTAAG
1201  CTCCATAAAA CTGTGCCTCT ACCTATAGGA ACGCTCTCCT CCACCCTAGG
1251  GAGTTCTCTG ATTTACTATA GCGATGTTCC TGAGATCTCC TCGCGCCATA
1301  GTCAGCTTTC CGCGAAGCTA CAACTTGATT ATCGCTTTCT ATTACATAAG
1351  TCCTACATTC AAAGACGCCA TATTATAGAG CCGTTCGTTA CCTTCATTAC
1401  AGAGACTCGT CCTCTAGCTA AGAATGAAGA TCATTATATC TTTTCTATTC
1451  AAGATGCCTT TCACTCCTTA AACCTTCTGA AAGCGGGTAT AGATACCTCG
1501  GTACTGAGTA AGACTAACCC TCGATTCCCG AGAATCCATG CGAAGCTGTG
1551  GACTACCCAC ATCTTGAGCA ATACAGAAAG CAAACCCACG TTTCCCAAAA
1601  CTGCATGCGA GCTATCTCTA CCTTTTGGAA AGAAAAATAC AGTCTCCTTA
1651  GATGCTGAAT GGATTTGGAA AAAGCACTGT TGGGATCACA TGAACATACG
1701  TTGGGAGTGG ATCGGAAATG ACAATGTGGC TATGACTCTA GAATCCCTGC
1751  ATAGAAGCAA ATACAGCCTG ATTAAGTGTG ACAGGGAGAA CTTCATTTTA
1801  GATGTCAGCC GTCCCATTGA CCAGCTTTTA GACTCCCCTC TCTCTGATCA
1851  TAGGAATCTC ATTTTAGGGA AATTATTTGT ACGACCTCAT CCCTGTTGGA
1901  ATTACCGCTT ATCCTTACGC TATGGCTGGC ATCGCCAGGA CACTCCGAAC
1951  TACCTAGAAT ACCAGATGAT TCTAGGGACG AAGATCTTCG AACATTGGCA
2001  GCTCTATGGG GTGTATGAAC GCCGAGAAGC AGATAGTCGA TTTTTCTTCT
2051  TCTTAAAGCT CGACAAACCT AAAAAACCTC CCTTCTAA
```

The PSORT algorithm predicts an outer membrane location (0.48).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 46A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot and for FACS analysis (Figure 46B). A his-tagged protein was also expressed.

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6272 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 47

The following *C.pneumoniae* protein (PID 4377111) was expressed <SEQ ID 93; cp7111>:

```
  1  MFEAVIADIQ AREILDSRGY PTLHVKVTTS TGSVGEARVP SGASTGKKEA
 51  LEFRDTDSPR YQGKGVLQAV KNVKEILFPL VKGCSVYEQS LIDSLMMDSD
101  GSPNKETLGA NAILGVSLAT AHAAAATLRR PLYRYLGGCF ACSLPCPMMN
151  LINGGMHADN GLEFQEFMIR PIGASSIKEA VNMGADVFHT LKKLLHERGL
201  STGVGDEGGF APNLASNEEA LELLLLAIEK AGFTPGKDIS LALDCAASSF
```

```
251  YNVKTGTYDG RHYEEQIAIL SNLCDRYPID SIEDGLAEED YDGWALLTEV
301  LGEKVQIVGD DLFVTNPELI LEGISNGLAN SVLIKPNQIG TLTETVYAIK
351  LAQMAGYTTI ISHRSGETTD TTIADLAVAF NAGQIKTGSL SRSERVAKYN
401  RLMEIEEELG SEAIFTDSNV FSYEDSEE*
```

A predicted signal peptide is highlighted.

The cp7111 nucleotide sequence <SEQ ID 94> is:

```
   1  ATGTTTGAAG CTGTCATTGC CGATATCCAG GCTAGGGAAA TCTTGGATTC
  51  TCGCGGGTAT CCCACTTTAC ATGTTAAAGT AACCACTAGC ACAGGTTCTG
 101  TTGGAGAAGC TCGGGTTCCT TCAGGAGCAT CCACAGGGAA AAAAGAAGCC
 151  TTAGAGTTTC GTGATACAGA TTCTCCTCGT TATCAAGGCA AAGGGGTTTT
 201  GCAAGCTGTA AAAAACGTAA AAGAAATTCT TTTTCCCCTC GTCAAGGGAT
 251  GTAGTGTTTA TGAGCAATCC TTAATTGATT CTCTGATGAT GGATTCTGAC
 301  GGCTCTCCGA ACAAAGAAAC TCTAGGGGCC AATGCTATTT TAGGAGTCTC
 351  TCTAGCTACA GCACATGCAG CAGCAGCAAC ACTACGCAGA CCTCTGTATC
 401  GTTATTTAGG AGGGTGTTTT GCCTGCAGTC TTCCCTGTCC TATGATGAAT
 451  CTGATCAATG GAGGCATGCA TGCCGATAAC GGCTTGGAGT TCCAAGAATT
 501  TATGATCCGT CCTATTGGAG CCTCTTCCAT CAAAGAAGCT GTCAACATGG
 551  GTGCTGACGT TTTTCATACT TTGAAAAAAT TACTCCATGA AAGAGGCTTA
 601  TCTACTGGAG TGGGTGACGA AGGAGGCTTC GCCCCGAATC TTGCTTCTAA
 651  TGAAGAAGCT CTAGAGCTCC TATTGCTGGC TATTGAAAAA GCAGGCTTTA
 701  CTCCAGGAAA AGATATATCG CTAGCCTTAG ACTGCGCAGC ATCCTCATTC
 751  TATAACGTAA AAACAGGCAC GTATGATGGG AGGCACTATG AAGAGCAAAT
 801  CGCAATCCTT TCTAATTTAT GTGATCGCTA TCCTATAGAC TCCATAGAAG
 851  ATGGTCTTGC TGAAGAAGAC TATGACGGGT GGGCCTTGTT AACTGAAGTT
 901  CTTGGAGAAA AAGTACAGAT TGTGGGTGAT GACCTATTTG TTACAAATCC
 951  GGAATTAATA TTAGAGGGTA TTAGCAATGG ATTAGCGAAC TCTGTGTTGA
1001  TTAAACCAAA TCAGATAGGG ACGCTTACTG AAACAGTGTA TGCTATCAAG
1051  CTTGCGCAAA TGGCTGGCTA TACTACAATT ATTTCTCATC GCTCAGGAGA
1101  AACTACGGAC ACTACGATTG CAGATCTTGC TGTTGCCTTC AACGCCGGTC
1151  AAATCAAAAC AGGCTCTTTA TCACGTTCTG AGCGTGTTGC AAAATACAAT
1201  AGACTCATGG AAATTGAAGA AGAGCTTGGA TCCGAAGCAA TTTTCACAGA
1251  TTCTAATGTA TTTTCTTAC GAGGATTCT GAGGAATAG
```

The PSORT algorithm predicts an inner membrane location (0.100).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 47A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 47B) and for FACS analysis (Figure 47C). A his-tagged protein was also expressed.

The cp7111 protein was also identified in the 2D-PAGE experiment and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp7111 is a surfaee-exposed and immunoaceessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 48

The following *C.pneumoniae* protein (PID 4455886) was expressed <SEQ ID 95; cp0010>:

```
  1  MKSQFSWLVL SSTLACFTSC STVFAATAEN IGPSDSFDGS TNTGTYTPKN
 51  TTTGIDYTLT GDITLQNLGD SAALTKGCFS DTTESLSFAG KGYSLSFLNI
101  KSSAEGAALS VTTDKNLSLT GFSSLTFLAA PSSVITTPSG KGAVKCGGDL
151  TFDNNGTILF KQDYCEENGG AISTKNLSLK NSTGSISFEG NKSSATGKKG
201  GAICATGTVD ITNNTAPTLF SNNIAEAAGG AINSTGNCTI TGNTSLVFSE
251  NSVTATAGNG GALSGDADVT ISGNQSVTFS GNQAVANGGA IYAKKLTLAS
301  GGGGVSPFLT IIVQGTTAGN GGAISILAAG ECSLSAEAGD ITFNGNAIVA
351  TTPQTTKRNS IDIGSTAKIT NLRAISGHSI FFYDPITANT AADSTDTLNL
401  NKADAGNSTD YSGSIVFSGE KLSEDEAKVA DNLTSTLKQP VTLTAGNLVL
451  KRGVTLDTKG FTQTAGSSVI MDAGTTLKAS TEEVTLTGLS IPVDSLGEGK
501  KVVIAASAAS KNVALSGPIL LLDNQGNAYE NHDLGKTQDF SFVQLSALGT
```

```
551  ATTTDVPAVP TVATPTHYGY QGTWGMTWVD DTASTPKTKT ATLAWTNTGY
601  LPNPERQGPL VPNSLWGSFS DIQAIQGVIE RSALTLCSDR GFWAAGVANF
651  LDKDKKGEKR KYRHKSGGYA IGGAAQTCSE NLISFAFCQL FGSDKDFLVA
701  KNHTDTYAGA FYIQHITECS GFIGCLLDKL PGSWSHKPLV LEGQLAYSHV
751  SNDLKTKYTA YPEVKGSWGN NAFNMMLGAS SHSYPEYLHC FDTYAPYIKL
801  NLTYIRQDSF SEKGTEGRSF DDSNLFNLSL PIGVKFEKFS DCNDFSYDLT
851  LSYVPDLIRN DPKCTTALVI SGASWETYAN NLARQALQVR AGSHYAFSPM
901  FEVLGQFVFE VRGSSRIYNV DLGGKFQF*
```

A predicted signal peptide is highlighted.

The cp0010 nucleotide sequence <SEQ ID 96> is:

```
   1  ATGAAATCGC AATTTTCCTG GTTAGTGCTC TCTTCGACAT TGGCATGTTT
  51  TACTAGTTGT TCCACTGTTT TTGCTGCAAC TGCTGAAAAT ATAGGCCCCT
 101  CTGATAGCTT TGACGGAAGT ACTAACACAG GCACCTATAC TCCTAAAAAT
 151  ACGACTACTG GAATAGACTA TACTCTGACA GGAGATATAA CTCTGCAAAA
 201  CCTTGGGGAT TCGGCAGCTT TAACGAAGGG TTGTTTTTCT GACACTACGG
 251  AATCTTTAAG CTTTGCCGGT AAGGGGTACT CACTTTCTTT TTTAAATATT
 301  AAGTCTAGTG CTGAAGGCGC AGCACTTTCT GTTACAACTG ATAAAAATCT
 351  GTCGCTAACA GGATTTTCGA GTCTTACTTT CTTAGCGGCC CCATCATCGG
 401  TAATCACAAC CCCCTCAGGA AAAGGTGCAG TTAAATGTGG AGGGGATCTT
 451  ACATTTGATA ACAATGGAAC TATTTTATTT AAACAAGATT ACTGTGAGGA
 501  AAATGGCGGA GCCATTTCTA CCAAGAATCT TTCTTTGAAA AACAGCACGG
 551  GATCGATTTC TTTTGAAGGG AATAAATCGA GCGCAACAGG GAAAAAAGGT
 601  GGGGCTATTT GTGCTACTGG TACTGTAGAT ATTACAAATA ATACGGCTCC
 651  TACCCTCTTC TCGAACAATA TTGCTGAAGC TGCAGGTGGA GCTATAAATA
 701  GCACAGGAAA CTGTACAATT ACAGGGAATA CGTCTCTTGT ATTTTCTGAA
 751  AATAGTGTGA CAGCGACCGC AGGAAATGGA GGAGCTCTTT CTGGAGATGC
 801  CGATGTTACC ATATCTGGGA ATCAGAGTGT AACTTTCTCA GGAAACCAAG
 851  CTGTAGCTAA TGGCGGAGCC ATTTATGCTA AGAAGCTTAC ACTGGCTTCC
 901  GGGGGGGGGG GGGTATCTCC TTTTCTAACA ATAaTAGTCC AAGGTACCAC
 951  TGCAGGTAAT GGTGGAGCCA TTTCTATACT GGCAGCTGGA GAGTGTAGTC
1001  TTTCAGCAGA AGCAGGGGAC ATTACCTTCA ATGGGAATGC CATTGTTGCA
1051  ACTACACCAC AAACTACAAA AAGAAATTCT ATTGACATAG GATCTACTGC
1101  AAAGATCACG AATTTACGTG CAATATCTGG GCATAGCATC TTTTTCTACG
1151  ATCCGATTAC TGCTAATACG GCTGCGGATT CTACAGATAC TTTAAATCTC
1201  AATAAGGCTG ATGCAGGTAA TAGTACAGAT TATAGTGGGT CGATTGTTTT
1251  TTCTGGTGAA AAGCTCTCTG AAGATGAAGC AAAAGTTGCA GACAACCTCA
1301  CTTCTACGCT GAAGCAGCCT GTAACTCTAA CTGCAGGAAA TTTAGTACTT
1351  AAACGTGGTG TCACTCTCGA TACGAAAGGC TTTACTCAGA CCGCGGGTTC
1401  CTCTGTTATT ATGGATGCGG GCACAACGTT AAAAGCAAGT ACAGAGGAGG
1451  TCACTTTAAC AGGTCTTTCC ATTCCTGTAG ACTCTTTAGG CGAGGGTAAG
1501  AAAGTTGTAA TTGCTGCTTC TGCAGCAAGT AAAAATGTAG CCCTTAGTGG
1551  TCCGATTCTT CTTTTGGATA ACCAAGGGAA TGCTTATGAA AATCACGACT
1601  TAGGAAAAAC TCAAGACTTT TCATTTGTGC AGCTCTCTGC TCTGGGTACT
1651  GCAACAACTA CAGATGTTCC AGCGGTTCCT ACAGTAGCAA CTCCTACGCA
1701  CTATGGGTAT CAAGGTACTT GGGGAATGAC TTGGGTTGAT GATACCGCAA
1751  GCACTCCAAA GACTAAGACA GCGACATTAG CTTGGACCAA TACAGGCTAC
1801  CTTCCGAATC CTGAGCGTCA AGGACCTTTA GTTCCTAATA GCCTTTGGGG
1851  ATCTTTTTCA GACATCCAAG CGATTCAAGG TGTCATAGAG AGAAGTGCTT
1901  TGACTCTTTG TTCAGATCGA GGCTTCTGGG CTGCGGGAGT CGCCAATTTC
1951  TTAGATAAAG ATAAGAAAGG GGAAAAACGC AAATACCGTC ATAAATCTGG
2001  TGGATATGCT ATCGGAGGTG CAGCGCAAAC TTGTTCTGAA AACTTAATTA
2051  GCTTTGCCTT TTGCCAACTC TTTGGTAGCG ATAAAGATTT CTTAGTCGCT
2101  AAAAATCATA CTGATACCTA TGCAGGAGCC TTCTATATCC AACACATTAC
2151  AGAATGTAGT GGGTTCATAG GTTGTCTCTT AGATAAACTT CCTGGCTCTT
2201  GGAGTCATAA ACCCCTCGTT TTAGAAGGGC AGCTCGCTTA TAGCCACGTC
2251  AGTAATGATC TGAAGACAAA GTATACTGCG TATCCTGAGG TGAAAGGTTC
2301  TTGGGGGAAT AATGCTTTTA ACATGATGTT GGGAGCTTCT TCTCATTCTT
2351  ATCCTGAATA CCTGCATTGT TTTGATACCT ATGCTCCATA CATCAAACTG
2401  AATCTGACCT ATATACGTCA GGACAGCTTC TCGGAGAAAG GTACAGAAGG
2451  AAGATCTTTT GATGACAGCA ACCTCTTCAA TTTATCTTTG CCTATAGGGG
2501  TGAAGTTTGA GAAGTTCTCT GATTGTAATG ACTTTTCTTA TGATCTGACT
2551  TTATCCTATG TTCCTGATCT TATCCGCAAT GATCCCAAAT GCACTACAGC
2601  ACTTGTAATC AGCGGAGCCT CTTGGGAAAC TTATGCCAAT AACTTAGCAC
2651  GACAGGCCTT GCAAGTGCGT GCAGGCAGTC ACTACGCCTT CTCTCCTATG
2701  TTTGAAGTGC TCGGCCAGTT TGTCTTTGAA GTTCGTGGAT CCTCACGGAT
```

```
2751  TTATAATGTA GATCTTGGGG GTAAGTTCCA ATTCTAG
```

The PSORT algorithm predicts an outer membrane location (0.922).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 48A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 48B) and for FACS analysis (Figure 48C). A his-tagged protein was also expressed.

The cp0010 protein was also identified in the 2D-PAGE experiment and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp0010 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 49

The following *C.pneumoniae* protein (PID 4376296) was expressed <SEQ ID 97; cp6296>:

```
  1  MEEVSEYLQQ VENQLESCSK RLTKMETFAL GVRLEAKEEI ESIILSDVVN
 51  RFEVLCRDIE DMLSRVEEIE RMLRMAELPL LPIKEALTKA FVQHNSCKEK
101  LTKVEPYFKE SPAYLTSEER LQSLNQTLQR AYKESQKVSG LESEVRACRE
151  QLKDQVRQFE TQGVSLIKEE ILFVTSTFRT KFSYHSFRLH VPCMRLYEEY
201  YDDIDLERTR ARWMAMSERY RDAFQAFQEM LKEGLVEEAQ ALRETEYWLY
251  REERKSKKKH*
```

The cp6296 nucleotide sequence <SEQ ID 98> is:

```
  1  ATGGAGGAGG TGTCTGAGTA TCTTCAGCAA GTAGAAAATC AGTTGGAATC
 51  CTGTTCCAAG CGATTAACCA AGATGGAAAC TTTTGCCTTA GGTGTGAGGT
101  TGGAAGCTAA AGAAGAGATA GAGTCTATCA TACTTTCTGA TGTAGTGAAC
151  CGTTTTGAGG TTTTATGTAG AGATATTGAA GATATGCTAT CTCGAGTCGA
201  GGAGATAGAG CGGATGTTAC GTATGGCGGA GCTTCCTCTA CTTCCTATAA
251  AAGAAGCGCT TACCAAGGCT TTTGTACAAC ATAACAGCTG TAAAGAGAAG
301  TTAACCAAGG TAGAGCCTTA CTTTAAAGAG AGCCCTGCAT ATCTAACTAG
351  TGAAGAGCGA TTGCAGAGTT TGAATCAGAC TTTACAACGT GCGTACAAAG
401  AGTCCCAAAA GGTTTCAGGT TTAGAATCGG AAGTGAGAGC CTGTCGAGAG
451  CAGCTTAAAG ATCAAGTAAG ACAGTTTGAA ACTCAAGGAG TGAGCTTGAT
501  AAAAGAAGAG ATTCTCTTTG TGACTAGTAC CTTTAGAACT AAATTTAGCT
551  ATCATTCATT TCGATTACAT GTTCCTTGCA TGAGGTTGTA TGAGGAGTAT
601  TATGATGACA TTGATCTAGA GAGAACTCGA GCTCGATGGA TGGCGATGTC
651  TGAGAGGTAT AGAGATGCTT TTCAGGCATT CCAGGAGATG TTGAAGGAAG
701  GCCTAGTTGA AGAAGCTCAG GCTCTTAGAG AAACCGAGTA CTGGTTATAT
751  CGAGAGGAGA GAAAGAGTAA AAAGAAACAT TGA
```

The PSORT algorithm predicts a cytoplasmic location (0.523).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 49A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 49B) and for FACS analysis (Figure 49C). A his-tagged protein was also expressed.

These experiments show that cp6296 is a surfaee-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 50

The following *C.pneumoniae* protein (PID 4376664) was expressed <SEQ ID 99; cp6664>:

```
  1  MVLFHAQASG RNRVKADAIV LPFWHFKDAK NAASFEAEFE PSYLPALENF
 51  QGKTGEIELL YSSPKAKEKR IVLLGLGKNE ELTSDVVFQT YATLTRVLRK
101  AKCSTVNIIL PTISELRLSA EEFLVGLSSG ILSLNYDYPR YNKVDRNLET
```

```
151  PLSKVTVIGI VPKMADAIFR KEAAIFEGVY LTRDLVNRNA DEITPKKLAE
201  VALNLGKEFP SIDTKVLGKD AIAKEKMGLL LAVSKGSCVD PHFIVVRYQG
251  RPKSKDHTVL IGKGVTFDSG GLDLKPGKSM LTMKEDMAGG ATVLGILSAL
301  AVLELPINVT GIIPATENAI DGASYKMGDV YVGMSGLSVE ICSTDAEGRL
351  ILADAITYAL KYCKPTRIID FATLTGAMVV SLGEEVAGFF SNNDVLAEDL
401  LEASAETSEP LWRLPLVKKY DKTLHSDIAD MKNLGSNRAG AITAALFLQR
451  FLEESSVAWA HLDIAGTAYH EKEEDRYPKY ASGFGVRSIL YYLENSLSK*
```

The cp6664 nucleotide sequence <SEQ ID 100> is:

```
   1  GTGGTTTTAT TTCATGCTCA AGCCTCTGGG CGTAATCGTG TTAAGGCAGA
  51  TGCTATAGTC CTGCCCTTTT GGCATTTTAA GGATGCAAAA AATGCAGCTT
 101  CTTTTGAAGC CGAGTTTGAA CCCTCGTATC TCCCCGCTTT AGAAAACTTT
 151  CAAGGAAAAA CCGGGGAGAT TGAACTCCTT TATAGTAGTC CTAAAGCTAA
 201  GGAAAAACGC ATTGTCCTCT TAGGCTTAGG GAAAAATGAA GAGCTCACCT
 251  CTGATGTTGT TTTCCAAACC TATGCGACAC TAACTCGTGT CTTACGTAAA
 301  GCAAAGTGTT CCACAGTCAA TATCATCTTA CCTACAATTT CTGAATTGCG
 351  GCTTTCTGCC GAAGAATTCT TAGTGGGGTT GTCCTCAGGA ATTTTGTCAT
 401  TAAACTATGA CTACCCACGT TATAATAAGG TAGATCGTAA TCTTGAAACT
 451  CCTCTTTCTA AAGTCACGGT TATCGGTATC GTTCCCAAAA TGGCGGATGC
 501  TATCTTTAGG AAAGAAGCAG CCATTTTCGA AGGCGTATAT CTCACTCGAG
 551  ATCTTGTGAA CAGGAATGCT GATGAAATTA CCCCTAAGAA ATTGGCAGAG
 601  GTTGCTCTGA ATCTGGGAAA AGAGTTCCCT AGTATTGATA CTAAGGTCTT
 651  GGGAAAAGAT GCCATCGCCA AAGAGAAAAT GGGACTCCTA TTGGCTGTTT
 701  CCAAGGGTTC TTGTGTGGAT CCACACTTTA TCGTTGTCCG TTATCAAGGA
 751  CGTCCTAAGT CTAAAGATCA CACCGTCTTG ATAGGGAAAG GGGTCACTTT
 801  TGACTCTGGA GGTTTAGACC TCAAGCCTGG AAAATCCATG CTTACTATGA
 851  AAGAAGACAT GGCAGGTGGG GCTACAGTCC TCGGGATTCT CTCGGCGTTA
 901  GCAGTTTTAG AGCTTCCTAT AAATGTCACG GGGATCATTC CTGCTACAGA
 951  GAATGCTATC GATGGCGCCT CCTATAAAAT GGGAGATGTC TATGTAGGAA
1001  TGTCGGGGCT TTCTGTTGAG ATTTGTAGTA CCGATGCTGA GGGACGTCTT
1051  ATCCTCGCTG ATGCGATTAC ATATGCTTTA AAATATTGTA AACCGACACG
1101  TATTATAGAT TTTGCAACTC TAACAGGAGC TATGGTAGTC TCTCTAGGAG
1151  AAGAGGTTGC AGGTTTCTTT TCCAATAACG ATGTTTTAGC TGAAGATCTT
1201  TTAGAGGCGT CAGCCGAAAC CTCCGAGCCG TTATGGAGAC TTCCTCTAGT
1251  TAAGAAGTAT GATAAAACAT TGCATTCTGA TATTGCTGAT ATGAAAAATC
1301  TAGGCAGTAA CCGTGCAGGG GCTATTACAG CAGCATTATT CTTGCAGAGA
1351  TTTTTGGAAG AATCTTCGGT AGCTTGGGCA CATCTTGATA TTGCAGGTAC
1401  TGCATATCAT GAAAAAGAAG AAGACCGTTA TCCAAAATAT GCTTCAGGTT
1451  TTGGTGTTCG TTCTATTCTT TATTACTTAG AAAATAGTCT TTCTAAGTAG
```

The PSORT algorithm predicts an inner membrane location (0.268).

The protein was expressed in *E.coli* and purified as a GST-fusion (Figure 50A), as a his-tagged protein, and as a GST/His fusion. The proteins were used to immunise mice, whose sera were used in Western blot Western blot (50B) and FACS (50C) analyses.

The cp6664 protein was also identified in the 2D-PAGE experiment (Cpn0385) and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6664 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 51

The following *C.pneumoniae* protein (PID 4376696) was expressed <SEQ ID 101; cp6696>:

```
  1  MTLIFVIIIV WCNAFLIKLC VIMGLQSRLQ HCIEVSQNSN FDSQVKQFIY
 51  ACQDKTLRQS VLKIFRYHPL LKIHDIARAV YLLMALEEGE DLGLSFLNVQ
101  QYPSGAVELF SCGGFPWKGL PYPAEHAEFG LLLLQIAEFY EESQAYVSKM
151  SHFQQALFDH QGSVFPSLWS QENSRLLKEK TTLSQSFLFQ LGMQIHPEYS
201  LEDPALGFWM QRTRSSSAFV AASGCQSSLG AYSSGDVGVI AYGPCSGDIS
251  DCYYFGCCGI AKEFVCQKSH QTTEISFLTS TGKPHPRNTG FSYLRDSYVH
301  LPIRCKITIS DKQYRVHAAL AEATSAMTFS IFCKGKNCQV VDGPRLRSCS
```

```
351  LDSYKGPGND IMILGENDAI NIVSASPYME IFALQGKEKF WNADFLINIP
401  YKEEGVMLIF EKKVTSEKGR FFTKMN*
```

A predicted signal peptide is highlighted.

The cp6696 nucleotide sequence <SEQ ID 102> is:

```
   1  TTGACTCTAA TTTTTGTTAT TATTATCGTT TGGTGCAATG CTTTTCTGAT
  51  CAAATTGTGC GTGATAATGG GGCTGCAATC CAGGTTACAA CATTGTATAG
 101  AAGTGTCCCA GAATTCGAAC TTTGATTCAC AAGTAAAACA GTTTATCTAT
 151  GCGTGCCAAG ATAAGACATT AAGGCAGTCT GTACTCAAGA TTTTCCGCTA
 201  CCATCCTTTA CTAAAAATTC ATGATATTGC TCGGGCCGTC TATCTTTTGA
 251  TGGCCTTAGA AGAAGGCGAG GATTTAGGCT TAAGCTTTTT AAATGTACAG
 301  CAGTACCCTT CAGGTGCTGT AGAACTGTTT TCTTGTGGGG GATTTCCTTG
 351  GAAAGGATTA CCTTATCCTG CAGAACATGC GGAATTTGGC CTACTCCTGT
 401  TACAGATCGC AGAGTTTTAT GAAGAGAGTC AGGCATACGT CTCTAAAATG
 451  AGTCATTTTC AACAGGCACT CTTTGATCAC CAAGGGAGCG TCTTTCCCTC
 501  TCTCTGGAGC CAGGAGAACT CTCGACTCCT AAAAGAAAAG ACAACTCTTA
 551  GCCAATCGTT TCTCTTCCAA TTAGGAATGC AAATTCACCC AGAATACAGT
 601  CTTGAGGATC CTGCACTAGG GTTCTGGATG CAAAGAACGC GTTCTTCATC
 651  CGCTTTTGTA GCCGCTTCAG GATGTCAAAG TAGCTTGGGA GCGTATTCCT
 701  CAGGGGATGT CGGTGTTATC GCTTATGGAC CTTGCTCTGG AGACATTAGT
 751  GATTGTTATT ATTTTGGATG TTGTGGAATC GCTAAAGAGT TCGTGTGCCA
 801  AAAATCTCAC CAAACTACAG AGATTTCTTT TCTCACCTCT ACAGGAAAGC
 851  CTCATCCCAG AAATACGGGA TTTTCCTACC TTCGAGATTC CTATGTACAT
 901  CTGCCGATCC GCTGTAAGAT CACTATTTCC GACAAGCAAT ATCGCGTGCA
 951  CGCTGCGTTG GCTGAGGCCA CCTCTGCCAT GACGTTTTCT ATTTTCTGTA
1001  AGGGGAAGAA TTGTCAGGTT GTTGACGGCC CTCGCTTGCG CTCCTGTTCC
1051  CTAGATTCTT ATAAAGGTCC CGGAAACGAC ATTATGATTC TTGGGGAAAA
1101  TGACGCAATC AACATTGTTT CTGCAAGTCC CTATATGGAA ATTTTTGCTT
1151  TGCAAGGCAA AGAAAAATTT TGGAATGCAG ACTTTTTGAT TAATATTCCT
1201  TACAAAGAAG AGGGCGTCAT GTTAATTTTT GAAAAAAAAG TGACCTCTGA
1251  GAAAGGAAGA TTCTTTACGA AGATGAATTA A
```

The PSORT algorithm predicts an inner membrane location (0.463).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 51A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 51B) and for FACS analysis (Figure 51C). A his-tagged protein was also expressed.

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6696 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 52

The following *C.pneumoniae* protein (PID 4376790) was expressed <SEQ ID 103; cp6790>:

```
  1  MSEHKKSSKI IGIDLGTTNS CVSVMEGGQA KVITSSEGTR TTPSIVAFKG
 51  NEKLVGIPAK RQAVTNPEKT LGSTKRFIGR KYSEVASEIQ TVPYTVTSGS
101  KGDAVFEVDG KQYTPEEIGA QILMKMKETA EAYLGETVTE AVITVPAYFN
151  DSQRASTKDA GRIAGLDVKR IIPEPTAAAL AYGIDKVGDK KIAVFDLGGG
201  TFDISILEIG DGVFEVLSTN GDTLLGGDDF DEVIIKWMIE EFKKQEGIDL
251  SKDNMALQRL KDAAEKAKIE LSGVSSTEIN QPFITMDAQG PKHLALTLTR
301  AQFEKLAASL IERTKSPCIK ALSDAKLSAK DIDDVLLVGG MSRMPAVQET
351  VKELFGKEPN KGVNPDEVVA IGAAIQGGVL GGEVKDVLLL DVIPLSLGIE
401  TLGGVMTTLV ERNTTIPTQK KQIFSTAADN QPAVTIVVLQ GERPMAKDNK
451  EIGRFDLTDI PPAPRGHPQI EVSFDIDANG IFHVSAKDVA SGKEQKIRIE
501  ASSGLQEDEI QRMVRDAEIN KEEDKKRREA SDAKNEADSM IFRAEKAIKD
551  YKEQIPETLV KEIEERIENV RNALKDDAPI EKIKEVTEDL SKHMQKIGES
601  MQSQSASAAA SSAANAKGGP NINTEDLKKH SFSTKPPSNN GSSEDHIEEA
```

```
651  DVEIIDNDDK*
```

The cp6790 nucleotide sequence <SEQ ID 104> is:

```
   1  ATGAGTGAAC ACAAAAAATC AAGCAAAATT ATAGGTATAG ACTTAGGCAC
  51  AACAAACTCC TGCGTATCTG TTATGGAAGG AGGACAAGCT AAAGTAATTA
 101  CATCATCCGA AGGAACAAGA ACCACGCCAT CGATCGTTGC CTTCAAAGGT
 151  AATGAGAAAT TAGTGGGGAT TCCAGCAAAA CGTCAAGCAG TGACAAATCC
 201  AGAAAAAACT CTCGGCTCTA CAAAACGCTT TATTGGCCGT AAGTACTCTG
 251  AAGTAGCTTC GGAAATCCAA ACCGTTCCTT ATACAGTCAC CTCCGGATCT
 301  AAAGGTGATG CCGTTTTCGA AGTTGATGGC AAACAATACA CTCCAGAAGA
 351  AATTGGCGCA CAAATCTTAA TGAAAATGAA AGAGACAGCA GAAGCTTATC
 401  TAGGCGAAAC TGTCACAGAA GCAGTGATCA CCGTCCCCGC ATACTTCAAT
 451  GATTCTCAAC GAGCATCCAC AAAAGATGCT GGACGCATTG CAGGTCTAGA
 501  TGTAAAACGT ATCATTCCAG AACCTACCGC AGCAGCTCTT GCCTACGGAA
 551  TCGATAAAGT CGGTGATAAA AAAATCGCTG TCTTCGACCT TGGTGGAGGA
 601  ACTTTTGATA TCTCCATCCT AGAAATCGGT GATGGCGTCT TCGAAGTTCT
 651  ATCTACAAAT GGAGATACTC TCCTCGGTGG AGACGACTTT GATGAAGTCA
 701  TTATCAAATG GATGATCGAA GAATTCAAAA AACAAGAAGG CATTGATCTT
 751  AGCAAAGATA ATATGGCCTT ACAAAGACTT AAAGATGCTG CTGAGAAAGC
 801  AAAAATAGAA CTTTCAGGAG TCTCTTCCAC AGAAATCAAT CAGCCATTCA
 851  TCACAATGGA TGCACAAGGA CCTAAACACC TTGCATTGAC ACTCACACGT
 901  GCGCAATTCG AGAAACTCGC AGCCTCTCTA ATCGAAAGAA CAAAATCTCC
 951  ATGCATCAAA GCACTCAGTG ACGCAAAACT TTCCGCTAAG GATATCGATG
1001  ATGTTCTCTT AGTTGGAGGT ATGTCAAGAA TGCCCGCAGT GCAAGAAACT
1051  GTAAAAGAAC TCTTCGGCAA AGAGCCTAAT AAAGGAGTCA ACCCCGACGA
1101  AGTTGTTGCT ATTGGAGCCG CAATTCAAGG TGGTGTTCTT GGCGGAGAAG
1151  TTAAGGATGT TCTACTTCTA GACGTTATCC CCCTATCTCT GGGTATCGAA
1201  ACTCTAGGAG GCGTCATGAC GACTCTGGTA GAGAGAAATA CTACAATCCC
1251  TACACAGAAA AAACAAATCT TCTCCACAGC TGCTGATAAC CAGCCTGCGG
1301  TTACCATCGT AGTTCTCCAA GGAGAGCGTC CCATGGCCAA AGATAACAAG
1351  GAAATCGGAA GATTCGATCT TACAGATATC CCTCCGGCTC CTCGAGGCCA
1401  TCCTCAAATC GAAGTCTCCT TCGATATCGA TGCAAACGGA ATTTTCCATG
1451  TCTCAGCTAA AGATGTTGCC AGCGGTAAAG AACAGAAAAT TCGTATCGAA
1501  GCAAGCTCAG GACTTCAAGA AGATGAAATC CAAAGAATGG TTCGAGATGC
1551  CGAAATTAAT AAGGAAGAAG ATAAAAAACG TCGTGAAGCT TCAGATGCTA
1601  AAAATGAAGC CGATAGCATG ATCTTCAGAG CCGAAAAAGC TATTAAAGAT
1651  TATAAGGAGC AAATTCCTGA AACTTTAGTT AAAGAAATCG AAGAGCGAAT
1701  CGAAAACGTG CGCAACGCAC TCAAAGATGA CGCTCCTATT GAAAAAATTA
1751  AAGAGGTTAC TGAAGACCTA AGCAAGCATA TGCAAAAAAT TGGAGAGTCT
1801  ATGCAATCGC AGTCTGCATC AGCAGCAGCA TCATCGGCAG CCAATGCTAA
1851  AGGTGGACCT AACATCAATA CAGAAGATTT GAAAAAACAT AGTTTCAGTA
1901  CGAAGCCTCC TTCAAATAAC GGTTCTTCAG AAGACCATAT CGAAGAAGCT
1951  GATGTAGAAA TTATTGATAA CGACGATAAG TAA
```

The PSORT algorithm predicts an inner membrane location (0.151).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 52A) and a his-tagged product. The proteins were used to immunise mice, whose sera were used in Western blot (Figure 52B) and FACS (Figure 52C) analyses.

The cp6790 protein was also identified in the 2D-PAGE experiment (Cpn0503).

These experiments show that cp6790 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 53

The following *C.pneumoniae* protein (PID 4376878) was expressed <SEQ ID 105; cp6878>:

```
  1  MNVPDSKNLH PPAYELLEIK ARITQSYKEA SAILTAIPDG ILLLSETGHF
 51  LICNSQAREI LGIDENLEIL NRSFTDVLPD TCLGFSIQEA LESLKVPKTL
101  RLSLCKESKE KEVELFIRKN EISGYLFIQI RDRSDYKQLE NAIERYKNIA
151  ELGKMTATLA HEIRNPLSGI VGFASILKKE ISSPRHQRML SSIISGTRSL
201  NNLVSSMLEY TKSQPLNLKI INLQDFFSSL IPLLSVSFPN CKFVREGAQP
```

```
251  LFRSIDPDRM NSVVWNLVKN AVETGNSPIT LTLHTSGDIS VTNPGTIPSE
301  IMDKLFTPFF TTKREGNGLG LAEAQKIIRL HGGDIQLKTS DSAVSFFIII
351  PELLAALPKE RAAS*
```

The cp6878 nucleotide sequence <SEQ ID 106> is:

```
1    ATGAACGTCC CTGATTCCAA GAACCTCCAT CCTCCTGCAT ACGAACTCCT
51   AGAGATCAAG GCTCGCATCA CACAATCTTA TAAAGAAGCG AGTGCTATAC
101  TGACAGCGAT TCCTGATGGT ATCCTATTAC TTTCTGAAAC AGGACACTTT
151  CTTATCTGCA ATTCACAAGC ACGTGAAATT CTAGGAATTG ATGAAAATCT
201  AGAAATTCTT AATAGATCCT TTACCGATGT TCTCCCCGAT ACGTGTCTTG
251  GATTTTCTAT TCAAGAGGCT CTTGAATCTC TAAAAGTCCC TAAAACTCTT
301  AGACTCTCTC TCTGTAAAGA ATCTAAAGAA AAAGAAGTGG AACTCTTCAT
351  CCGTAAAAAC GAGATCAGTG GATACCTGTT TATCCAAATC CGCGATCGGT
401  CCGACTATAA ACAACTAGAA AACGCTATAG AAAGATATAA AAATATCGCA
451  GAACTTGGGA AAATGACGGC TACCCTAGCT CACGAAATCC GCAATCCGCT
501  AAGTGGAATC GTTGGATTTG CCTCTATCCT AAAGAAAGAG ATTTCCTCTC
551  CTCGCCACCA ACGAATGCTC TCCTCAATCA TCTCCGGCAC AAGGTCTCTA
601  AATAACCTTG TCTCTTCTAT GTTAGAATAT ACAAAATCAC AACCGTTGAA
651  CCTAAAGATT ATAAATTTAC AAGACTTCTT CTCTTCTCTT ATCCCTCTGC
701  TCTCCGTCTC TTTCCCGAAT TGCAAGTTTG TAAGAGAGGG CGCACAACCT
751  CTATTCAGAT CTATAGATCC TGATCGGATG AACAGTGTCG TTTGGAACCT
801  AGTGAAAAAT GCTGTAGAAA CAGGGAACTC TCCGATCACT CTGACCCTGC
851  ATACATCGGG AGACATCTCG GTAACGAACC CCGGAACGAT TCCTTCCGAG
901  ATCATGGACA AGCTCTTCAC TCCATTCTTC ACAACAAAGA GAGAGGGAAA
951  TGGTTTGGGA CTTGCTGAAG CTCAAAAAAT TATAAGACTC CATGGAGGAG
1001 ATATCCAATT AAAAACAAGC GACTCCGCCG TTAGCTTCTT CATAATCATC
1051 CCCGAACTTC TAGCGGCCCT ACCCAAAGAA AGAGCCGCTA G
```

The PSORT algorithm predicts an inner membrane location (0.204).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 53A) and as a GST-fusion product. The recombinant GST-fusion protein was used to immunise mice, whose sera were used in a Western blot (Figure 53B) and for FACS analysis.

These experiments show that cp6878 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 54

The following *C.pneumoniae* protein (PID 4377224) was expressed <SEQ ID 107; cp7224>:

```
  1  MMKKIRKVAL AVGGSGGHIV PALSVKEAFS REGIDVLLLG KGLKNHPSLQ
 51  QGISYREIPS GLPTVLNPIK IMSRTLSLCS GYLKARKELK IFDPDLVIGF
101  GSYHSLPVLL AGLSHKIPLF LHEQNLVPGK VNQLFSRYAR GIGVNFSPVT
151  KHFRCPAEEV FLPKRSFSLG SPMMKRCTNH TPTICVVGGS QGAQILNTCV
201  PQALVKLVNK YPNMYVHHIV GPKSDVMKVQ HVYNRGEVLC CVKPFEEQLL
251  DVLLAADLVI SRAGATILEE ILWAKVPGIL IPYPGAYGHQ EVNAKFFVDV
301  LEGGTMILEK ELTEKLLVEK VTFALDSHNR EKQRNSLAAY SQQRSTKTFH
351  AFICECL*
```

The cp7224 nucleotide sequence <SEQ ID 108> is:

```
  1  ATGATGAAGA AAATTCGAAA AGTAGCCTTG GCTGTAGGAG GTTCAGGAGG
 51  CCACATTGTC CCAGCTCTCT CGGTAAAGGA AGCTTTTTCT CGTGAAGGAA
101  TAGACGTATT ACTACTAGGG AAAGGTCTCA AGAACCATCC TTCTTTGCAA
151  CAGGGAATCA GCTATCGGGA AATCCCCTCA GGACTTCCTA CAGTCCTTAA
201  TCCCATAAAG ATCATGAGCA GGACCCTTTC TCTATGTTCA GGATACCTGA
251  AAGCAAGAAA GGAACTTAAA ATTTTTGACC CTGACCTGGT CATAGGATTT
301  GGGAGCTACC ACTCTCTTCC CGTGTTGCTC GCAGGACTGT CCCATAAAAT
351  TCCCTTATTT CTACACGAAC AAAATCTAGT TCCTGGAAAA GTAAATCAAT
401  TGTTTTCCCG CTATGCTCGA GGTATTGGAG TGAATTTCTC CCCCGTTACT
451  AAACACTTCC GCTGCCCCGC AGAAGAGGTC TTCCTTCCTA AACGAAGCTT
501  CTCCTTAGGA AGCCCTATGA TGAAGCGATG TACAAATCAT ACCCCTACAA
551  TCTGTGTTGT TGGAGGTTCT CAGGGAGCAC AGATATTAAA TACTTGTGTT
601  CCCCAAGCTC TTGTCAAGCT AGTCAATAAG TACCCAAATA TGTACGTCCA
```

```
 651  TCATATTGTA GGACCTAAAA GTGATGTTAT GAAGGTGCAA CATGTTTACA
 701  ATCGTGGAGA GGTCCTCTGC TGTGTGAAGC CGTTCGAAGA GCAACTCCTA
 751  GATGTCTTGC TTGCCGCAGA TTTGGTCATC AGTAGGGCAG GAGCCACAAT
 801  TTTAGAAGAA ATTCTTTGGG CAAAAGTTCC CGGAATTTTA ATTCCCTATC
 851  CAGGAGCTTA TGGACATCAG GAAGTTAATG CTAAATTCTT TGTAGACGTC
 901  TTAGAAGGGG GAACTATGAT CCTAGAAAAA GAATTAACAG AGAAGCTATT
 951  AGTAGAAAAA GTAACGTTTG CTTTAGACTC CCATAACAGA GAAAAACAAC
1001  GCAATTCCCT AGCGGCGTAT AGTCAGCAAA GGTCAACAAA AACATTCCAT
1051  GCATTCATTT GTGAATGCTT ATAG
```

The PSORT algorithm predicts an inner membrane location (0.164).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 54A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 54B) and for FACS analysis (Figure 54C). A his-tagged protein was also expressed.

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp7224 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 55

The following *C.pneumoniae* protein (PID 4377140) was expressed <SEQ ID 109; cp7140>:

```
  1  MVRRSISFCL FFLMTLLCCT SCNSRSLIVH GLPGREANEI VVLLVSKGVA
 51  AQKLPQAAAA TAGAATEQMW DIAVPSAQIT EALAILNQAG LPRMKGTSLL
101  DLFAKQGLVP SELQEKIRYQ EGLSEQMAST IRKMDGVVDA SVQISFTTEN
151  EDNLPLTASV YIKHRGVLDN PNSIMVSKIK RLIASAVPGL VPENVSVVSD
201  RAAYSDITIN GPWGLTEEID YVSVWGIILA KSSLTKFRLI FYVLILILFV
251  ISCGLLWVIW KTHTLIMTMG GTKGFFNPTP YTKNALEAKK AEGAAADKEK
301  KEDADSQGES KNAETSDKDS SDKDAPEGSN EIEGA*
```

A predicted signal peptide is highlighted.

The cp7140 nucleotide sequence <SEQ ID 110> is:

```
   1  ATGGTTCGTC GATCTATTTC TTTTTGCTTG TTCTTTCTAA TGACATTGCT
  51  GTGCTGTACA AGCTGTAACA GCAGGTCTCT AATTGTGCAC GGTCTTCCTG
 101  GCAGAGAAGC GAATGAGATT GTGGTGCTTT TGGTAAGCAA AGGGGTGGCT
 151  GCACAAAAAT TGCCTCAAGC TGCAGCGGCT ACAGCCGGAG CAGCTACTGA
 201  GCAAATGTGG GATATCGCGG TTCCGTCAGC ACAAATCACA GAGGCCCTTG
 251  CCATTCTAAA TCAAGCGGGT CTTCCACGTA TGAAAGGGAC AAGCCTGTTA
 301  GATCTTTTTG CAAAACAAGG TCTTGTTCCT TCCGAGCTTC AGGAAAAAAT
 351  CCGTTATCAA GAAGGCTTAT CAGAACAGAT GGCCTCTACG ATTAGAAAAA
 401  TGGATGGCGT TGTCGATGCC TCAGTACAGA TTTCCTTCAC TACAGAAAAT
 451  GAAGATAATC TTCCTTTAAC AGCCTCTGTG TATATTAAGC ATCGAGGGGT
 501  TTTGGACAAT CCGAACAGCA TTATGGTTTC CAAAATTAAG CGCCTTATTG
 551  CAAGTGCTGT TCCAGGACTT GTGCCAGAGA ACGTCTCTGT AGTGAGCGAT
 601  CGCGCAGCTT ATAGTGATAT TACAATTAAT GGTCCTTGGG GATTAACAGA
 651  AGAAATCGAT TATGTTTCTG TTTGGGGTAT TATTCTTGCG AAGTCTTCGC
 701  TCACCAAATT CCGTCTCATT TTTTATGTCT TGATTCTCAT TTTATTTGTT
 751  ATTTCTTGTG GTCTCCTTTG GGTCATTTGG AAAACTCATA CTCTCATTAT
 801  GACTATGGGA GGTACAAAAG GGTTCTTCAA CCCTACACCA TATACAAAGA
 851  ATGCCTTGGA AGCCAAGAAA GCCGAGGGAG CAGCTGCTGA CAAAGAGAAA
 901  AAAGAAGATG CAGATTCACA GGGGGAAAGC AAAAATGCGG AAACCAGTGA
 951  TAAAGACTCT AGTGATAAAG ATGCTCCAGA AGGAAGCAAT GAAATTGAGG
1001  GTGCTTAG
```

The PSORT algorithm predicts an inner membrane location (0.650).

The protein was expressed in *E.coli* and purified as a GST-fusion produet, as shown in Figure 55A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 55B) and for FACS analysis (Figure 55C). A his-tagged protein was also expressed.

These experiments show that cp7140 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 56

The following *C.pneumoniae* protein (PID 4377306) was expressed <SEQ ID 111; cp7306>:

```
  1  MITKQLRSWL AVLVGSSLLA LPLSGQAVGK KESRVSELPQ DVLLKEISGG
 51  FSKVATKATP AVVYIESFPK SQAVTHPSPG RRGPYENPFD YFNDEFFNRF
101  FGLPSQREKP QSKEAVRGTG FLVSPDGYIV TNNHVVEDTG KIHVTLHDGQ
151  KYPATVIGLD PKTDLAVIKI KSQNLPYLSF GNSDHLKVGD WAIAIGNPFG
201  LQATVTVGVI SAKGRNQLHI ADFEDFIQTD AAINPGNSGG PLLNIDGQVI
251  GVNTAIVSGS GGYIGIGFAI PSLMANRIID QLIRDGQVTR GFLGVTLQPI
301  DAELAACYKL EKVYGALVTD VVKGSPADKA GLKQEDVIIA YNGKEVDSLS
351  MFRNAVSLMN PDTRIVLKVV REGKVIEIPV TVSQAPKEDG MSALQRVGIR
401  VQNLTPETAK KLGIAPETKG ILIISVEPGS VAASSGIAPG QLILAVNRQK
451  VSSIEDLNRT LKDSNNENIL LMVSQGDVIR FIALKPEE*
```

A predieted signal peptide is highlighted.

The cp7306 nucleotide sequence <SEQ ID 112> is:

```
   1  ATGATAACTA AGCAATTGCG TTCGTGGCTA GCTGTACTTG TTGGTTCAAG
  51  TCTGCTAGCT CTTCCTTTAT CAGGGCAAGC TGTCGGGAAA AAAGAATCTC
 101  GAGTTTCCGA GCTGCCTCAA GACGTTCTTC TTAAAGAGAT CTCGGGAGGG
 151  TTTTCTAAGG TCGCTACCAA GGCGACTCCC GCTGTTGTGT ACATAGAAAG
 201  TTTCCCAAAG AGCCAGGCTG TAACACATCC TTCTCCTGGA CGCCGTGGGC
 251  CTTATGAAAA TCCTTTTGAT TATTTTAATG ATGAGTTTTT CAATCGTTTT
 301  TTTGGTCTAC CTTCACAGAG GGAAAAACCT CAAAGTAAAG AGGCGGTTCG
 351  AGGAACAGGT TTCCTAGTAT CTCCAGATGG CTATATTGTG ACTAATAACC
 401  ATGTTGTCGA AGATACAGGT AAGATTCACG TAACTCTTCA TGATGGGCAA
 451  AAGTACCCAG CAACTGTAAT CGGACTCGAT CCTAAAACAG ACCTTGCAGT
 501  CATTAAAATT AAATCCCAAA ACCTCCCGTA TCTTTCTTTT GGAAACTCCG
 551  ACCACTTAAA AGTCGGAGAT TGGGCAATTG CAATTGGAAA TCCCTTCGGT
 601  CTTCAAGCTA CGGTCACCGT AGGTGTCATC AGTGCTAAAG GAAGAAATCA
 651  ACTCCACATT GCAGATTTTG AAGATTTTAT TCAGACAGAT GCTGCGATTA
 701  ATCCAGGCAA CTCTGGAGGC CCTCTTCTAA ATATTGATGG ACAGGTCATC
 751  GGTGTTAATA CTGCCATTGT CAGTGGTAGT GGTGGCTATA TTGGAATCGG
 801  GTTTGCGATT CCTAGCCTTA TGGCAAATAG AATCATAGAT CAGCTGATTC
 851  GTGATGGTCA AGTTACCCGA GGATTCTTAG GAGTGACTTT ACAACCTATA
 901  GATGCGGAAC TCGCTGCTTG CTACAAACTC GAAAAGGTTT ATGGCGCTTT
 951  AGTCACAGAT GTTGTTAAAG GATCTCCAGC AGATAAAGCA GGGCTAAAAC
1001  AAGAAGATGT GATCATTGCT TATAATGGGA AAGAAGTCGA TTCACTGAGT
1051  ATGTTCCGTA ATGCTGTTTC TTTAATGAAT CCAGATACAC GTATTGTTCT
1101  AAAGGTAGTT CGTGAAGGAA AGGTTATCGA AATACCCGTG ACAGTTTCTC
1151  AAGCTCCAAA AGAAGATGGA ATGTCGGCTT TACAGCGTGT GGGAATCCGT
1201  GTGCAAAACC TAACTCCTGA AACTGCTAAG AAGCTGGGAA TTGCTCCAGA
1251  GACTAAAGGC ATTTTGATTA TAAGTGTTGA ACCAGGGTCT GTAGCAGCTT
1301  CTTCAGGAAT TGCTCCTGGT CAGCTGATCC TTGCTGTGAA TAGACAAAAA
1351  GTATCTTCGA TTGAAGATCT GAATAGAACG TTAAAAGATT CTAACAATGA
1401  GAATATTCTT CTTATGGTTT CTCAAGGAGA TGTTATTCGC TTCATTGCCC
1451  TGAAACCTGA AGAATAA
```

The PSORT algorithm prediets a periplasmic location (0.923).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 56A) and as a GST-fusion product (Figure 56B). The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 56C) and for FACS (Figure 56D) analyses.

The ep7306 protein was also identified in the 2D-PAGE experiment (Cpn0979) and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp7306 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 57

The following *C.pneumoniae* protein (PID 4377132) was expressed <SEQ ID 113; cp7132>:

```
  1  MCNSIAMKKQ KRGFVLMELL MSFTLIALLL GTLGFWYRKI YTVQKQKERI
 51  YNFYIEESRA YKQLRTLFSM SLSSSYEEPG SLFSLIFDRG VYRDPKLAGA
101  VRASLHHDTK DQRLELRICN IKDQSYFETQ RLLSHVTHVV LSFQRNPDPE
151  KLPETIALTI TREPKAYPPR TLTYQFAVGK*
```

A predicted signal peptide is highlighted.

The cp7132 nucleotide sequence <SEQ ID 114> is:

```
  1  ATGTGTAACT CTATAGCTAT GAAAAAGCAA AAGCGTGGCT TTGTGCTTAT
 51  GGAATTACTC ATGTCGTTCA CTCTAATTGC TTTGTTATTA GGGACTTTAG
101  GATTTTGGTA TCGGAAAATT TATACTGTAC AAAAGCAAAA AGAACGTATT
151  TATAACTTTT ATATCGAAGA AAGCCGAGCC TACAAGCAGC TCAGAACCCT
201  GTTTAGCATG TCCTTGTCTT CATCTTACGA GGAGCCTGGA TCATTATTTT
251  CTTTAATCTT TGATCGGGGT GTTTATCGAG ATCCTAAGCT GGCAGGTGCG
301  GTACGAGCTT CTCTCCATCA TGACACCAAG GATCAGAGAT TGGAACTTCG
351  TATTTGTAAT ATTAAGGATC AGTCTTACTT TGAAACACAG CGACTGCTCT
401  CCCACGTGAC CCATGTTGTA CTTTCCTTCC AGAGAAATCC TGATCCTGAA
451  AAACTTCCTG AAACAATTGC TTTAACTATA ACACGGGAAC CTAAAGCATA
501  TCCTCCAAGG ACGTTAACAT ACCAATTTGC GGTTGGGAAA TAA
```

The PSORT algorithm predicts a periplasmie loeation (0.915).

The protein was expressed in *E.coli* and purified as a his-tag produet (Figure 57A) or as a GST-fusion. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 57B) and FACS (Figure 57C) analyses.

These experiments show that cp7132 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 58

The following *C.pneumoniae* protein (PID 4376733) was expressed <SEQ ID 115; cp6733>:

```
  1  MKTSIPWVLV SSVLAFSCHL QSLANEELLS PDDSFNGNID SGTFTPKTSA
 51  TTYSLTGDVF FYEPGKGTPL SDSCFKQTTD NLTFLGNGHS LTFGFIDAGT
101  HAGAAASTTA NKNLTFSGFS LLSFDSSPST TVTTGQGTLS SAGGVNLENI
151  RKLVVAGNFS TADGGAIKGA SFLLTGTSGD ALFSNNSSST KGGAIATTAG
201  ARIANNTGYV RFLSNIASTS GGAIDDEGTS ILSNNKFLYF EGNAAKTTGG
251  AICNTKASGS PELIISNNKT LIFASNVAET SGGAIHAKKL ALSSGGFTEF
301  LRNNVSSATP KGGAISIDAS GELSLSAETG NITFVRNTLT TTGSTDTPKR
351  NAINIGSNGK FTELRAAKNH TIFFYDPITS EGTSSDVLKI NNGSAGALNP
401  YQGTILFSGE TLTADELKVA DNLKSSFTQP VSLSGGKLLL QKGVTLESTS
451  FSQEAGSLLG MDSGTTLSTT AGSITITNLG INVDSLGLKQ PVSLTAKGAS
501  NKVIVSGKLN LIDIEGNIYE SHMFSHDQLF SLLKITVDAD VDTNVDISSL
551  IPVPAEDPNS EYGFQGQWNV NWTTDTATNT KEATATWTKT GFVPSPERKS
601  ALVCNTLWGV FTDIRSLQQL VEIGATGMEH KQGFWVSSMT NFLHKTGDEN
651  RKGFRHTSGG YVIGGSAHTP KDDLFTFAFC HLFARDKDCF IAHNNSRTYG
701  GTLFFKHSHT LQPQNYLRLG RAKFSESAIE KFPREIPLAL DVQVSFSHSD
751  NRMETHYTSL PESEGSWSNE CIAGGIGLDL PFVLSNPHPL FKTFIPQMKV
801  EMVYVSQNSF FESSSDGRGF SIGRLLNLSI PVGAKFVQGD IGDSYTYDLS
```

```
851  GFFVSDVYRN NPQSTATLVM SPDSWKIRGG NLSRQAFLLR GSNNYVYNSN
901  CELFGHYAME LRGSSRNYNV DVGTKLRF*
```

A predicted signal peptide is highlighted.

The cp6733 nucleotide sequence <SEQ ID 116> is:

```
   1  ATGAAGACTT CGATTCCTTG GGTTTTAGTT TCCTCCGTGT TAGCTTTCTC
  51  ATGTCACCTA CAGTCACTAG CTAACGAGGA ACTTTTATCA CCTGATGATA
 101  GCTTTAATGG AAATATCGAT TCAGGAACGT TTACTCCAAA AACTTCAGCC
 151  ACAACATATT CTCTAACAGG AGATGTCTTC TTTTACGAGC CTGGAAAAGG
 201  CACTCCCTTA TCTGACAGTT GTTTTAAGCA AACCACGGAC AATCTTACCT
 251  TCTTGGGGAA CGGTCATAGC TTAACGTTTG GCTTTATAGA TGCTGGCACT
 301  CATGCAGGTG CTGCTGCATC TACAACAGCA AATAAGAATC TTACCTTCTC
 351  AGGGTTTTCC TTACTGAGTT TTGATTCCTC TCCTAGCACA ACGGTTACTA
 401  CAGGTCAGGG AACGCTTTCC TCAGCAGGAG GCGTAAATTT AGAAAATATT
 451  CGTAAACTTG TAGTTGCTGG GAATTTTTCT ACTGCAGATG GTGGAGCTAT
 501  CAAAGGAGCG TCTTTCCTTT TAACTGGCAC TTCTGGAGAT GCTCTTTTTA
 551  GTAACAACTC TTCATCAACA AAGGGAGGAG CAATTGCTAC TACAGCAGGC
 601  GCTCGCATAG CAAATAACAC AGGTTATGTT AGATTCCTAT CTAACATAGC
 651  GTCTACGTCA GGAGGCGCTA TCGATGATGA AGGCACGTCG ATACTATCGA
 701  ACAACAAATT TCTATATTTT GAAGGGAATG CAGCGAAAAC TACTGGCGGT
 751  GCGATCTGCA ACACCAAGGC GAGTGGATCT CCTGAACTGA TAATCTCTAA
 801  CAATAAGACT CTGATCTTTG CTTCAAACGT AGCAGAAACA AGCGGTGGCG
 851  CCATCCATGC TAAAAAGCTA GCCCTTTCCT CTGGAGGCTT TACAGAGTTT
 901  CTACGAAATA ATGTCTCATC AGCAACTCCT AAGGGGGGTG CTATCAGCAT
 951  CGATGCCTCA GGAGAGCTCA GTCTTTCTGC AGAGACAGGA AACATTACCT
1001  TTGTAAGAAA TACCCTTACA ACAACCGGAA GTACCGATAC TCCTAAACGT
1051  AATGCGATCA ACATAGGAAG TAACGGGAAA TTCACGGAAT TACGGGCTGC
1101  TAAAAATCAT ACAATTTTCT TCTATGATCC CATCACTTCA GAAGGAACCT
1151  CATCAGACGT ATTGAAGATA AATAACGGCT CTGCGGGAGC TCTCAATCCA
1201  TATCAAGGAA CGATTCTATT TTCTGGAGAA ACCCTAACAG CAGATGAACT
1251  TAAAGTTGCT GACAATTTAA AATCTTCATT CACGCAGCCA GTCTCCCTAT
1301  CCGGAGGAAA GTTATTGCTA CAAAAGGGAG TCACTTTAGA GAGCACGAGC
1351  TTCTCTCAAG AGGCCGGTTC TCTCCTCGGC ATGGATTCAG GAACGACATT
1401  ATCAACTACA GCTGGGAGTA TTACAATCAC GAACCTAGGA ATCAATGTTG
1451  ACTCCTTAGG TCTTAAGCAG CCCGTCAGCC TAACAGCAAA AGGTGCTTCA
1501  AATAAAGTGA TCGTATCTGG GAAGCTCAAC CTGATTGATA TTGAAGGGAA
1551  CATTTATGAA AGTCATATGT TCAGCCATGA CCAGCTCTTC TCTCTATTAA
1601  AAATCACGGT TGATGCTGAT GTTGATACTA ACGTTGACAT CAGCAGCCTT
1651  ATCCCTGTTC CTGCTGAGGA TCCTAATTCA GAATACGGAT TCCAAGGACA
1701  ATGGAATGTT AATTGGACTA CGGATACAGC TACAAATACA AAAGAGGCCA
1751  CGGCAACTTG GACCAAAACA GGATTTGTTC CCAGCCCCGA AAGAAAATCT
1801  GCGTTAGTAT GCAATACCCT ATGGGGAGTC TTTACTGACA TTCGCTCTCT
1851  GCAACAGCTT GTAGAGATCG GCGCAACTGG TATGGAACAC AAACAAGGTT
1901  TCTGGGTTTC CTCCATGACG AACTTCCTGC ATAAGACTGG AGATGAAAAT
1951  CGCAAAGGCT TCCGTCATAC CTCTGGAGGC TACGTCATCG GTGGAAGTGC
2001  TCACACTCCT AAAGACGACC TATTTACCTT TGCGTTCTGC CATCTCTTTG
2051  CTAGAGACAA AGATTGTTTT ATCGCTCACA ACAACTCTAG AACCTACGGT
2101  GGAACTTTAT TCTTCAAGCA CTCTCATACC CTACAACCCC AAAACTATTT
2151  GAGATTAGGA AGAGCAAAGT TTTCTGAATC AGCTATAGAA AAATTCCCTA
2201  GGGAAATTCC CCTAGCCTTG GATGTCCAAG TTTCGTTCAG CCATTCAGAC
2251  AACCGTATGG AAACGCACTA TACCTCATTG CCAGAATCCG AAGGTTCTTG
2301  GAGCAACGAG TGTATAGCTG GTGGTATCGG CCTAGACCTT CCTTTTGTTC
2351  TTTCCAACCC ACATCCTCTT TTCAAGACCT TCATTCCACA GATGAAAGTC
2401  GAAATGGTTT ATGTATCACA AAATAGCTTC TTCGAAAGCT CTAGTGATGG
2451  CCGTGGTTTT AGTATTGGAA GGCTGCTTAA CCTCTCGATT CCTGTGGGTG
2501  CGAAATTCGT GCAGGGGGAT ATCGGAGATT CCTACACCTA TGATCTCTCA
2551  GGATTCTTTG TTTCCGATGT CTATCGTAAC AATCCCCAAT CTACAGCGAC
2601  TCTTGTGATG AGCCCAGACT CTTGGAAAAT TCGCGGTGGC AATCTTTCAA
2651  GACAGGCATT TTTACTGAGG GGTAGCAACA ACTACGTCTA CAACTCCAAT
2701  TGTGAGCTCT TCGGACATTA CGCTATGGAA CTCCGTGGAT CTTCAAGGAA
2751  CTACAATGTA GATGTTGGTA CCAAACTCCG ATTCTAG
```

The PSORT algorithm predicts an outer membrane location (0.924).

The protein was expressed in *E.coli* and purified as a his-tag product, as shown in Figure 58A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 58B) and for FACS (Figure 58C) analyses. A GST-fusion protein was also expressed.

The cp6733 protein was also identified in the 2D-PAGE experiment (Cpn0451).

These experiments show that cp6733 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 59

The following *C.pneumoniae* protein (PID 4376814) was expressed <SEQ ID 117; cp6814>:

```
  1  MHDALLSILA IQELDIKMIR LMRVKKEHQK ELAKVQSLKS DIRRKVQEKE
 51  LEMENLKTQI RDGENRIQEI SEQINKLENQ QAAVKKMDEF NALTQEMTTA
101  NKERRSLEHQ LSDLMDKQAG GEDLIVSLKE SLASTENSSS VIEKEIFESI
151  KKINEEGKAL LEQRTELKHA TNPELLSIYE RLLNNKKDRV VVPIENRVCS
201  GCHIVLTPQH ENLVRKKDRL IFCEHCSRIL YWQESQVNAQ ENSTAKRRRR
251  RAAV*
```

The cp6814 nueleotide sequence <SEQ ID 118> is:

```
  1  ATGCATGACG CACTTCTAAG CATTTTGGCT ATTCAAGAGC TTGATATTAA
 51  AATGATTCGC CTTATGCGCG TAAAGAAAGA ACATCAGAAA GAATTGGCTA
101  AAGTCCAATC TTTAAAAAGT GATATTCGTA GAAAAGTTCA GGAAAAAGAA
151  CTCGAAATGG AGAATTTGAA AACTCAAATT CGAGATGGAG AGAATCGCAT
201  CCAAGAGATT TCTGAACAAA TCAATAAATT AGAAAATCAG CAAGCTGCTG
251  TAAAAAAAAT GGATGAGTTT AACGCTCTTA CCCAAGAAAT GACTACAGCA
301  AACAAAGAAC GTCGCTCTTT AGAGCACCAG CTTAGCGATC TCATGGATAA
351  GCAAGCTGGA GGCGAAGACC TTATTGTCTC TCTAAAAGAA AGCTTAGCTT
401  CTACAGAAAA TAGTAGCAGT GTCATTGAAA AAGAAATTTT TGAAAGCATC
451  AAAAAGATTA ATGAAGAAGG CAAAGCTTTG CTTGAACAAC GGACAGAGTT
501  AAAGCATGCG ACGAATCCCG AACTACTCAG CATCTATGAG CGTCTATTAA
551  ACAATAAAAA AGATCGCGTT GTTGTTCCTA TTGAAAATCG TGTCTGCAGT
601  GGTTGTCATA TTGTTCTAAC TCCTCAACAC GAAAATCTTG TAAGAAAGAA
651  AGACCGACTC ATTTTTTGCG AACATTGCTC TCGAATTCTC TATTGGCAAG
701  AATCCCAAGT CAATGCTCAG GAAAATTCCA CAGCAAAACG TCGTCGTCGT
751  CGCGCAGCTG TATAA
```

The PSORT algorithm predicts an inner membrane location (0.070).

The protein was expressed in *E.coli* and purified as a GST-fusion (Figure 59A) or his-tagged product. The recombinant proteins were used to immunise mice, whose sera were used in Western blot (Figure 59B) and FACS (Figure 59C) analyses.

These experiments show that cp6814 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 60

The following *C.pneumoniae* protein (PID 4376830) was expressed <SEQ ID 119; cp6830>:

```
  1  MKWLPATAVF AAVLPALTAF GDPASVEIST SHTGSGDPTS DAALTGFTQS
 51  STETDGTTYT IVGDITFSTF TNIPVPVVTP DANDSSSNSS KGGSSSSGAT
101  SLIRSSNLHS DFDFTKDSVL DLYHLFFPSA SNTLNPALLS SSSSGGSSSS
151  SSSSSSGSAS AVVAADPKGG AAFYSNEANG TLTFTTDSGN PGSLTLQNLK
201  MTGDGAAIYS KGPLVFTGLK NLTFTGNESQ KSGGAAYTEG ALTTQAIVEA
251  VTFTGNTSAG QGGAIYVKEA TLFNALDSLK FEKNTSGQAG GGIYTESTLT
301  ISNITKSIEF ISNKASVPAP APEPTSPAPS SLINSTTIDT STLQTRAASA
351  TPAVAPVAAV TPTPISTQET AGNGGAIYAK QGISISTFKD LTFKSNSASV
```

```
 401  DATLTVDSST IGESGGAIFA ADSIQIQQCT GTTLFSGNTA NKSGGGIYAV
 451  GQVTLEDIAN LKMTNNTCKG EGGAIYTKKA LTINNGAILT TFSGNTSTDN
 501  GGAIFAVGGI TLSDLVEVRF SKNKTGNYSA PITKAASNTA PVVSSSTTAA
 551  SPAVPAAAAA PVTNAAKGGA LYSTEGLTVS GITSILSFEN NECQNQGGGA
 601  YVTKTFQCSD SHRLQFTSNK AADEGGGLYC GDDVTLTNLT GKTLFQENSS
 651  EKHGGGLSLA SGKSLTMTSL ESFCLNANTA KENGGGANVP ENIVLTFTYT
 701  PTPNEPAPVQ QPVYGEALVT GNTATKSGGG IYTKNAAFSN LSSVTFDQNT
 751  SSENGGALLT QKAADKTDCS FTYITNVNIT NNTATGNGGG IAGGKAHFDR
 801  IDNLTVQSNQ AKKGGGVYLE DALILEKVIT GSVSQNTATE SGGGIYAKDI
 851  QLQALPGSFT ITDNKVETSL TTSTNLYGGG IYSSGAVTLT NISGTFGITG
 901  NSVINTATSQ DADIQGGGIY ATTSLSINQC NTPILFSNNS AATKKTSTTK
 951  QIAGGAIFSA AVTIENNSQP IIFLNNSAKS EATTAATAGN KDSCGGAIAA
1001  NSVTLTNNPE ITFKGNYAET GGAIGCIDLT NGSPPRKVSI ADNGSVLFQD
1051  NSALNRGGAI YGETIDISRT GATFIGNSSK HDGSAICCST ALTLAPNSQL
1101  IFENNKVTET TATTKASINN LGAAIYGNNE TSDVTISLSA ENGSIFFKNN
1151  LCTATNKYCS IAGNVKFTAI EASAGKAISF YDAVNVSTKE TNAQELKLNE
1201  KATSTGTILF SGELHENKSY IPQKVTFAHG NLILGKNAEL SVVSFTQSPG
1251  TTITMGPGSV LSNHSKEAGG IAINNVIIDF SEIVPTKDNA TVAPPTLKLV
1301  SRTNADSKDK IDITGTVTLL DPNGNLYQNS YLGEDRDITL FNIDNSASGA
1351  VTATNVTLQG NLGAKKGYLG TWNLDPNSSG SKIILKWTFD KYLRWPYIPR
1401  DNHFYINSIW GAQNSLVTVK QGILGNMLNN ARFEDPAFNN FWASAIGSFL
1451  RKEVSRNSDS FTYHGRGYTA AVDAKPRQEF ILGAAFSQVF GHAESEYHLD
1501  NYKHKGSGHS TQASLYAGNI FYFPAIRSRP ILFQGVATYG YMQHDTTTYY
1551  PSIEEKNMAN WDSIAWLFDL RFSVDLKEPQ PHSTARLTFY TEAEYTRIRQ
1601  EKFTELDYDP RSFSACSYGN LAIPTGFSVD GALAWREIIL YNKVSAAYLP
1651  VILRNNPKAT YEVLSTKEKG NVVNVLPTRN AARAEVSSQI YLGSYWTLYG
1701  TYTIDASMNT LVQMANGGIR FVF*
```

A predicted signal peptide is highlighted.

The cp6830 nucleotide sequence <SEQ ID 120> is:

```
   1  ATGAAGTGGC TACCAGCTAC AGCTGTTTTT GCTGCCGTAC TCCCCGCACT
  51  AACAGCCTTC GGAGATCCCG CGTCTGTTGA AATAAGTACC AGCCATACAG
 101  GATCCGGGGA TCCTACAAGC GACGCTGCCT TAACAGGATT TACACAAAGT
 151  TCCACAGAAA CTGACGGTAC TACCTATACC ATTGTCGGTG ATATCACCTT
 201  CTCTACTTTT ACGAATATTC CTGTTCCCGT AGTAACTCCA GACGCCAACG
 251  ATAGTTCCAG CAATAGCTCT AAAGGAGGAA GTAGCAGTAG TGGAGCTACA
 301  TCTCTAATCC GATCCTCAAA CCTACACTCC GATTTTGATT TTACAAAAGA
 351  TAGCGTGTTA GACCTCTATC ACCTTTTCTT TCCTTCAGCT TCAAATACTC
 401  TCAATCCTGC ACTCCTTTCT TCCAGTAGCA GCGGTGGATC CTCGAGCAGC
 451  AGTAGCTCCT CATCATCTGG AAGTGCATCT GCTGTTGTTG CTGCGGACCC
 501  AAAAGGAGGC GCTGCCTTTT ATAGTAACGA GGCTAACGGA ACTTTAACCT
 551  TCACTACAGA CTCTGGAAAT CCCGGCTCCC TGACTCTTCA GAATCTTAAA
 601  ATGACCGGAG ATGGAGCCGC CATCTACTCG AAGGGTCCTC TAGTATTTAC
 651  TGGTTTAAAA AATCTAACCT TTACAGGAAA TGAATCTCAG AAATCTGGAG
 701  GTGCTGCCTA TACTGAAGGC GCACTCACAA CACAAGCAAT CGTTGAAGCC
 751  GTAACTTTTA CTGGCAACAC CTCGGCAGGG CAAGGAGGCG CTATCTATGT
 801  TAAAGAAGCT ACCCTATTCA ATGCTCTAGA CAGCCTCAAA TTTGAAAAAA
 851  ACACTTCTGG GCAAGCTGGT GGTGGAATCT ATACAGAGTC TACGCTCACA
 901  ATCTCGAACA TCACAAAATC TATTGAATTT ATCTCTAATA AAGCTTCTGT
 951  CCCTGCCCCC GCTCCTGAGC CCACCTCTCC GGCTCCAAGT AGCTTAATAA
1001  ATTCTACAAC GATCGATACC TCGACTCTCC AAACCCGAGC AGCATCCGCA
1051  ACTCCAGCAG TGGCTCCTGT TGCTGCCGTA ACTCCAACAC CAATCTCTAC
1101  TCAAGAGACC GCAGGAAATG GAGGCGCTAT CTATGCTAAA CAAGGTATTT
1151  CGATATCCAC GTTTAAAGAT CTGACCTTCA AGTCTAACTC TGCATCGGTA
1201  GATGCCACCC TTACTGTCGA TTCTAGCACT ATTGGAGAAT CTGGAGGTGC
1251  TATCTTTGCA GCAGACTCTA TACAAATCCA ACAGTGCACG GGAACCACCT
1301  TATTCAGTGG CAATACTGCC AATAAGTCTG GTGGGGGTAT TTACGCTGTA
1351  GGACAAGTCA CCCTAGAAGA TATAGCGAAT CTGAAGATGA CCAACAACAC
1401  CTGTAAAGGT GAAGGTGGAG CCATCTACAC TAAAAAGGCT TTAACTATCA
1451  ACAACGGTGC CATTCTCACT ACATTTTCTG GAAATACATC GACAGATAAT
1501  GGTGGGGCTA TTTTTGCTGT AGGTGGCATC ACTCTCTCTG ATCTTGTAGA
1551  AGTCCGCTTT AGTAAAAATA AGACCGGAAA TTATTCCGCT CCTATTACCA
1601  AAGCGGCTAG CAACACAGCT CCTGTAGTTT CTAGCTCTAC AACTGCTGCA
1651  TCTCCTGCGG TCCCTGCTGC CGCTGCAGCA CCTGTTACAA ACGCAGCAAA
1701  AGGAGGGGCT TTATATAGTA CAGAAGGACT GACTGTATCT GGAATCACAT
1751  CGATATTGTC GTTTGAAAAC AACGAATGCC AGAATCAAGG AGGTGGGGCT
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1801  TACGTTACTA AAACCTTCCA GTGTTCCGAT TCTCATCGCC TCCAGTTTAC
1851  TAGTAATAAA GCAGCAGATG AAGGCGGGGG CCTGTATTGT GGTGACGATG
1901  TCACGCTAAC GAACCTGACA GGGAAAACAC TATTTCAAGA GAATAGCAGT
1951  GAGAAACATG GAGGTGGGCT CTCTCTCGCC TCAGGAAAAT CTCTGACTAT
2001  GACATCGTTA GAGAGCTTCT GCTTAAATGC AAATACAGCA AAGGAAAACG
2051  GAGGCGGTGC GAATGTCCCT GAAAATATTG TACTCACCTT CACCTATACT
2101  CCCACTCCAA ATGAACCTGC GCCTGTGCAG CAGCCCGTGT ATGGAGAAGC
2151  TCTTGTTACT GGAAATACAG CCACAAAAAG TGGTGGGGGC ATTTACACGA
2201  AAAATGCGGC CTTCTCAAAT TTATCTTCTG TAACTTTTGA TCAAAATACC
2251  TCTTCAGAAA ATGGTGGTGC CTTACTTACC CAAAAAGCTG CAGATAAAAC
2301  GGACTGTTCT TTCACCTATA TTACAAATGT CAATATCACC AACAATACAG
2351  CTACAGGAAA TGGTGGGGGC ATTGCTGGGG GAAAAGCACA TTTCGATCGC
2401  ATTGATAATC TTACAGTCCA AAGCAACCAA GCAAAGAAAG GTGGTGGGGT
2451  TTATCTTGAA GATGCCCTCA TCCTGGAAAA GGTTATTACA GGTTCTGTCT
2501  CACAAAATAC AGCTACAGAA AGTGGTGGGG GTATCTACGC TAAGGATATT
2551  CAACTACAAG CTCTACCTGG AAGCTTCACA ATTACCGATA ATAAAGTCGA
2601  AACTAGTCTT ACTACTAGCA CTAATTTATA TGGTGGGGGC ATCTATTCCA
2651  GTGGAGCTGT CACGCTAACC AATATATCTG GAACCTTTGG CATTACAGGA
2701  AACTCTGTTA TCAATACAGC GACATCCCAG GATGCAGATA TACAAGGTGG
2751  GGGCATTTAT GCAACCACGT CTCTCTCAAT AAATCAATGT AATACACCCA
2801  TTCTATTTAG CAACAACTCT GCTGCCACTA AAAAAACATC AACAACAAAG
2851  CAAATTGCTG GTGGGGCTAT CTTCTCCGCT GCAGTAACTA TCGAGAATAA
2901  CTCTCAGCCC ATTATTTTCT TAAATAATTC CGCAAAGTCG GAAGCAACTA
2951  CAGCAGCAAC TGCAGGAAAT AAAGATAGCT GTGGAGGAGC CATTGCAGCT
3001  AACTCTGTTA CTTTAACAAA TAACCCTGAA ATAACCTTTA AAGGAAATTA
3051  TGCAGAAACT GGAGGAGCGA TTGGCTGTAT TGATCTTACT AATGGCTCAC
3101  CTCCCCGTAA AGTCTCTATT GCAGACAACG GTTCTGTCCT TTTTCAAGAC
3151  AACTCTGCGT TAAATCGCGG AGGCGCTATC TATGGAGAGA CTATCGATAT
3201  CTCCAGGACA GGTGCGACTT TCATCGGTAA CTCTTCAAAA CATGATGGAA
3251  GTGCAATTTG CTGTTCAACA GCCCTAACTC TTGCGCCAAA CTCCCAACTT
3301  ATCTTTGAAA ACAATAAGGT TACGGAAACC ACAGCCACTA CAAAAGCTTC
3351  CATAAAATAAT TTAGGAGCTG CAATTTATGG AAATAATGAG ACTAGTGACG
3401  TCACTATCTC TTTATCAGCT GAGAATGGAA GTATTTTCTT TAAAAACAAT
3451  CTATGCACAG CAACAAACAA ATACTGCAGT ATTGCTGGAA ACGTAAAATT
3501  TACAGCAATA GAAGCTTCAG CAGGGAAAGC TATATCTTTC TATGATGCAG
3551  TTAACGTTTC CACCAAAGAA ACAAATGCTC AAGAGCTAAA ATTAAATGAA
3601  AAAGCGACAA GTACAGGAAC GATTCTATTT TCTGGGGAAC TTCACGAAAA
3651  TAAATCCTAT ATTCCACAGA AAGTCACTTT CGCACATGGG AATCTCATTC
3701  TAGGTAAAAA TGCAGAACTT AGCGTAGTTT CCTTTACCCA ATCTCCAGGC
3751  ACCACAATCA CTATGGGCCC AGGATCGGTT CTTTCCAACC ATAGCAAAGA
3801  AGCAGGAGGA ATCGCTATAA ACAATGTCAT CATTGATTTT AGTGAAATCG
3851  TTCCTACTAA AGATAATGCA ACAGTAGCTC CACCCACTCT TAAATTAGTA
3901  TCGAGAACTA ATGCAGATAG TAAAGATAAG ATTGATATTA CAGGAACTGT
3951  GACTCTTCTA GATCCTAATG GCAACTTATA TCAAAATTCT TATCTTGGTG
4001  AAGACCGCGA TATCACTCTT TTCAATATAG ACAATTCTGC AAGTGGGGCA
4051  GTTACAGCCA CGAATGTCAC CCTTCAAGGG AATTTAGGAG CTAAAAAAGG
4101  ATATTTAGGA ACCTGGAATT TGGATCCAAA TTCCTCGGGT TCAAAAATTA
4151  TTCTAAAATG GACCTTTGAC AAATACCTGC GCTGGCCCTA CATCCCTAGA
4201  GACAACCACT TCTACATCAA CTCTATTTGG GGAGCACAAA ACTCTTTAGT
4251  GACTGTGAAA CAAGGGATCT TAGGGAACAT GTTGAACAAT GCAAGGTTTG
4301  AAGATCCTGC TTTCAACAAC TTCTGGGCTT CGGCTATAGG ATCTTTCCTT
4351  AGGAAAGAAG TATCTCGAAA TTCTGACTCA TTCACCTATC ATGGCAGAGG
4401  CTATACCGCT GCTGTGGATG CCAAACCTCG CCAAGAATTT ATTTTAGGAG
4451  CTGCCTTCAG TCAGGTTTTT GGTCACGCCG AGTCTGAATA TCACCTTGAC
4501  AACTATAAGC ATAAAGGCTC AGGTCACTCT ACACAAGCAT CTCTTTATGC
4551  TGGCAATATC TTCTATTTTC CTGCGATACG GTCTCGGCCT ATTCTATTCC
4601  AAGGTGTGGC GACCTATGGT TATATGCAAC ATGACACCAC AACCTACTAT
4651  CCTTCTATTG AAGAAAAAAA TATGGCAAAC TGGGATAGCA TTGCTTGGTT
4701  ATTTGATCTG CGTTTCAGTG TGGATCTTAA AGAACCTCAA CCTCACTCTA
4751  CAGCAAGGCT TACCTTCTAT ACAGAAGCTG AGTATACCAG AATTCGCCAG
4801  GAGAAATTCA CAGAGCTAGA CTATGATCCT AGATCTTTCT CTGCATGCTC
4851  TTATGGAAAC TTAGCAATTC CTACTGGATT CTCTGTAGAC GGAGCATTAG
4901  CTTGGCGTGA GATTATTCTA TATAATAAAG TATCAGCTGC GTACCTCCCT
4951  GTGATTCTCA GGAATAATCC AAAAGCGACC TATGAAGTTC TCTCTACAAA
5001  AGAAAAGGGC AACGTAGTCA ACGTTCTCCC TACAAGAAAC GCAGCTCGTG
5051  CAGAGGTGAG CTCTCAAATT TATCTTGGAA GTTACTGGAC ACTCTACGGC
5101  ACGTATACTA TTGATGCTTC AATGAATACT TTAGTGCAAA TGGCCAACGG
5151  AGGGATCCGG TTTGTATTCT AG
```

The PSORT algorithm predicts an outer membrane location (0.926).

The protein was expressed in *E.coli* and purified as a GST-fusion (Figure 60A) or his-tagged product. The recombinant proteins were used to immunise mice, whose sera were used in Western blot (Figure 60B) and FACS (Figure 60C) analyses.

The cp6830 protein was also identified in the 2D-PAGE experiment (Cpn0540) and showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp6830 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 61

The following *C.pneumoniae* protein (PID 4376854) was expressed <SEQ ID 121; cp6854>:

```
  1 MSIAIAREQY AAILDMHPKP SIAMFSSEQA RTSWEKRQAH PYLYRLLEII
 51 WGVVKFLLGL IFFIPLGLFW VLQKICQNFI LLGAGGWIFR PICRDSNLLR
101 QAYAARLFSA SFQDHVSSVR RVCLQYDEVF IDGLELRLPN AKPDRWMLIS
151 NGNSDCLEYR TVLQGEKDWI FRIAEESQSN ILIFNYPGVM KSQGNITRNN
201 VVKSYQACVR YLRDEPAGPQ ARQIVAYGYS LGASVQAEAL SKEIADGSDS
251 VRWFVVKDRG ARSTGAVAKQ FIGSLGVWLA NLTHWNINSE KRSKDLHCPE
301 LFIYGKDSQG NLIGDGLFKK ETCFAAPFLD PKNLEECSGK KIPVAQTGLR
351 HDHILSDDVI KEVAGHIQRH FDN*
```

The cp6854 nucleotide sequence <SEQ ID 122> is:

```
   1 ATGTCAATAG CTATTGCAAG GGAACAATAC GCAGCTATAT TGGATATGCA
  51 TCCTAAACCT TCGATCGCCA TGTTTTCTTC GGAGCAGGCG AGAACTTCTT
 101 GGGAGAAACG ACAGGCTCAT CCTTACCTTT ATCGTCTTCT TGAGATCATA
 151 TGGGGTGTTG TGAAATTTCT TCTCGGCTTA ATCTTCTTTA TTCCCTTGGG
 201 TCTTTTCTGG GTCCTTCAGA AGATATGTCA GAATTTTATT CTTCTTGGTG
 251 CAGGAGGGTG GATTTTTAGA CCCATATGCA GGGACTCTAA TTTATTGCGA
 301 CAAGCTTACG CCGCGCGTCT TTTCTCCGCT TCATTCCAAG ATCATGTCTC
 351 CTCTGTGCGA AGGGTTTGCT TACAGTATGA CGAGGTCTTT ATTGACGGAT
 401 TGGAGTTACG TCTTCCCAAT GCTAAGCCAG ATCGATGGAT GTTAATCTCC
 451 AATGGAAACT CCGATTGCTT AGAGTATAGG ACAGTGCTGC AAGGGGAAAA
 501 GGACTGGATA TTCCGTATTG CTGAAGAGTC TCAATCCAAC ATTTTAATCT
 551 TCAATTACCC AGGAGTCATG AAGAGCCAAG GGAATATAAC AAGAAACAAT
 601 GTAGTCAAAT CTTATCAAGC ATGCGTACGC TATCTTAGAG ATGAACCCGC
 651 AGGACCTCAG GCGCGTCAAA TCGTTGCTTA TGGCTATTCT TTAGGAGCTA
 701 GTGTTCAAGC CGAAGCATTA AGTAAAGAGA TCGCAGACGG AAGTGATAGC
 751 GTCCGTTGGT TTGTCGTTAA AGATCGAGGA GCTCGCTCTA CAGGAGCCGT
 801 TGCTAAACAG TTTATTGGAA GTCTAGGAGT TTGGCTGGCG AATCTTACCC
 851 ATTGGAATAT TAATTCTGAA AAGAGAAGCA AGGACTTGCA TTGCCCAGAA
 901 CTCTTTATTT ATGGCAAGGA TTCCCAAGGT AATCTTATCG GGGATGGATT
 951 GTTCAAAAAA GAGACGTGCT TCGCAGCACC ATTTTTAGAT CCTAAAAACT
1001 TGGAAGAGTG TTCAGGGAAG AAAATCCCTG TAGCTCAGAC CGGTCTAAGA
1051 CACGATCATA TCCTTTCCGA TGATGTGATT AAAGAAGTTG CAGGTCATAT
1101 TCAAAGACAT TTCGATAATT A
```

The PSORT algorithm predicts an inner membrane location (0.461).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 61A. The recombinant protein was used to immunise mice, whose sera were used in Western blot (Figure 61B) and FACS (Figure 61C) analyses. A his-tagged protein was also expressed.

These experiments show that cp6854 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 62

The following *C.pneumoniae* protein (PID 4377101) was expressed <SEQ ID 123; cp7101>:

```
  1 MYSCYSKGIS HNYLLHPMSR LDIFVFDSLI ANQDQNLLEE IFCSEDTVLF
 51 KAYRTTALQS PLAAKNLNIA RKVANYILAD NGEIDTVKLV EAIHHLSQCT
101 YPLGPHRHNE AQDREHLLKM LKALKENPKL KESIKTLFVP SYSTIQNLIR
151 HTLALNPQTI LSTIHVRQAA LTALFTYLRQ DVGSCFATAP AILIHQEYPE
201 RFLKDLNDLI SSGKLSRIVN QREIAVPINL SGCIGELFKP LRILDLYPDP
251 LVKLSSSPGL KKAFSAANLI ETLGDSEAQI QQLLSHQYLM QKLQNVHETL
301 TANDIIKSTL LHYYQLQEST VRAIFFKEGL FSKEQVAFST QHPRELSEIQ
351 RVYHYLHAYE EAKSAFIHDT QNPLLKAWEY TLATLADASQ PTISNHIRLA
401 LGWKSEDPHS LVSLVTHFVE EEVENIRILV QQCEQTYHEA RSQLEYIEGR
451 MRNPLNNQDS QILTMDHMRF RQELNKALYE WDSAQEKAKK FLHLPEFLLS
501 FYTKQIPLYF RSSYDAFIQE FAHLYANAPA GFRILFTHGR THPNTWSPIY
551 SINEFIRFLS EFFTSTESEL LGKHAVINLE KETSRLVHNI TAMLHTDVFQ
601 EALLTRILEA YQLPVPPSIL NHLDQLSQTP WVYVSGGTVD TLLLDYFESS
651 EPLTLTEKHP ENPHELAAFY ADALKDLPTG IKSYLEEGSH SLLSSSPTHV
701 FSIIAGSPLF REAWDNDWYS YTWLRDVWVK QHQDFLQDTI LPQLSIYAFI
751 ENFCNKYALQ HVVHDFHDFC SDHSLTLPEL YDKGSRFLSS LFTKDKTVAL
801 IYIRRLLYLM VREVPYVSEQ QLPEVLDNVS SYLGISSRIT YEKFRSLIEE
851 TIPKMTLLSS ADLRHIYKGL LMQSYQKIYT EEDTYLRLTT AMRHHNLAYP
901 APLLFADSNW PSIYFGFILN PGTTEIDLWK FNYAGLQGQP LDNIQELFAT
951 SRPWTLYANP IDYGMPPPPG YRSRLPKEFF *
```

The cp7101 nucleotide sequence <SEQ ID 124> is:

```
   1 ATGTATTCGT GTTACAGCAA AGGAATATCC CATAACTATC TTCTACATCC
  51 TATGTCACGT TTGGATATTT TTGTTTTCGA TTCTCTGATC GCAAACCAGG
 101 ATCAAAATCT TCTTGAGGAA ATTTTCTGTT CTGAAGACAC AGTTTTATTT
 151 AAAGCCTACC GTACTACGGC TCTACAATCC CCTCTAGCTG CTAAGAACCT
 201 AAATATCGCC CGTAAAGTCG CAAATTATAT CTTAGCTGAC AATGGGGAAA
 251 TCGATACAGT AAAGCTTGTC GAAGCCATTC ACCATCTCTC ACAATGTACC
 301 TATCCTTTAG GGCCTCATCG CCATAATGAA GCTCAAGATC GTGAACACCT
 351 CCTTAAAATG CTAAAAGCTC TAAAGGAAAA TCCTAAATTA AAAGAAAGCA
 401 TCAAAACTCT CTTTGTCCCT TCATACTCTA CAATCCAAAA CCTAATTCGC
 451 CATACACTAG CATTGAATCC ACAGACAATT CTCTCTACGA TTCATGTGCG
 501 TCAAGCAGCA CTCACAGCGC TCTTCACCTA CCTTCGGCAA GATGTAGGTT
 551 CCTGTTTTGC TACGGCTCCT GCCATTCTCA TTCACCAAGA ATATCCAGAA
 601 CGATTCCTTA AAGATCTCAA TGATCTCATT AGCAGTGGCA AACTCTCTAG
 651 AATCGTAAAC CAAAGGGAAA TTGCGGTTCC TATAAACCTT TCGGGATGCA
 701 TTGGAGAGCT ATTCAAGCCT TTAAGGATTC TAGATCTTTA TCCTGATCCT
 751 CTGGTTAAGC TCTCCTCATC TCCAGGACTC AAAAAAGCCT TTTCTGCTGC
 801 CAATCTTATT GAAACTCTTG GGGATTCTGA AGCACAAATC CAACAGTTGC
 851 TCTCGCATCA ATATTTGATG CAAAAACTAC AAAATGTCCA TGAGACCTTA
 901 ACTGCTAACG ACATTATCAA ATCGACACTT CTGCACTACT ATCAGCTCCA
 951 AGAAAGTACT GTACGAGCTA TTTTCTTCAA AGAAGGGTTG TTCAGCAAAG
1001 AACAAGTGGC ATTCTCGACG CAACACCCCA GAGAGCTCTC AGAAATACAA
1051 CGGGTATACC ACTACTTACA TGCCTATGAA GAAGCAAAAT CTGCTTTTAT
1101 CCATGACACT CAAAATCCCT TACTGAAAGC CTGGGAGTAT ACTTTAGCGA
1151 CTCTTGCGGA TGCTAGCCAA CCTACCATCT CAAACCATAT CCGCCTTGCC
1201 TTAGGATGGA AAAGTGAAGA CCCTCACAGT CTTGTATCTC TAGTTACACA
1251 CTTTGTTGAA GAGGAAGTAG AAAACATCCG AATTTTAGTC CAACAATGTG
1301 AACAGACCTA TCACGAAGCA CGCTCCCAAC TAGAATATAT TGAAGGGCGG
1351 ATGCGCAACC CACTAAATAA TCAAGACAGT CAGATTTTGA CGATGGATCA
1401 CATGCGCTTC CGTCAAGAAC TCAATAAAGC TCTTTATGAG TGGGATAGTG
1451 CTCAAGAAAA GGCAAAGAAA TTTCTACATC TTCCTGAATT CTTACTTTCT
1501 TTCTATACAA AGCAAATTCC CTTATACTTT CGTAGTTCTT ACGATGCCTT
1551 CATTCAAGAA TTTGCTCATC TCTATGCTAA TGCTCCCGCT GGCTTCCGTA
1601 TTCTTTTCAC GCATGGACGC ACCCATCCGA ACACATGGTC CCCCATCTAT
1651 TCGATTAATG AATTTATACG TTTTCTTTCT GAATTCTTCA CCTCCACAGA
1701 GTCAGAACTT CTGGGGAAAC ATGCCGTGAT CAATTTAGAG AAAGAAACAT
1751 CTCGGCTCGT CCACAACATC ACTGCCATGC TACACACGGA TGTTTTCCAA
1801 GAAGCTCTCC TTACAAGAAT TTTAGAAGCC TATCAGCTTC CTGTGCCTCC
1851 CTCCATCTTA AACCACTTAG ATCAGCTGTC ACAAACTCCC TGGGTTTATG
1901 TTTCTGGAGG AACAGTGGAC ACTCTTCTTT TGGATTATTT TGAAAGCTCA
1951 GAACCTCTGA CACTTACAGA AAAGCATCCT GAAAATCCTC ATGAGCTTGC
2001 AGCTTTCTAC GCAGACGCCC TTAAAGATCT CCCTACAGGA ATTAAAAGTT
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2051  ATCTAGAAGA AGGATCCCAC TCTCTACTTA GCTCATCACC CACCCACGTT
2101  TTCTCTATAA TCGCAGGATC TCCTTTATTT CGGGAAGCTT GGGATAATGA
2151  TTGGTACAGC TATACCTGGC TTCGTGATGT CTGGGTGAAA CAACACCAAG
2201  ATTTCCTTCA AGATACTATA TTACCTCAGC TAAGTATCTA TGCTTTCATA
2251  GAGAATTTTT GTAACAAATA TGCTTTGCAA CATGTAGTTC ATGACTTTCA
2301  TGATTTCTGC TCCGACCACT CCTTGACTCT TCCGGAGCTC TATGACAAAG
2351  GATCGCGTTT TCTAAGCTCC TTATTCACCA AAGATAAGAC CGTAGCTCTT
2401  ATCTATATAC GCCGTCTTCT CTACCTTATG GTCCGTGAAG TCCCTTATGT
2451  TTCAGAACAA CAGCTTCCAG AAGTCTTAGA TAACGTCTCT TCATATCTCG
2501  GGATTTCCTC TCGTATTACC TATGAGAAAT TCCGCTCCCT GATAGAGGAA
2551  ACCATCCCTA AAATGACCTT ACTCTCCTCA GCAGACCTGA GGCATATCTA
2601  TAAAGGTCTC CTCATGCAAA GTTATCAAAA GATCTACACC GAAGAAGATA
2651  CGTACCTCCG CCTCACCACG GCAATGAGGC ATCATAATCT TGCCTATCCC
2701  GCTCCTTTGC TCTTTGCAGA CAGTAACTGG CCTTCTATTT ATTTTGGATT
2751  CATCCTAAAT CCAGGAACCA CAGAGATCGA TCTTTGGAAA TTTAACTATG
2801  CAGGGCTGCA AGGACAGCCT CTTGACAATA TCCAGGAGCT GTTCGCAACG
2851  TCAAGACCCT GGACCCTCTA TGCAAATCCT ATAGATTATG GCATGCCACC
2901  GCCTCCAGGC TACCGCAGCC GCCTCCCTAA AGAATTTTTC TAG
```

The PSORT algorithm predicts a cytoplasmic location (0.206).

The protein was expressed in *E.coli* and purified as a GST-fusion (Figure 62A) or his-tagged product. The proteins were used to immunise mice, whose sera were used in Western blot (Figure 62B) and FACS (Figure 62C) analyses.

This protein also showed good cross-reactivity with human sera, including sera from patients with pneumonitis.

These experiments show that cp7101 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 63

The following *C.pneumoniae* protein (PID 4377107) was expressed <SEQ ID 125; cp7107>:

```
  1  MSIVRNSALP LPCLSRSETF KKVRSHMKFM KVLTPWIYRK DLWVTAFLLT
 51  AIPGSFAHTL VDIAGEPRHA AQATGVSGDG KIVIGMKVPD DPFAITVGFQ
101  YIDGHLQPLE AVRPQCSVYP NGITPDGTVI VGTNYAIGMG SVAVKWVNGK
151  VSELPMLPDT LDSVASAVSA DGRVIGGNRN INLGASVAVK WEDDVITQLP
201  SLPDAMNACV NGISSDGSII VGTMVDVSWR NTAVQWIGDQ LSVIGTLGGT
251  TSVASAISTD GTVIVGGSEN ADSQTHAYAY KNGVMSDIGT LGGFYSLAHA
301  VSSDGSVIVG VSTNSEHRYH AFQYADGQMV DLGTLGGPES YAQGVSGDGK
351  VIVGRAQVPS GDWHAFLCPF QAPSPAPVHG GSTVVTSQNP RGMVDINATY
401  SSLKNSQQQL QRLLIQHSAK VESVSSGAPS FTSVKGAISK QSPAVQNDVQ
451  KGTFLSYRSQ VHGNVQNQQL LTGAFMDWKL ASAPKCGFKV ALHYGSQDAL
501  VERAALPYTE QGLGSSVLSG FGGQVQGRYD FNLGETVVLQ PFMGIQVLHL
551  SREGYSEKNV RFPVSYDSVA YSAATSFMGA HVFASLSPKM STAATLGVER
601  DLNSHIDEFK GSVSAMGNFV LENSTVSVLR PFASLAMYYD VRQQQLVTLS
651  VVMNQQPLTG TLSLVSQSSY NLSF*
```

The cp7107 nucleotide sequenee <SEQ ID 126> is:

```
  1  ATGAGTATAG TCAGAAATTC TGCATTGCCA CTTCCGTGTT TAAGCAGATC
 51  CGAAACCTTT AAAAAAGTTA GGTCGCATAT GAAATTTATG AAAGTCCTTA
101  CTCCATGGAT TTATCGAAAA GATCTTTGGG TAACAGCATT CTTACTGACA
151  GCAATTCCAG GATCTTTTGC ACATACTCTT GTTGATATAG CAGGAGAACC
201  TCGGCATGCT GCTCAAGCAA CAGGAGTTTC TGGAGATGGT AAAATTGTTA
251  TAGGAATGAA AGTTCCGGAT GATCCTTTTG CTATAACTGT AGGATTTCAA
301  TATATTGATG GGCATTTGCA ACCCTTAGAG GCAGTACGTC CTCAATGCTC
351  TGTATACCCT AATGGTATAA CCCCGGACGG AACGGTTATT GTGGGTACAA
401  ACTATGCCAT CGGGATGGGT AGTGTTGCTG TGAAATGGGT AAATGGCAAG
451  GTTTCTGAAC TTCCCATGCT CCCTGACACC CTCGATTCTG TAGCATCGGC
501  AGTTTCTGCA GATGGAAGAG TGATTGGAGG GAATAGAAAT ATAAATCTTG
551  GCGCTTCTGT TGCTGTGAAA TGGGAGGACG ACGTGATTAC ACAACTTCCT
601  TCTCTTCCTG ATGCTATGAA TGCTTGTGTT AACGGAATTT CTTCAGATGG
```

```
 651  TTCTATAATT GTAGGAACCA TGGTAGACGT GTCATGGAGA AATACCGCAG
 701  TACAATGGAT CGGGGATCAG CTCTCTGTTA TTGGGACTTT AGGAGGAACT
 751  ACTTCTGTTG CTAGTGCAAT CTCAACAGAT GGCACTGTGA TTGTAGGAGG
 801  TTCTGAAAAT GCAGATTCTC AGACTCATGC CTATGCTTAT AAAAACGGTG
 851  TTATGAGCGA TATAGGGACC CTCGGAGGTT TTTATTCTTT AGCACATGCA
 901  GTATCTTCAG ATGGTTCTGT GATTGTAGGA GTATCCACGA ACTCTGAGCA
 951  TAGATATCAT GCATTCCAAT ATGCTGATGG ACAGATGGTA GATTTAGGAA
1001  CTTTAGGAGG GCCTGAATCT TATGCTCAAG GTGTGTCTGG AGATGGAAAG
1051  GTAATTGTGG GTAGAGCACA AGTACCATCT GGAGATTGGC ATGCGTTCCT
1101  ATGTCCTTTC CAAGCTCCGA GCCCTGCTCC TGTCCATGGG GGAAGCACTG
1151  TCGTAACTAG CCAGAATCCA CGTGGAATGG TAGATATCAA TGCTACGTAC
1201  TCCTCTTTGA AAAATAGCCA ACAACAACTA CAAAGATTGC TTATCCAGCA
1251  TAGTGCAAAA GTTGAAAGTG TATCCTCAGG AGCACCATCT TTTACAAGTG
1301  TGAAAGGTGC GATCTCAAAA CAGAGCCCTG CAGTGCAAAA TGATGTACAG
1351  AAAGGGACGT TTTTAAGTTA CCGTTCCCAA GTTCATGGAA ACGTGCAGAA
1401  TCAGCAATTG CTCACAGGAG CTTTTATGGA CTGGAAACTC GCTTCAGCTC
1451  CTAAATGCGG CTTTAAAGTA GCTCTCCACT ATGGCTCTCA AGATGCTCTC
1501  GTAGAACGTG CAGCTCTTCC TTACACAGAA CAAGGCTTAG GAAGCAGTGT
1551  CTTGTCAGGT TTTGGAGGAC AAGTTCAAGG ACGCTATGAC TTTAATTTAG
1601  GAGAAACTGT TGTTCTGCAA CCCTTTATGG GCATTCAAGT TCTCCACCTA
1651  AGTAGAGAAG GGTATTCTGA GAAGAATGTT CGATTTCCTG TAAGCTATGA
1701  TTCTGTAGCC TACTCAGCAG CTACTAGCTT TATGGGTGCG CATGTATTTG
1751  CCTCCCTAAG CCCTAAAATG AGTACAGCAG CAACTTTAGG TGTGGAGAGA
1801  GATCTGAATT CACATATAGA TGAATTTAAG GGATCCGTCT CTGCTATGGG
1851  AAACTTTGTC TTGGAAAATT CTACAGTGAG TGTTTTAAGA CCTTTTGCTT
1901  CTCTTGCTAT GTACTATGAC GTAAGACAAC AGCAACTCGT GACGTTGTCA
1951  GTAGTTATGA ATCAACAACC CTTAACAGGC ACACTAAGCT TAGTAAGCCA
2001  AAGTAGCTAT AATCTTAGCT TCTAA
```

The PSORT algorithm predicts an inner membrane location (0.100).

The protein was expressed in *E.coli* and purified as a GST-fusion (Figure 63A) or his-tagged product. The proteins were used to immunise miee, whose sera were used in Western blot (Figure 63B) and FACS (Figure 63C) analyses.

These experiments show that cp7107 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 64

The following *C.pneumoniae* protein (PID 4376467) was expressed <SEQ ID 127; cp6467>:

```
   1  MLRFFAVFIS TLWLITSGCS PSQSSKGIFV VNMKEMPRSL DPGKTRLIAD
  51  QTLMRHLYEG LVEEHSQNGE IKPALAESYT ISEDGTRYTF KIKNILWSNG
 101  DPLTAQDFVS SWKEILKEDA SSVYLYAFLP IKNARAIFDD TESPENLGVR
 151  ALDKRHLEIQ LETPCAHFLH FLTLPIFFPV HETLRNYSTS FEEMPITCGA
 201  FRPVSLEKGL RLHLEKNPMY HNKSRVKLHK IIVQFISNAN TAAILFKHKK
 251  LDWQGPPWGE PIPPEISASL HQDDQLFSLP GASTTWLLFN IQKKPWNNAK
 301  LRKALSLAID KDMLTKVVYQ GLAEPTDHIL HPRLYPGTYP ERKRQNERIL
 351  EAQQLFEEAL DELQMTREDL EKETLTFSTF SFSYGRICQM LREQWKKVLK
 401  FTIPIVGQEF FTIQKNFLEG NYSLTVNQWT AAFIDPMSYL MIFANPGGIS
 451  PYHLQDSHFQ TLLIKITQEH KKHLRNQLII EALDYLEHCH ILEPLCHPNL
 501  RIALNKNIKN FNLFVRRTSD FRFIEKL*
```

A predicted signal peptide is highlighted.

The cp6467 nucleotide sequenee <SEQ ID 128> is:

```
   1  ATGCTCCGTT TCTTCGCTGT ATTTATATCA ACTCTTTGGC TCATTACCTC
  51  AGGATGTTCC CCATCCCAAT CCTCTAAAGG AATTTTTGTG GTAAATATGA
 101  AGGAAATGCC ACGCTCCTTG GATCCTGGAA AAACTCGTCT CATTGCAGAC
 151  CAAACTCTAA TGCGTCATCT ATATGAAGGA CTCGTCGAAG AACATTCCCA
 201  AAATGGAGAG ATTAAACCAG CCCTTGCAGA AAGCTACACC ATCTCCGAAG
 251  ACGGGACTCG GTACACATTT AAAATCAAAA ACATCCTTTG GAGTAACGGA
 301  GACCCTCTGA CAGCTCAAGA CTTTGTCTCC TCTTGGAAGG AAATCCTAAA
```

```
 351  GGAAGATGCG TCCTCCGTAT ATCTCTATGC GTTTTTACCT ATCAAAAATG
 401  CTCGGGCAAT CTTTGATGAT ACTGAGTCTC CAGAAAATCT AGGAGTCCGA
 451  GCTTTAGATA AGCGTCATCT CGAAATTCAG TTAGAAACTC CCTGCGCGCA
 501  TTTCCTACAT TTCTTGACTC TTCCTATTTT TTTCCCTGTT CATGAAACTC
 551  TGCGAAACTA TAGCACCTCT TTTGAAGAGA TGCCCATTAC CTGCGGTGCT
 601  TTCCGCCCTG TGTCTCTAGA AAAAGGCCTG AGACTCCATC TAGAGAAAAA
 651  CCCTATGTAC CATAATAAAA GCCGTGTGAA ACTACATAAA ATTATTGTAC
 701  AGTTTATCTC AAACGCTAAC ACTGCAGCCA TTCTATTCAA ACATAAGAAA
 751  TTAGATTGGC AAGGACCTCC TTGGGGAGAA CCTATCCCTC CAGAAATCTC
 801  AGCTTCTCTA CATCAAGATG ACCAGCTCTT TTCTCTTCCG GGCGCTTCGA
 851  CTACATGGTT ACTCTTTAAT ATACAAAAAA AACCTTGGAA CAATGCTAAA
 901  TTACGCAAGG CATTGAGCCT TGCAATAGAC AAAGATATGT TAACCAAAGT
 951  GGTATACCAA GGTCTTGCAG AACCTACAGA TCATATCCTA CATCCAAGAC
1001  TTTATCCAGG GACCTATCCC GAACGGAAAA GACAAAACGA AAGAATTCTT
1051  GAGGCTCAAC AACTCTTTGA AGAAGCTCTA GACGAACTTC AAATGACACG
1101  CGAAGATCTA GAAAAGGAAA CTTTGACTTT CTCAACCTTT TCTTTTTCTT
1151  ACGGAAGGAT TTGCCAAATG CTAAGAGAAC AATGGAAGAA AGTCTTAAAA
1201  TTTACTATCC CTATAGTAGG CCAAGAGTTT TTCACAATAC AAAAAAACTT
1251  CCTAGAGGGG AACTATTCCC TAACCGTGAA CCAATGGACC GCAGCATTTA
1301  TTGATCCGAT GTCTTATCTC ATGATCTTTG CCAATCCTGG AGGAATTTCC
1351  CCCTATCACC TCCAAGATTC ACACTTTCAA ACTCTTCTCA TAAAGATCAC
1401  TCAAGAACAT AAAAAACACC TACGAAATCA GCTTATTATT GAAGCCCTTG
1451  ACTATTTAGA ACACTGTCAC ATTCTCGAAC CACTATGTCA TCCAAATCTT
1501  CGAATTGCTT TGAACAAAAA CATTAAAAAC TTTAATCTTT TTGTTCGACG
1551  AACTTCAGAC TTTCGTTTTA TAGAAAAACT ATAG
```

The PSORT algorithm predicts an outer membrane lipoprotein (0.790).

The protein was expressed in *E.coli* and purified as a his-tag product and a GST-fusion protein, as shown in Figure 64A. The recombinant his-tag protein was used to immunise mice, whose sera were used in a Western blot (Figure 64B). The recombinant GST-fusion protein was also used to immunise mice, whose sera were used in a Western blot (Figure 64C) and for FACS analysis (Figure 64D).

These experiments show that cp6467 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 65

The following *C.pneumoniae* protein (PID 4376679) was expressed <SEQ ID 129; cp6679>:

```
  1  MRKMLVLLAS LGLLSPTLSS CTHLGSSGSY HPKLYTSGSK TKGVIAMLPV
 51  FHRPGKSLEP LPWNLQGEFT EEISKRFYAS EKVFLIKHNA SPQTVSQFYA
101  PIANRLPETI IEQFLPAEFI VATELLEQKT GKEAGVDSVT ASVRVRVFDI
151  RHHKIALIYQ EIIECSQPLT TLVNDYHRYG WNSKHFDSTP MGLMHSRLFR
201  EVVARVEGYV CANYS*
```

A predicted signal peptide is highlighted.

The cp6679 nucleotide sequence <SEQ ID 130> is:

```
  1  ATGCGAAAAA TGTTGGTATT ATTGGCATCT TTAGGACTTC TATCCCCAAC
 51  CCTATCCAGC TGCACTCACT TAGGCTCTTC AGGAAGTTAT CATCCTAAGC
101  TATACACTTC AGGGAGCAAA ACTAAAGGTG TGATTGCGAT GCTTCCTGTA
151  TTTCATCGCC CAGGAAAGAG TCTTGAACCT TTACCTTGGA ACCTCCAAGG
201  AGAATTTACT GAAGAGATCA GCAAAAGGTT TTATGCTTCG GAAAAGGTCT
251  TCCTGATCAA GCACAATGCT TCACCTCAGA CAGTCTCTCA GTTCTATGCT
301  CCGATTGCGA ATCGTCTACC CGAAACAATT ATTGAGCAAT TTCTTCCTGC
351  AGAATTCATT GTTGCTACAG AACTGTTAGA ACAAAAGACA GGGAAAGAAG
401  CAGGTGTCGA TTCTGTAACA GCGTCTGTAC GTGTTCGCGT TTTTGATATC
451  CGTCATCATA AAATAGCTCT CATTTATCAA GAGATTATCG AATGCAGCCA
501  GCCTTTAACT ACCCTAGTCA ATGATTATCA TCGCTATGGC TGGAACTCAA
551  AACATTTTGA TTCAACGCCC ATGGGCTTAA TGCATAGCCG TCTTTTCCGC
```

```
601  GAAGTTGTTG CCAGAGTTGA GGGCTATGTT TGTGCTAACT ACTCGTAG
```

The PSORT algorithm predicts an inner membrane location (0.149).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 65A) and as a GST-fusion product (Figure 65B). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 65C) and for FACS analysis.

These experiments show that cp6679 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 66

The following *C.pneumoniae* protein (PID 4376890) was expressed <SEQ ID 131; cp6890>:

```
  1  MKQLLFCVCV FAMSCSAYAS PRRQDPSVMK ETFRNNYGII VSGQEWVKRG
 51  SDGTITKVLK NGATLHEVYS GGLLHGEITL TFPHTTALDV VQIYDQGRLV
101  SRKTFFVNGL PSQEELFNED GTFVLTRWPD NNDSDTITKP YFIETTYQGH
151  VIEGSYTSFN GKYSSSIHNG EGVRSVFSSN NILLSEETFN EGVMVKYTTF
201  YPNRDPESIT HYQNGQPHGL RLTYLQGGIP NTIEEWRYGF QDGTTIVFKN
251  GCKTSEIAYV KGVKEGLELR YNEQEIVAEE VSWRNDFLHG ERKIYAGGIQ
301  KHEWYYRGRS VSKAKFERLN AAG*
```

A predicted signal peptide is highlighted.

The cp6890 nucleotide sequence <SEQ ID 132> is:

```
  1  ATGAAACAAT TACTTTTCTG TGTTTGCGTA TTTGCTATGT CATGTTCTGC
 51  TTACGCATCC CCACGACGAC AAGATCCTTC TGTTATGAAG GAAACATTCC
101  GAAATAATTA TGGCATTATT GTTTCCGGTC AAGAATGGGT AAAGCGTGGT
151  TCTGACGGCA CCATCACCAA AGTACTCAAA AATGGAGCTA CCCTGCATGA
201  AGTTTATTCT GGAGGCCTCC TTCATGGGGA AATTACCTTA ACGTTTCCCC
251  ATACCACAGC ATTGGACGTT GTTCAAATCT ATGATCAAGG TAGACTCGTT
301  TCTCGCAAAA CCTTTTTTGT GAACGGTCTT CCATCTCAAG AAGAGCTGTT
351  CAATGAAGAT GGCACGTTTG TCCTCACACG ATGGCCGGAC AACAACGACA
401  GTGATACCAT CACAAAGCCT TACTTCATAG AAACGACATA TCAAGGGCAT
451  GTCATAGAAG GAAGTTATAC TTCCTTTAAT GGGAAATACT CCTCATCCAT
501  CCACAATGGA GAGGGAGTTC GTTCTGTGTT CTCCTCCAAT AACATCCTTC
551  TTTCTGAAGA GACCTTCAAT GAAGGTGTCA TGGTGAAATA TACCACATTC
601  TATCCGAATC GCGATCCCGA ATCGATTACT CATTATCAAA ATGGACAGCC
651  TCACGGCTTA CGGCTAACAT ATCTACAAGG TGGCATCCCC AATACGATAG
701  AGGAGTGGCG TTATGGCTTT CAAGACGGAA CGACCATCGT ATTTAAAAAT
751  GGTTGTAAGA CATCTGAGAT CGCTTATGTT AAGGGAGTGA AAGAAGGTTT
801  AGAACTGCGC TACAATGAAC AGGAAATTGT AGCTGAAGAA GTTTCTTGGC
851  GTAATGATTT TCTGCATGGA GAACGTAAGA TCTATGCTGG AGGAATCCAA
901  AAGCATGAAT GGTATTACCG CGGGAGATCT GTATCTAAAG CCAAATTCGA
951  GCGGCTAAAT GCTGCAGGAT AG
```

The PSORT algorithm predicts an outer membrane location (0.940).

The protein was expressed in *E.coli* and purified as a GST-fusion product, as shown in Figure 66A. The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 66B) and for FACS analysis. A his-tagged protein was also expressed.

These experiments show that cp6890 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 67

The following *C.pneumoniae* protein (PID 6172323) was expressed <SEQ ID 133; cp0018>:

```
  1 MKTSVSMLLA LLCSGASSIV LHAATTPLNP EDGFIGEGNT NTFSPKSTTD
 51 AAGTTYSLTG EVLYIDPGKG GSITGTCFVE TAGDLTFLGN GNTLKFLSVD
101 AGANIAVAHV QGSKNLSFTD FLSLVITESP KSAVTTGKGS LVSLGAVQLQ
151 DINTLVLTSN ASVEDGGVIK GNSCLIQGIK NSAIFGQNTS SKKGGAISTT
201 QGLTIENNLG TLKFNENKAV TSGGALDLGA ASTFTANHEL IFSQNKTSGN
251 AANGGAINCS GDLTFTDNTS LLLQENSTMQ DGGALCSTGT ISITGSDSIN
301 VIGNTSGQKG GAISAASLKI LGGQGGALFS NNVVTHATPL GGAIFINTGG
351 SLQLFTQGGD IVFEGNQVTT TAPNATTKRN VIHLESTAKW TGLAASQGNA
401 IYFYDPITTN DTGASDNLRI NEVSANQKLS GSIVFSGERL STAEAIAENL
451 TSRINQPVTL VEGSLVLKQG VTLITQGFSQ EPESTLLLDL GTSL*
```

A predicted signal peptide is highlighted.

The cp0018 nucleotide sequence <SEQ ID 134> is:

```
   1 ATGAAGACTT CAGTTTCTAT GTTGTTGGCC CTGCTTTGCT CGGGGGCTAG
  51 CTCTATTGTA CTCCATGCCG CAACCACTCC ACTAAATCCT GAAGATGGGT
 101 TTATTGGGGA GGGCAATACA AATACTTTTT CTCCGAAATC TACAACGGAT
 151 GCTGCAGGAA CTACCTACTC TCTCACAGGA GAGGTTCTGT ATATAGATCC
 201 GGGGAAAGGT GGTTCAATTA CAGGAACTTG CTTTGTAGAA ACTGCTGGCG
 251 ATCTTACATT TTTAGGTAAT GGAAATACCC TAAAGTTCCT GTCGGTAGAT
 301 GCAGGTGCTA ATATCGCGGT TGCTCATGTA CAAGGAAGTA AGAATTTAAG
 351 CTTCACAGAT TTCCTTTCTC TGGTGATCAC AGAATCTCCA AAATCCGCTG
 401 TTACTACAGG AAAAGGTAGC CTAGTCAGTT TAGGTGCAGT CCAACTGCAA
 451 GATATAAACA CTCTAGTTCT TACAAGCAAT GCCTCTGTCG AAGATGGTGG
 501 CGTGATTAAA GGAAACTCCT GCTTGATTCA GGGAATCAAA AATAGTGCGA
 551 TTTTTGGACA AAATACATCT TCGAAAAAAG GAGGGGCGAT CTCCACGACT
 601 CAAGGACTTA CCATAGAGAA TAACTTAGGG ACGCTAAAGT TCAATGAAAA
 651 CAAAGCAGTG ACCTCAGGAG GCGCCTTAGA TTTAGGAGCC GCGTCTACAT
 701 TCACTGCGAA CCATGAGTTG ATATTTTCAC AAAATAAGAC TTCTGGGAAT
 751 GCTGCAAATG GCGGAGCCAT AAATTGCTCA GGGGACCTTA CATTTACTGA
 801 TAACACTTCT TTGTTACTTC AAGAAAATAG CACAATGCAG GATGGTGGAG
 851 CTTTGTGTAG CACAGGAACC ATAAGCATTA CCGGTAGTGA TTCTATCAAT
 901 GTGATAGGAA ATACTTCAGG ACAAAAAGGA GGAGCGATTT CTGCAGCTTC
 951 TCTCAAGATT TTGGGAGGGC AGGGAGGCGC TCTCTTTTCT AATAACGTAG
1001 TGACTCATGC CACCCCTCTA GGAGGTGCCA TTTTTATCAA CACAGGAGGA
1051 TCCTTGCAGC TCTTCACTCA AGGAGGGGAT ATCGTATTCG AGGGGAATCA
1101 GGTCACTACA ACAGCTCCAA ATGCTACCAC TAAGAGAAAT GTAATTCACC
1151 TCGAGAGCAC CGCGAAGTGG ACGGGACTTG CTGCAAGTCA AGGTAACGCT
1201 ATCTATTTCT ATGATCCCAT TACCACCAAC GATACGGGAG CAAGCGATAA
1251 CTTACGTATC AATGAGGTCA GTGCAAATCA AAAGCTCTCG GGATCTATAG
1301 TATTTTCTGG AGAGAGATTG TCGACAGCAG AAGCTATAGC TGAAAATCTT
1351 ACTTCGAGGA TCAACCAGCC TGTCACTTTA GTAGAGGGGA GCTTAGTACT
1401 TAAACAGGGA GTGACCTTGA TCACACAAGG ATTCTCGCAG GAGCCAGAAT
1451 CCACGCTTCT TTTGGATCTG GGGACCTCAT TATAA
```

The PSORT algorithm predicts outer membrane (0.935).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 67A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 67B) and for FACS analysis.

These experiments show that cp0018 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 68

The following *C.pneumoniae* protein (PID 4376262) was expressed <SEQ ID 135; cp6262>:

```
  1 MRKLRILAIV LIALSIILIA GGVVLLTVAI PGLSSVISSP AGMGACALGC
 51 VMLALGIDVL LKKREVPIVL ASVTTTPGTG SPRSGISISG ADSTIRSLPT
101 YLLDEGHPQS MRKLRILAIV LIVFSIILIA SGVVLLTVAI PGLSSVISSP
151 AGMGACALGC VMLALGIDVL LKKREVPIVL ASVTTTPGTG SPRSGISISG
201 ADSTIRSLPT YPLDEGHPQS MRKLRILAIV LIVFSIILIA SGVVLLTVAI
251 PGLSSIISSP AEMGACALGC VMLALGIDVL LKKREVPIVV PAPIPEEVVI
```

```
301  DDIDEESIRL QQEAEAALAR LPEEMSAFEG YIKVVESHLE NMKSLPYDGH
351  GLEEKTKHQI RVVRSSLKAM VPEFLDIRRI FEEEEFFFLS ARKRLIDLAT
401  TLVERKILTE QLERNNLRKA FSYLYQDSIF KKIIDNFEKL AWKFMILSKS
451  ICRFTIIFEN HEHGVAKSLL HKNAVLLEKV IYRSLQKSYR DIGMSSAKMK
501  ILHGNPFFSL EDNKKTIMKE HAEMLESLSS YRKVFLALSD ENVVDTPSDP
551  KKWDLSGIPC RDALSEISRD EQWQKKAHLK HQESLYTQAR DRLTDQSSKE
601  NQKELEKAEQ EYISSWERVK KFEIERVQER IRAIQKLYPN ILEREEETTG
651  QETVTPTVQG TTASSDLTDI LGRIEVSSRE DNQNQESCVK VLRSHEVEMS
701  WEVKQEYGPK KKEFQDQMGS LERFFTEHIE ELEVLQKDYS KHLSYFKKVN
751  NKKEVQYAKF RLKVLESDLE GILAQTESAE SLLTQEELPI LATRGALEKA
801  VFKGSLCCAL ASKAKPYFEE DPRFQDSDTQ LRALTLRLQE AKASLEEEIK
851  RFSNLENDIA EERRLLKESK QTFERAGLGV LREIAVESTY DLRSLTNTWE
901  GTPESEKVYF SMYLNYYNEE KRRAKTRLVE MTQRYRDFKM ALEAMQFNEE
951  ALLQEELSIQ APSE*
```

A predicted signal peptide is highlighted.

The cp6262 nucleotide sequence <SEQ ID 136> is:

```
   1  ATGAGGAAAC TTCGTATTCT TGCGATCGTT CTCATAGCTT TGAGCATTAT
  51  TTTGATTGCA GGTGGTGTGG TATTGCTTAC TGTAGCGATC CCTGGATTAA
 101  GTTCAGTCAT TTCTTCCCCG GCAGGGATGG GTGCCTGTGC TTTGGGATGT
 151  GTGATGCTTG CTTTAGGGAT CGATGTTCTT CTGAAGAAAC GAGAAGTCCC
 201  TATAGTTCTC GCATCTGTAA CTACGACACC AGGAACTGGC AGCCCTAGAA
 251  GTGGTATTTC TATTTCAGGA GCTGATAGCA CCATACGTTC TCTTCCTACG
 301  TATCTCTTGG ACGAGGGACA TCCACAATCC ATGAGGAAAC TTCGTATTCT
 351  TGCGATCGTT CTCATAGTTT TTAGCATTAT TTTGATTGCA AGTGGTGTGG
 401  TATTGCTTAC TGTAGCGATC CCTGGATTAA GTTCAGTCAT TTCTTCCCCG
 451  GCAGGGATGG GTGCCTGTGC TTTGGGATGT GTGATGCTTG CTTTAGGGAT
 501  CGATGTTCTT CTGAAGAAAC GAGAAGTCCC TATAGTTCTC GCATCTGTAA
 551  CTACGACACC AGGAACTGGC AGCCCTAGAA GTGGTATTTC TATTTCAGGA
 601  GCTGATAGCA CCATACGTTC TCTTCCTACG TATCCCTTGG ACGAGGGACA
 651  TCCACAATCC ATGAGGAAAC TTCGTATTCT TGCGATCGTT CTCATAGTTT
 701  TTAGCATTAT TTTGATTGCA AGTGGTGTGG TATTGCTTAC TGTAGCGATC
 751  CCTGGATTAA GCTCGATCAT TTCTTCCCCA GCGGAGATGG GTGCTTGTGC
 801  TTTGGGATGT GTGATGCTTG CTTTGGGGAT CGACGTTCTT CTGAAGAAAC
 851  GAGAAGTCCC TATAGTAGTT CCCGCACCTA TTCCTGAAGA AGTCGTCATA
 901  GATGATATAG ATGAAGAGAG TATACGGCTG CAGCAGGAAG CTGAAGCCGC
 951  TTTAGCAAGA CTTCCTGAGG AGATGAGTGC ATTTGAAGGT TACATAAAAG
1001  TTGTCGAGAG TCATTTGGAG AACATGAAAA GCCTGCCTTA TGATGGTCAT
1051  GGGCTAGAAG AGAAAACGAA ACATCAGATA AGAGTCGTCA GATCTTCTTT
1101  GAAGGCTATG GTTCCAGAAT TTTTAGATAT CAGAAGAATT TTTGAAGAAG
1151  AAGAGTTCTT TTTTCTCTCA GCTCGCAAAC GACTTATAGA TTTAGCTACT
1201  ACTTTAGTAG AGAGAAAAAT TTTAACAGAG CAACTTGAGC GCAATAATTT
1251  AAGGAAAGCG TTTTCTTATT TATATCAGGA CTCAATTTTT AAAAAAATTA
1301  TTGATAACTT CGAGAAGTTA GCATGGAAAT TTATGATTTT GAGTAAATCA
1351  ATTTGTCGAT TTACAATTAT TTTTGAAAAT CATGAACATG GTGTAGCAAA
1401  GAGCCTGTTA CACAAGAATG CAGTGTTACT GGAGAAGGTA ATCTATAGGA
1451  GTTTGCAAAA AAGCTATAGA GATATAGGCA TGTCATCTGC AAAGATGAAA
1501  ATCTTGCACG GCAACCCTTT TTTCTCTTTG GAAGATAATA AAAAGACGAT
1551  AATGAAAGAA CACGCAGAGA TGCTTGAAAG TCTCAGTAGC TATAGGAAGG
1601  TATTTTTAGC TCTATCTGAT GAGAACGTTG TAGATACACC TAGCGATCCA
1651  AAGAAATGGG ATTTGTCAGG AATCCCCTGT AGGGACGCGT TGTCTGAGAT
1701  TTCTCGTGAT GAACAGTGGC AGAAGAAAGC ACATCTAAAG CATCAAGAGT
1751  CCCTCTATAC GCAAGCTAGG GATCGTTTAA CAGACCAGAG CTCTAAAGAA
1801  AATCAGAAAG AGTTAGAGAA AGCTGAACAA GAGTACATAT CTTCTTGGGA
1851  ACGGGTTAAA AAATTTGAGA TTGAGAGAGT ACAGGAGAGG ATACGGGCAA
1901  TTCAAAAGCT TTATCCTAAT ATCCTCGAGA GAGAAGAAGA AACCACAGGT
1951  CAGGAGACTG TGACTCCAAC TGTTCAAGGG ACGACGGCTT CATCCGATTT
2001  AACAGATATT TTAGGAAGAA TAGAGGTCTC CAGTAGGGAG GATAATCAGA
2051  ATCAAGAGTC TTGTGTAAAA GTCTTAAGAA GTCATGAGGT AGAAATGAGC
2101  TGGGAAGTCA AACAAGAGTA TGGCCCTAAG AAAAAAGAAT TTCAGGATCA
2151  AATGGGTTCT TTAGAGAGGT TTTTTACAGA GCATATTGAA GAGTTAGAAG
2201  TATTACAGAA GGACTACTCT AAACACTTGT CTTATTTTAA AAAAGTAAAC
2251  AATAAGAAAG AGGTTCAATA TGCGAAGTTT AGGTTGAAGG TTTTAGAGTC
2301  AGATTTAGAA GGGATTCTAG CTCAGACTGA GAGTGCTGAG AGTCTGTTAA
2351  CTCAAGAAGA ACTTCCGATT CTTGCAACTC GGGGAGCCTT AGAGAAAGCT
2401  GTTTTCAAAG GGAGTCTATG TTGCGCGCTA GCAAGCAAAG CAAAACCCTA
```

```
2451  TTTTGAAGAG GATCCCAGAT TCCAAGATTC TGATACGCAA TTGCGAGCTC
2501  TGACTCTAAG GTTACAGGAG GCTAAGGCAA GCCTGGAAGA AGAGATAAAG
2551  AGATTTTCAA ATCTTGAGAA CGATATTGCA GAGGAAAGAC GCCTTCTTAA
2601  AGAGAGCAAG CAGACGTTCG AAAGAGCAGG TTTAGGGGTT CTCCGAGAAA
2651  TTGCAGTCGA GTCTACTTAT GATTTGCGTT CCTTAACAAA TACATGGGAA
2701  GGGACCCCAG AGAGTGAGAA GGTCTATTTT AGCATGTATC TTAATTATTA
2751  CAACGAAGAG AAACGTAGGG CTAAAACAAG ATTGGTTGAA ATGACACAGA
2801  GGTATAGAGA TTTTAAAATG GCCTTGGAAG CTATGCAGTT TAATGAAGAA
2851  GCCCTTTTGC AAGAGGAACT CTCTATTCAA GCTCCCAGTG AATAA
```

The PSORT algorithm prediets inner membrane (0.660).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 68A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 68B) and for FACS analysis.

These experiments show that cp6262 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 69

The following *C.pneumoniae* protein (PID 4376269) was expressed <SEQ ID 137; cp6269>:

```
  1  MYQENLRLLE RLLYNSVQKS YADRLFSYEK TKMVHDTPLI PWEEDKEKCA
 51  EAEKAFLEQQ KILLDYGKSI FWLNENDEIN LNDPWSWGLN TVRTRKVFQE
101  VDDSERWNHK VLIQKLEDDY EKLLEESSKE STEANKKLLS DLVDRLEDAK
151  TKFFLKKQEE VETRVKDLRA RYGGTVDPKQ DTEAKKKVEL EASLETFLDS
201  IESELVQCLE DQDIYWKEQD VKDLARTQEL EEQDIEAKRE EAAEDLRSLN
251  ERLKKSKTML DRAKWHIENA EDSITWWTSQ IEMKDMKARL KILKEDITSV
301  LPEIDEIETC LSLEELPLLT TRELLTKSYL KFKICSETLL KMTSVFENNI
351  YVQEYEVQLQ NLGFKLQGIS QRFGKKQDDF ANLEEQVALQ KKRLRELTQN
401  FEIQGFNFMK EDFKAAAKDL YIRSTAEQKM NFDVPCMELF RRYHEEVNKP
451  LLELMYNCAD SYRDAKKKLC SLRLDEKELL QKEIKKEEFY QKKQQRHADR
501  SRHTTYQKLR IAEELALELK KKI*
```

The cp6269 nucleotide sequence <SEQ ID 138> is:

```
   1  ATGTACCAGG AGAATCTAAG ATTGTTGGAA AGGCTTCTTT ATAATAGTGT
  51  TCAAAAGAGC TATGCGGATC GGCTGTTTTC CTATGAAAAG ACAAAGATGG
 101  TGCACGATAC TCCGCTGATT CCTTGGGAAG AGGATAAGGA AAAATGTGCT
 151  GAAGCTGAGA AAGCTTTCTT AGAGCAACAG AAGATTCTCC TAGATTATGG
 201  AAAATCTATC TTTTGGCTGA ATGAGAACGA TGAGATCAAT TTAAACGATC
 251  CTTGGAGTTG GGGTCTTAAT ACGGTGAGGA CTAGGAAAGT ATTCCAAGAG
 301  GTTGACGACA GTGAACGTTG GAATCATAAG GTACTCATTC AAAAACTCGA
 351  GGACGATTAT GAGAAACTTC TAGAGGAAAG TTCAAAAGAG TCTACTGAAG
 401  CAAATAAGAA GCTTTTATCT GACTTAGTAG ATCGTCTTGA AGATGCTAAG
 451  ACAAAATTTT TCCTGAAGAA ACAGGAGGAG GTGGAGACTC GCGTTAAGGA
 501  TCTTAGAGCT CGATATGGAG GCACAGTAGA TCCTAAGCAG GATACGGAAG
 551  CTAAGAAGAA AGTCGAATTG GAGGCTAGCT TAGAAACCTT TTTAGATTCC
 601  ATCGAATCAG AGCTAGTACA GTGTTTAGAA GATCAAGATA TATATTGGAA
 651  AGAACAGGAT GTCAAAGATC TAGCACGTAC GCAAGAGCTC GAGGAACAAG
 701  ATATTGAAGC GAAGAGGGAA GAAGCTGCCG AAGACCTAAG AAGTCTTAAT
 751  GAGCGTTTAA AGAAGTCAAA AACTATGTTA GATAGGGCTA AATGGCATAT
 801  TGAAAATGCT GAGGACAGTA TTACCTGGTG GACTAGTCAG ATAGAAATGA
 851  AGGATATGAA AGCAAGACTG AAGATCTTAA AAGAAGATAT AACAAGTGTT
 901  CTACCTGAAA TAGATGAGAT TGAAACGTGT TTAAGCTTAG AGGAGCTTCC
 951  TTTGCTTACG ACCAGGGAAC TCTTAACTAA GTCCTACCTA AAGTTTAAGA
1001  TTTGTTCGGA AACACTATTA AAAATGACTT CTGTGTTTGA GAACAATATC
1051  TATGTTCAGG AGTACGAGGT TCAGCTGCAA AATCTAGGGT TTAAGTTACA
1101  AGGTATATCT CAGAGATTCG GAAAGAAACA AGACGATTTT GCGAATCTAG
1151  AGGAACAGGT TGCTTTGCAA AAGAAACGAC TCAGAGAGCT CACTCAGAAT
1201  TTTGAAATAC AAGGATTCAA TTTCATGAAA GAAGATTTTA AGGCAGCCGC
1251  TAAAGATCTT TATATAAGAA GTACAGCTGA ACAAAAGATG AACTTTGATG
1301  TGCCTTGCAT GGAGCTCTTC CGTAGGTATC ATGAGGAGGT CAACAAGCCG
1351  CTTCTTGAGT TGATGTACAA TTGTGCAGAC AGTTATAGAG ATGCTAAGAA
```

```
1401  AAAGCTTTGC TCTCTACGTC TTGATGAAAA AGAGTTATTA CAAAAAGAAA
1451  TCAAGAAAGA GGAATTTTAT CAAAAGAAAC AACAAAGGCA TGCAGATAGA
1501  TCACGTCATA CTACGTATCA AAAGCTACGA ATTGCTGAAG AGCTTGCTCT
1551  TGAGCTGAAG AAGAAAATCT AA
```

The PSORT algorithm predicts cytoplasmic location (0.412).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 69A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 69B) and for FACS analysis.

These experiments show that cp6269 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 70

The following *C.pneumoniae* protein (PID 4376270) was expressed <SEQ ID 139; cp6270>:

```
  1  MKIPLRFLLI SLVPTLSMSN LLGAATTEEL SASNSFDGTT STTSFSSKTS
 51  SATDGTNYVF KDSVVIENVP KTGETQSTSC FKNDAAAGDL NFLGGGFSFT
101  FSNIDATTAS GAAIGSEAAN KTVTLSGFSA LSFLKSPAST VTNGLGAINV
151  KGNLSLLDND KVLIQDNFST GDGGAINCAG SLKIANNKSL SFIGNSSSTR
201  GGAIHTKNLT LSSGGETLFQ GNTAPTAAGK GGAIAIADSG TLSISGDSGD
251  IIFEGNTIGA TGTVSHSAID LGTSAKITAL RAAQGHTIYF YDPITVTGST
301  SVADALNINS PDTGDNKEYT GTIVFSGEKL TEAEAKDEKN RTSKLLQNVA
351  FKNGTVVLKG DVVLSANGFS QDANSKLIMD LGTSLVANTE SIELTNLEIN
401  IDSLRNGKKI KLSAATAQKD IRIDRPVVLA ISDESFYQNG FLNEDHSYDG
451  ILELDAGKDI VISADSRSID AVQSPYGYQG KWTINWSTDD KKATVSWAKQ
501  SFNPTAEQEA PLVPNLLWGS FIDVRSFQNF IELGTEGAPY EKRFWVAGIS
551  NVLHRSGREN QRKFRHVSGG AVVGASTRMP GGDTLSLGFA QLFARDKDYF
601  MNTNFAKTYA GSLRLQHDAS LYSVVSILLG EGGLREILLP YVSKTLPCSF
651  YGQLSYGHTD HRMKTESLPP PPPTLSTDHT SWGGYVWAGE LGTRVAVENT
701  SGRGFFQEYT PFVKVQAVYA RQDSFVELGA ISRDFSDSHL YNLAIPLGIK
751  LEKRFAEQYY HVVAMYSPDV CRSNPKCTTT LLSNQGSWKT KGSNLARQAG
801  IVQASGFRSL GAAAELFGNF GFEWRGSSRS YNVDAGSKIK F*
```

A predicted signal peptide is highlighted.

The cp6270 nucleotide sequence <SEQ ID 140> is:

```
   1  ATGAAGATTC CACTCCGCTT TTTATTGATA TCATTAGTAC CTACGCTTTC
  51  TATGTCGAAT TTATTAGGAG CTGCTACTAC CGAAGAGTTA TCGGCTAGCA
 101  ATAGCTTCGA TGGAACTACA TCAACAACAA GCTTTTCTAG TAAAACATCA
 151  TCGGCTACAG ATGGCACCAA TTATGTTTTT AAAGATTCTG TAGTTATAGA
 201  AAATGTACCC AAAACAGGGG AAACTCAGTC TACTAGTTGT TTTAAAAATG
 251  ACGCTGCAGC TGGAGATCTA AATTTCTTAG GAGGGGGATT TTCTTTCACA
 301  TTTAGCAATA TCGATGCAAC CACGGCTTCT GGAGCTGCTA TTGGAAGTGA
 351  AGCAGCTAAT AAGACAGTCA CGTTATCAGG ATTTTCGGCA CTTTCTTTTC
 401  TTAAATCCCC AGCAAGTACA GTGACTAATG GATTGGGAGC TATCAATGTT
 451  AAAGGGAATT TAAGCCTATT GGATAATGAT AAGGTATTGA TTCAGGACAA
 501  TTTCTCAACA GGAGATGGCG GAGCAATTAA TTGTGCAGGC TCCTTGAAGA
 551  TCGCAAACAA TAAGTCCCTT TCTTTTATTG GAAATAGTTC TTCAACACGT
 601  GGCGGAGCGA TTCATACCAA AAACCTCACA CTATCTTCTG GTGGGGAAAC
 651  TCTATTTCAG GGGAATACAG CGCCTACGGC TGCTGGTAAA GGAGGTGCTA
 701  TCGCGATTGC AGACTCTGGC ACCCTATCCA TTTCTGGAGA CAGTGGCGAC
 751  ATTATCTTTG AAGGCAATAC GATAGGAGCT ACAGGAACCG TCTCTCATAG
 801  TGCTATTGAT TTAGGAACTA GCGCTAAGAT AACTGCGTTA CGTGCTGCGC
 851  AAGGACATAC GATATACTTT TATGATCCGA TTACTGTAAC AGGATCGACA
 901  TCTGTTGCTG ATGCTCTCAA TATTAATAGC CCTGATACTG GAGATAACAA
 951  AGAGTATACG GGAACCATAG TCTTTTCTGG AGAGAAGCTC ACGGAGGCAG
1001  AAGCTAAAGA TGAGAAGAAC CGCACTTCTA AATTACTTCA AAATGTTGCT
1051  TTTAAAAATG GGACTGTAGT TTTAAAAGGT GATGTCGTTT TAAGTGCGAA
1101  CGGTTTCTCT CAGGATGCAA ACTCTAAGTT GATTATGGAT TTAGGGACGT
1151  CGTTGGTTGC AAACACCGAA AGTATCGAGT TAACGAATTT GGAAATTAAT
1201  ATAGACTCTC TCAGGAACGG GAAAAAGATA AAACTCAGTG CTGCCACAGC
```

1251 TCAGAAAGAT ATTCGTATAG ATCGTCCTGT TGTACTGGCA ATTAGCGATG
1301 AGAGTTTTTA TCAAAATGGC TTTTTGAATG AGGACCATTC CTATGATGGG
1351 ATTCTTGAGT TAGATGCTGG GAAAGACATC GTGATTTCTG CAGATTCTCG
1401 CAGTATAGAT GCTGTACAAT CTCCGTATGG CTATCAGGGA AAGTGGACGA
1451 TCAATTGGTC TACTGATGAT AAGAAAGCTA CGGTTTCTTG GGCGAAGCAG
1501 AGTTTTAATC CCACTGCTGA GCAGGAGGCT CCGTTAGTTC CTAATCTTCT
1551 TTGGGGTTCT TTTATAGATG TTCGTTCCTT CCAGAATTTT ATAGAGCTAG
1601 GTACTGAAGG TGCTCCTTAC GAAAAGAGAT TTTGGGTTGC AGGCATTTCC
1651 AATGTTTTGC ATAGGAGCGG TCGTGAAAAT CAAAGGAAAT TCCGTCATGT
1701 GAGTGGAGGT GCTGTAGTAG GTGCTAGCAC GAGGATGCCG GGTGGTGATA
1751 CCTTGTCTCT GGGTTTTGCT CAGCTCTTTG CGCGTGACAA AGACTACTTT
1801 ATGAATACCA ATTTCGCAAA GACCTACGCA GGATCTTTAC GTTTGCAGCA
1851 CGATGCTTCC CTATACTCTG TGGTGAGTAT CCTTTTAGGA GAGGGAGGAC
1901 TCCGCGAGAT CCTGTTGCCT TATGTTTCCA AGACTCTGCC GTGCTCTTTC
1951 TATGGGCAGC TTAGCTACGG CCATACGGAT CATCGCATGA AGACCGAGTC
2001 TCTACCCCCC CCCCCCCCGA CGCTCTCGAC GGATCATACT TCTTGGGGAG
2051 GATATGTCTG GGCTGGAGAG CTGGGAACTC GAGTTGCTGT TGAAAATACC
2101 AGCGGCAGAG GATTTTTCCA AGAGTACACT CCATTTGTAA AAGTCCAAGC
2151 TGTTTACGCT CGCCAAGATA GCTTTGTAGA ACTAGGAGCT ATCAGTCGTG
2201 ATTTTAGTGA TTCGCATCTT TATAACCTTG CGATTCCTCT TGGAATCAAG
2251 TTAGAGAAAC GGTTTGCAGA GCAATATTAT CATGTTGTAG CGATGTATTC
2301 TCCAGATGTT TGTCGTAGTA ACCCCAAATG TACGACTACC CTACTTTCCA
2351 ACCAAGGGAG TTGGAAGACC AAAGGTTCGA ACTTAGCAAG ACAGGCTGGT
2401 ATTGTTCAGG CCTCAGGTTT TCGATCTTTG GGAGCTGCAG CAGAGCTTTT
2451 CGGGAACTTT GGCTTTGAAT GGCGGGGATC TTCTCGTAGC TATAATGTAG
2501 ATGCGGGTAG CAAAATCAAA TTTTAG

The PSORT algorithm predicts outer membrane (0.92).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 70A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot and for FACS analysis (Figure 70B).

The cp6270 protein was also identified in the 2D-PAGE experiment (Cpn0013).

These experiments show that cp6270 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 71

The following *C.pneumoniae* protein (PID 4376402) was expressed <SEQ ID 141; cp6402>:

1 MNVADLLSHL ETLLSSKIFQ DYGPNGLQVG DPQTPVKKIA VAVTADLETI
51 KQAVAAEANV LIVHHGIFWK GMPYPITGMI HKRIQLLIEH NIQLIAYHLP
101 LDAHPTLGNN WRVALDLNWH DLKPFGSSLP YLGVQGSFSP IDIDSFIDLL
151 SQYYQAPLKG SALGGPSRVS SAALISGGAY RELSSAATSQ VDCFITGNFD
201 EPAWSTALES NINFLAFGHT ATEKVGPKSL AEHLKSEFPI STTFIDTANP
251 F*

The cp6402 nucleotide sequence <SEQ ID 142> is:

1 ATGAATGTTG CGGATCTCCT TTCTCATCTT GAGACTCTTC TCTCATCAAA
51 AATATTTCAG GATTATGGAC CCAACGGACT TCAAGTTGGA GATCCCCAAA
101 CTCCGGTAAA GAAAATCGCT GTTGCAGTTA CCGCAGATCT AGAAACCATA
151 AAACAAGCTG TTGCGGCCGA AGCAAACGTT CTCATTGTAC ACCACGGAAT
201 TTTTTGGAAA GGTATGCCCT ATCCTATTAC CGGCATGATC CATAAGCGCA
251 TCCAATTACT AATAGAACAC AATATCCAAC TCATTGCCTA CCACCTTCCT
301 TTGGATGCTC ACCCTACCTT AGGAAATAAC TGGAGAGTTG CCCTGGATCT
351 AAATTGGCAT GACTTGAAGC CCTTTGGTTC TTCCCTCCCT TATTTAGGAG
401 TGCAAGGCTC TTTCTCTCCT ATCGATATAG ATTCTTTCAT TGACCTGTTA
451 TCTCAATATT ACCAAGCTCC CCTAAAAGGA TCTGCCTTGG GCGGCCCCTC
501 TAGAGTCTCC TCAGCAGCTC TGATCTCAGG AGGAGCTTAT AGAGAACTCT
551 CTTCGGCAGC CACGTCCCAA GTCGATTGCT TCATCACAGG AAATTTTGAT
601 GAACCTGCAT GGTCGACAGC TCTAGAAAGC AATATCAACT TCCTAGCATT
651 TGGACATACA GCCACAGAAA AAGTAGGTCC AAAATCTCTT GCAGAGCATC

```
701  TAAAAAGCGA ATTTCCTATT TCCACAACCT TTATAGATAC GGCCAACCCC
751  TTCTAA
```

The PSORT algorithm predicts cytoplasmic (0.158).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 71A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 71B) and for FACS analysis.

These experiments show that cp6402 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequenee alone.

Example 72

The following *C.pneumoniae* protein (PID 4376520) was expressed <SEQ ID 143; cp6520>:

```
  1  MKHYLSFSPS ADFFSKQGAI ETQVLFGERV LVKGSTCYAY SQLFHNELLW
 51  KPYPGHSFRS TLVPCTPEFH IHPNVSVVSV DAFLDPWGIP LPFGTLLHVN
101  SQNTVIFPKD ILNHMNTIWG SGTPQCDPRH LRRLNYNFFA ELLIKDADLL
151  LNFPYVWGGR SVHESLEKPG VDCSGFINIL YQAQGYNVPR NAADQYADCH
201  WISSFENLPS GGLIFLYPKE EKRISHVMLK QDSSTLIHAS GGGKKVEYFI
251  LEQDGKFLDS TYLFFRNNQR GRAFFGIPRK RKAFL*
```

The cp6520 nucleotide sequence <SEQ ID 144> is:

```
  1  ATGAAACACT ACCTATCATT TTCTCCTTCT GCTGATTTTT TCTCTAAACA
 51  GGGTGCTATT GAAACTCAAG TCCTTTTTGG AGAGCGCGTC TTAGTCAAAG
101  GGAGCACCTG CTATGCATAT TCCCAATTAT TCCACAATGA GCTGTTATGG
151  AAGCCCTATC CAGGTCATAG CTTTCGTTCT ACCCTAGTCC CCTGCACTCC
201  TGAATTTCAT ATCCATCCAA ATGTTTCTGT GGTTTCTGTG GATGCATTTT
251  TAGATCCTTG GGGGATCCCT CTTCCTTTTG GAACTTTACT CCATGTGAAT
301  TCTCAAAATA CCGTTATTTT CCCTAAGGAT ATTCTCAATC ATATGAACAC
351  CATCTGGGGC TCCGGCACAC CTCAATGCGA TCCTAGACAT CTACGTCGTC
401  TAAATTATAA CTTCTTTGCT GAACTTTTAA TTAAAGACGC AGACCTTTTA
451  CTGAACTTTC CCTATGTATG GGGAGGACGG TCTGTACACG AAAGTCTGGA
501  AAAGCCGGGT GTTGATTGTT CGGGATTTAT CAATATCCTT TACCAGGCAC
551  AGGGATACAA CGTCCCTAGA AACGCTGCAG ATCAATATGC GGATTGTCAT
601  TGGATCTCTA GCTTTGAGAA CCTTCCTTCT GGTGGGTTAA TATTTCTTTA
651  CCCTAAAGAA GAAAAGCGTA TTTCTCATGT TATGTTGAAA CAGGATAGTT
701  CCACCCTCAT TCATGCTTCT GGTGGAGGGA AAAAAGTGGA GTATTTCATT
751  TTAGAACAAG ATGGGAAGTT TTTAGATTCG ACTTATCTAT TTTTTAGAAA
801  TAATCAGAGG GGACGGGCAT TTTTTGGGAT CCCTAGAAAA AGAAAAGCCT
851  TTCTGTAA
```

The PSORT algorithm predicts cytoplasmic (0.265).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 72A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 72B) and for FACS analysis.

These experiments show that cp6520 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 73

The following *C.pneumoniae* protein (PID 4376567) was expressed <SEQ ID 145; cp6567>:

```
  1  MTSPIPFQSS GDASFLAEQP QQLPSTSESQ LVTQLLTMMK HTQALSETVL
 51  QQQRDRLPTA SIILQVGGAP TGGAGAPFQP GPADDHHHPI PPPVVPAQIE
101  TEITTIRSEL QLMRSTLQQS TKGARTGVLV VTAILMTISL LAIIIIILAV
151  LGFTGVLPQV ALLMQGETNL IWAMVSGSII CFIALIGTLG LILTNKNTPL
```

```
201  PAS*
```

The cp6567 nucleotide sequence <SEQ ID 146> is:

```
  1  ATGACCTCAC CGATCCCCTT TCAGTCTAGT GGCGATGCCT CTTTCCTTGC
 51  CGAGCAGCCA CAGCAACTCC CGTCTACTTC TGAATCTCAG CTAGTAACTC
101  AATTGCTAAC CATGATGAAG CATACTCAAG CATTATCCGA AACGGTTCTT
151  CAACAACAAC GCGATCGATT ACCAACCGCA TCTATTATCC TTCAAGTAGG
201  AGGAGCTCCT ACAGGAGGAG CGGGTGCGCC TTTTCAACCA GGACCGGCAG
251  ATGATCATCA TCATCCCATA CCGCCGCCTG TTGTACCAGC TCAAATAGAA
301  ACAGAAATCA CCACTATAAG ATCCGAGTTA CAGCTCATGC GATCTACTCT
351  ACAACAAAGC ACAAAAGGAG CTCGTACAGG AGTTCTAGTG GTTACTGCAA
401  TCTTAATGAC GATCTCCTTA TTGGCTATTA TTATCATAAT ACTAGCTGTG
451  CTTGGATTTA CGGGCGTCTT GCCTCAAGTA GCTTTATTGA TGCAGGGTGA
501  AACAAATCTG ATTTGGGCTA TGGTGAGCGG TTCTATTATT TGCTTTATTG
551  CGCTAATTGG AACTCTAGGA TTAATTTTAA CAAATAAGAA CACGCCTCTA
601  CCGGCTTCTT AA
```

The PSORT algorithm predicts inner membrane (0.694).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 73A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 73B) and for FACS analysis.

These experiments show that cp6567 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 74

The following *C.pneumoniae* protein (PID 4376576) was expressed <SEQ ID 147; cp6576>:

```
  1  MLIMRNKVIL QISILALIQT PLTLFSTEKV KEGHVVVDSI TIITEGENAS
 51  NKHPLPKLKT RSGALFSQLD FDEDLRILAK EYDSVEPKVE FSEGKTNIAL
101  HLIAKPSIRN IHISGNQVVP EHKILKTLQI YRNDLFEREK FLKGLDDLRT
151  YYLKRGYFAS SVDYSLEHNQ EKGHIDVLIK INEGPCGKIK QLTFSGISRS
201  EKSDIQEFIQ TKQHSTTTSW FTGAGLYHPD IVEQDSLAIT NYLHNNGYAD
251  AIVNSHYDLD DKGNILLYMD IDRGSRYTLG HVHIQGFEVL PKRLIEKQSQ
301  VGPNDLYCPD KIWDGAHKIK QTYAKYGYIN TNVDVLFIPH ATRPIYDVTY
351  EVSEGSPYKV GLIKITGNTH TKSDVILHET SLFPGDTFNR LKLEDTEQRL
401  RNTGYFQSVS VYTVRSQLDP MGNADQYRDI FVEVKETTTG NLGLFLGFSS
451  LDNLFGGIEL SESNFDLFGA RNIFSKGFRC LRGGGEHLFL KANFGDKVTD
501  YTLKWTKPHF LNTPWILGIE LDKSINRALS KDYAVQTYGG NVSTTYILNE
551  HLKYGLFYRG SQTSLHEKRK FLLGPNIDSN KGFVSAAGVN LNYDSVDSPR
601  TPTTGIRGGV TFEVSGLGGT YHFTKLSLNS SIYRKLTRKG ILKIKGEAQF
651  IKPYSNTTAE GVPVSERFFL GGETTVRGYK SFIIGPKYSA TEPQGGLSSL
701  LISEEFQYPL IRQPNISAFV FLDSGFVGLQ EYKISLKDLR SSAGFGLRFD
751  VMNNVPVMLG FGWPFRPTET LNGEKIDVSQ RFFFALGGMF *
```

A predicted signal peptide is highlighted.

The cp6576 nucleotide sequence <SEQ ID 148> is:

```
  1  ATGCTCATCA TGCGAAATAA AGTTATCTTG CAAATATCTA TTCTAGCGTT
 51  AATCCAAACC CCTTTAACTT TATTTTCTAC TGAAAAAGTT AAAGAAGGCC
101  ATGTGGTGGT AGACTCTATC ACAATCATAA CGGAAGGAGA AAATGCTTCA
151  AATAAACATC CCTTACCCAA ATTAAAGACC AGAAGTGGGG CTCTTTTTTC
201  TCAATTAGAT TTTGATGAAG ACTTGAGAAT TCTAGCTAAA GAATACGACT
251  CTGTTGAGCC TAAAGTAGAA TTTTCTGAAG GGAAAACTAA CATAGCCCTT
301  CACCTAATAG CTAAACCCTC AATTCGAAAT ATTCATATCT CAGGAAATCA
351  AGTCGTTCCT GAACATAAAA TTCTTAAAAC CCTACAAATT TACCGTAATG
401  ATCTCTTTGA ACGAGAAAAA TTTCTTAAGG GTCTTGATGA TCTAAGAACG
451  TATTATCTCA AGCGAGGATA TTTCGCATCC AGTGTAGACT ACAGTCTGGA
501  ACACAATCAA GAAAAAGGTC ACATCGATGT TTTAATTAAA ATCAATGAAG
551  GTCCTTGCGG GAAAATTAAA CAGCTTACGT TCTCAGGAAT CTCTCGATCA
601  GAAAAATCAG ATATCCAAGA ATTTATTCAA ACCAAGCAGC ACTCTACAAC
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```
 651  TACAAGTTGG TTTACTGGAG CTGGACTCTA TCACCCAGAT ATTGTTGAAC
 701  AAGATAGCTT GGCAATTACG AATTACCTAC ATAATAACGG GTACGCTGAT
 751  GCTATAGTCA ACTCTCACTA TGACCTTGAC GACAAAGGGA ATATTCTTCT
 801  TTACATGGAT ATTGATCGAG GGTCGCGATA TACCTTAGGA CACGTCCATA
 851  TCCAAGGGTT TGAGGTTTTG CCAAAACGCC TTATAGAAAA GCAATCCCAA
 901  GTCGGCCCCA ATGATCTTTA TTGCCCCGAT AAAATATGGG ATGGGGCTCA
 951  TAAGATCAAA CAAACTTATG CAAAGTATGG CTACATCAAT ACCAATGTAG
1001  ACGTTCTCTT CATCCCTCAC GCAACCCGCC CTATTTATGA TGTAACTTAT
1051  GAGGTAAGTG AAGGGTCTCC TTATAAAGTT GGGTTAATTA AAATTACTGG
1101  GAATACCCAT ACAAAATCTG ACGTTATTTT ACACGAAACC AGTCTCTTCC
1151  CAGGAGATAC ATTCAATCGC TTAAAGCTAG AAGATACTGA GCAACGTTTA
1201  AGAAATACAG GCTACTTCCA AAGCGTTAGT GTCTATACAG TTCGTTCTCA
1251  ACTTGATCCT ATGGGCAATG CGGATCAATA CCGAGATATT TTTGTAGAAG
1301  TCAAAGAAAC AACAACAGGA AACTTAGGCT TATTCTTAGG ATTTAGTTCT
1351  CTTGACAATC TTTTTGGAGG AATTGAACTA TCTGAAAGTA ATTTTGATCT
1401  ATTTGGAGCT AGAAATATAT TTTCTAAAGG TTTTCGTTGT CTAAGAGGCG
1451  GTGGAGAACA TCTATTCTTA AAAGCCAACT TCGGGGACAA AGTCACAGAC
1501  TATACTTTGA AGTGGACCAA ACCTCATTTT CTAAACACTC CTTGGATTTT
1551  AGGAATTGAA TTAGATAAAT CAATTAACAG AGCATTATCT AAAGATTATG
1601  CTGTCCAAAC CTATGGCGGG AACGTCAGCA CAACGTATAT CTTGAACGAA
1651  CACCTGAAAT ACGGTCTATT TTATCGAGGA AGTCAAACGA GTTTACATGA
1701  AAAACGTAAG TTCCTCCTAG GGCCAAATAT AGACAGCAAT AAAGGATTTG
1751  TCTCTGCTGC AGGTGTCAAC TTGAATTACG ATTCTGTAGA TAGTCCTAGA
1801  ACTCCAACTA CAGGGATTCG CGGGGGGGTG ACTTTTGAGG TTTCTGGTTT
1851  GGGAGGAACT TATCATTTTA CAAAACTCTC TTTAAACAGC TCTATCTATA
1901  GAAAACTTAC GCGTAAAGGT ATTTTGAAAA TCAAAGGGGA AGCTCAATTT
1951  ATTAAACCCT ATAGCAATAC TACAGCTGAA GGAGTTCCTG TCAGTGAGCG
2001  CTTCTTCCTA GGTGGAGAGA CTACAGTTCG GGGATATAAA TCCTTTATTA
2051  TCGGTCCAAA ATACTCTGCT ACAGAACCTC AGGGAGGACT CTCTTCGCTC
2101  CTTATTTCAG AAGAGTTTCA ATACCCTCTC ATCAGACAAC CTAATATTAG
2151  TGCCTTTGTA TTCTTAGACT CAGGTTTTGT CGGTTTACAA GAGTATAAGA
2201  TTTCGTTAAA AGATCTACGT AGTAGTGCTG GATTTGGTCT GCGCTTCGAT
2251  GTAATGAATA ATGTTCCTGT TATGTTAGGA TTTGGTTGGC CCTTCCGTCC
2301  AACCGAGACT TTGAATGGAG AAAAAATTGA TGTATCTCAG CGATTCTTCT
2351  TTGCTTTAGG GGGCATGTTC TAA
```

The PSORT algorithm predicts outer membrane (0.7658).

The protein was expressed in *E.coli* and purified as GST-fusion (Figure 74A), his-tag and his-tag/GST-fusion products. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 74B) and for FACS analysis (Figure 74C).

The cp6576 protein was also identified in the 2D-PAGE experiment (Cpn0300).

These experiments show that cp6576 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 75

The following *C.pneumoniae* protein (PID 4376607) was expressed <SEQ ID 149; cp6607>:

```
  1  MNKRQKDKLK ICVIISTLIL VGIFARAPRG DTFKTFLKSE EAIIYSNQCN
 51  EDMRKILCDA IEHADEEIFL RIYNLSEPKI QQSLTRQAQA KNKVTIYYQK
101  FKIPQILKQA SNVTLVEQPP AGRKLMHQKA LSIDKKDAWL GSANYTNLSL
151  RLDNNLILGM HSSELCDLII TNTSGDFSIK DQTGKYFVLP QDRKIAIQAV
201  LEKIQTAQKT IQVAMFALTH SEIIQALHQA KQRGIHVDII IDRSHSKLTF
251  KQLRQLNINK DFVSINTAPC TLHHKFAVID NKTLLAGSIN WSKGRFSLND
301  ESLIILENLT KQQNQKLRMI WKDLAKHSEH PTVDDEEKEI IEKSLPVEEQ
351  EAA*
```

A predicted signal peptide is highlighted.

The cp6607 nucleotide sequence <SEQ ID 150> is:

```
   1  ATGAATAAAA GACAAAAAGA TAAATTAAAA ATCTGTGTTA TTATTAGCAC
  51  GTTGATTTTA GTAGGAATTT TTGCAAGAGC TCCTCGTGGT GACACTTTTA
 101  AGACTTTTTT AAAGTCTGAA GAAGCTATCA TCTACTCAAA TCAATGCAAT
 151  GAGGACATGC GTAAAATTCT ATGCGATGCT ATAGAACACG CTGATGAAGA
 201  GATCTTCCTA CGTATTTATA ACCTCTCAGA ACCCAAGATC CAACAGAGTT
 251  TAACTCGACA AGCTCAAGCA AAAAACAAAG TTACGATCTA CTATCAAAAA
 301  TTTAAAATTC CCCAAATCTT AAAGCAAGCC AGCAATGTAA CTTTAGTCGA
 351  GCAACCTCCA GCAGGGCGTA AACTGATGCA TCAAAAAGCT CTTTCCATAG
 401  ATAAGAAAGA TGCTTGGCTA GGATCTGCGA ACTACACCAA TCTTTCTCTA
 451  CGTTTAGATA ATAATCTCAT TCTAGGAATG CATAGCTCGG AGCTCTGTGA
 501  TCTCATTATC ACAAATACCT CTGGAGACTT TTCTATAAAG GATCAAACAG
 551  GAAAGTATTT TGTTCTTCCT CAAGATCGTA AAATTGCAAT ACAAGCTGTA
 601  CTCGAAAAAA TCCAGACAGC TCAGAAAACC ATCCAAGTTG CTATGTTTGC
 651  TCTGACCCAC TCGGAGATTA TTCAAGCCTT ACATCAAGCA AAACAACGAG
 701  GAATCCATGT AGATATTATC ATTGATAGAA GTCATAGCAA ACTTACTTTT
 751  AAGCAATTAC GACAATTAAA TATCAATAAA GACTTTGTTT CTATAAATAC
 801  CGCACCCTGT ACTCTTCACC ATAAGTTTGC AGTTATAGAT AATAAAACTC
 851  TACTTGCAGG ATCTATAAAT TGGTCTAAAG GAAGATTCTC CTTAAATGAT
 901  GAAAGCTTGA TCATACTGGA AAACCTGACC AAACAACAAA ATCAGAAACT
 951  TCGAATGATT TGGAAAGATC TAGCTAAGCA TTCAGAACAT CCTACAGTAG
1001  ACGATGAAGA AAAAGAAATT ATAGAAAAAA GTCTTCCAGT AGAAGAGCAA
1051  GAAGCAGCGT GA
```

The PSORT algorithm predicts periplasmic (0.934).

The protein was expressed in *E.coli* and purified as a his-tagged product (Figure 75A) and also as a GST-fusion. The GST-fusion protein was used to immunise miee, whose sera were used in a Western blot (Figure 75B) and for FACS analysis.

These experiments show that cp6607 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 76

The following *C.pneumoniae* protein (PID 4376624) was expressed <SEQ ID 151; cp6624>:

```
   1  MDAKMGYIFK VMRWIFCFVA CGITFGCTNS GFQNANSRPC ILSMNRMIHD
  51  CVERVVGNRL ATAVLIKGSL DPHAYEMVKG DKDKIAGSAV IFCNGLGLEH
 101  TLSLRKHLEN NPNSVKLGER LIARGAFVPL EEDGICDPHI WMDLSIWKEA
 151  VIEITEVLIE KFPEWSAEFK ANSEELVCEM SILDSWAKQC LSTIPENLRY
 201  LVSGHNAFSY FTRRYLATPE EVASGAWRSR CISPEGLSPE AQISVRDIMA
 251  VVDYINEHDV SVVFPEDTLN QDALKKIVSS LKKSHLVRLA QKPLYSDNVD
 301  DNYFSTFKHN VCLITEELGG VALECQR*
```

The cp6624 nucleotide sequence <SEQ ID 152> is:

```
   1  ATGGATGCGA AAATGGGATA TATATTTAAA GTGATGCGTT GGATTTTCTG
  51  TTTCGTGGCA TGTGGTATAA CTTTTGGATG TACCAATTCT GGGTTTCAGA
 101  ATGCAAATTC ACGTCCTTGT ATACTATCCA TGAATCGCAT GATTCATGAT
 151  TGTGTTGAAA GAGTCGTGGG GAATAGGCTT GCTACCGCTG TTTTGATCAA
 201  AGGATCCTTA GACCCTCATG CGTATGAGAT GGTTAAAGGG GATAAGGACA
 251  AGATTGCTGG AAGTGCCGTA ATTTTTTGTA ACGGCCTGGG TCTTGAGCAT
 301  ACATTAAGTT TGCGGAAGCA TTTAGAAAAT AATCCCAATA GTGTCAAGTT
 351  AGGGGAGCGG TTGATAGCGC GTGGGGCCTT TGTTCCTCTA GAAGAAGACG
 401  GTATTTGCGA TCCTCATATC TGGATGGATC TTTCTATTTG GAAGGAAGCT
 451  GTCATAGAAA TTACAGAAGT TCTCATTGAA AAGTTCCCTG AATGGTCTGC
 501  TGAATTTAAA GCAAATAGTG AGGAACTTGT TTGTGAAATG TCTATTTTAG
 551  ATTCTTGGGC GAAACAATGC TTGAGCACAA TTCCTGAAAA TTTACGGTAT
 601  CTTGTCTCAG GTCATAATGC GTTCAGTTAC TTTACACGTC GCTATTTAGC
 651  TACTCCTGAA GAAGTGGCTT CCGGAGCATG GAGGTCTCGT TGTATTTCTC
 701  CTGAGGGTCT ATCTCCAGAA GCTCAAATCA GTGTTCGTGA TATTATGGCG
 751  GTTGTAGATT ATATTAATGA GCATGATGTC AGTGTGGTTT TCCCTGAGGA
 801  TACTCTGAAC CAAGATGCGT TGAAAAAAAT TGTTTCTTCT CTGAAGAAAA
 851  GTCATTTAGT TCGTCTAGCT CAAAAACCAT TGTATAGTGA TAATGTGGAC
 901  GACAATTATT TTAGCACCTT TAAACATAAT GTCTGCCTTA TCACAGAAGA
```

```
951  ATTAGGAGGG GTGGCTCTTG AATGTCAAAG ATGA
```

The PSORT algorithm predicts inner membrane (0.168).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 76A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 76B) and for FACS analysis.

The cp6624 protein was also identified in the 2D-PAGE experiment.

These experiments show that cp6624 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 77

The following *C.pneumoniae* protein (PID 4376728) was expressed <SEQ ID 153; cp6728>:

```
  1  MKSSVSWLFF SSIPLFSSLS IVAAEVTLDS SNNSYDGSNG TTFTVFSTTD
 51  AAAGTTYSLL SDVSFQNAGA LGIPLASGCF LEAGGDLTFQ GNQHALKFAF
101  INAGSSAGTV ASTSAADKNL LFNDFSRLSI ISCPSLLLSP TGQCALKSVG
151  NLSLTGNSQI IFTQNFSSDN GGVINTKNFL LSGTSQFASF SRNQAFTGKQ
201  GGVVYATGTI TIENSPGIVS FSQNLAKGSG GALYSTDNCS ITDNFQVIFD
251  GNSAWEAAQA QGGAICCTTT DKTVTLTGNK NLSFTNNTAL TYGGAISGLK
301  VSISAGGPTL FQSNISGSSA GQGGGGAINI ASAGELALSA TSGDITFNNN
351  QVTNGSTSTR NAINIIDTAK VTSIRAATGQ SIYFYDPITN PGTAASTDTL
401  NLNLADANSE IEYGGAIVFS GEKLSPTEKA IAANVTSTIR QPAVLARGDL
451  VLRDGVTVTF KDLTQSPGSR ILMDGGTTLS AKEANLSLNG LAVNLSSLDG
501  TNKAALKTEA ADKNISLSGT IALIDTEGSF YENHNLKSAS TYPLLELTTA
551  GANGTITLGA LSTLTLQEPE THYGYQGNWQ LSWANATSSK IGSINWTRTG
601  YIPSPERKSN LPLNSLWGNF IDIRSINQLI ETKSSGEPFE RELWLSGIAN
651  FFYRDSMPTR HGFRHISGGY ALGITATTPA EDQLTFAFCQ LFARDRNHIT
701  GKNHGDTYGA SLYFHHTEGL FDIANFLWGK ATRAPWVLSE ISQIIPLSFD
751  AKFSYLHTDN HMKTYYTDNS IIKGSWRNDA FCADLGASLP FVISVPYLLK
801  EVEPFVKVQY IYAHQQDFYE RHAEGRAFNK SELINVEIPI GVTFERDSKS
851  EKGTYDLTLM YILDAYRRNP KCQTSLIASD ANWMAYGTNL ARQGFSVRAA
901  NHFQVNPHME IFGQFAFEVR SSSRNYNTNL GSKFCF*
```

The cp6728 nucleotide sequence <SEQ ID 154> is:

```
   1  ATGAAGTCCT CTGTCTCTTG GTTGTTCTTT TCTTCAATCC CGCTCTTTTC
  51  ATCGCTCTCT ATAGTCGCGG CAGAGGTGAC CTTAGATAGC AGCAATAATA
 101  GCTATGATGG ATCTAACGGA ACTACCTTCA CGGTCTTTTC CACTACGGAC
 151  GCTGCTGCAG GAACTACCTA TTCCTTACTT TCCGACGTAT CCTTTCAAAA
 201  TGCAGGGGCT TTAGGAATTC CCTTAGCCTC AGGATGCTTC CTAGAAGCGG
 251  GCGGCGATCT TACTTTCCAA GGAAATCAAC ATGCACTGAA GTTTGCATTT
 301  ATCAATGCGG GCTCTAGCGC TGGAACTGTA GCCAGTACCT CAGCAGCAGA
 351  TAAGAATCTT CTCTTTAATG ATTTTTCTAG ACTCTCTATT ATCTCTTGTC
 401  CCTCTCTTCT TCTCTCTCCT ACTGGACAAT GTGCTTTAAA ATCTGTGGGG
 451  AATCTATCTC TAACTGGCAA TTCCCAAATT ATATTTACTC AGAACTTCTC
 501  GTCAGATAAC GGCGGTGTTA TCAATACGAA AAACTTCTTA TTATCAGGGA
 551  CATCTCAGTT TGCGAGCTTT TCGAGAAACC AAGCCTTCAC AGGGAAGCAA
 601  GGCGGTGTAG TTTACGCTAC AGGAACTATA ACTATCGAGA ACAGCCCTGG
 651  GATAGTTTCC TTCTCTCAAA ACCTAGCGAA AGGATCTGGC GGTGCTCTGT
 701  ACAGCACTGA CAACTGTTCG ATTACAGATA ACTTTCAAGT GATCTTTGAC
 751  GGCAATAGTG CTTGGGAAGC CGCTCAAGCT CAGGGCGGGG CTATTTGTTG
 801  CACTACGACA GATAAAACAG TGACTCTTAC TGGGAACAAA AACCTCTCTT
 851  TCACAAATAA TACAGCATTG ACATATGGCG GAGCCATCTC TGGACTCAAG
 901  GTCAGTATTT CCGCTGGAGG TCCTACTCTA TTTCAAAGTA ATATCTCAGG
 951  AAGTAGCGCC GGTCAGGGAG GAGGAGGAGC GATCAATATA GCATCTGCTG
1001  GGGAACTCGC TCTCTCTGCT ACTTCTGGAG ATATTACCTT CAATAACAAC
1051  CAAGTCACCA ACGGAAGCAC AAGTACAAGA AACGCAATAA ATATCATTGA
1101  TACCGCTAAA GTCACATCGA TACGAGCTGC TACGGGGCAA TCTATCTATT
1151  TCTATGATCC CATCACAAAT CCAGGAACCG CAGCTTCTAC CGACACATTG
1201  AACTTAAACT TAGCAGATGC GAACAGTGAG ATCGAGTATG GGGGTGCGAT
1251  TGTCTTTTCT GGAGAAAAGC TTTCCCCTAC AGAAAAAGCA ATCGCTGCAA
```

```
1301  ACGTCACCTC TACTATCCGA CAACCTGCAG TATTAGCGCG GGGAGATCTT
1351  GTACTTCGTG ATGGAGTCAC CGTAACTTTC AAGGATCTGA CTCAAAGTCC
1401  AGGATCCCGC ATCTTAATGG ATGGGGGGAC TACACTTAGT GCTAAAGAGG
1451  CAAATCTTTC GCTTAATGGC TTAGCAGTAA ATCTCTCCTC TTTAGATGGA
1501  ACCAACAAGG CAGCTTTAAA AACAGAAGCT GCAGATAAAA ATATCAGCCT
1551  ATCGGGAACG ATTGCGCTTA TTGACACGGA AGGGTCATTC TATGAGAATC
1601  ATAACTTAAA AAGTGCTAGT ACCTATCCTC TTCTTGAACT TACCACCGCA
1651  GGAGCCAACG GAACGATTAC TCTGGGAGCT CTTTCTACCC TGACTCTTCA
1701  AGAACCTGAA ACCCACTACG GGTATCAAGG AAACTGGCAG TTGTCTTGGG
1751  CAAATGCAAC ATCCTCAAAA ATAGGAAGCA TCAACTGGAC CCGTACAGGA
1801  TACATTCCTA GTCCTGAGAG AAAAAGTAAT CTCCCTCTAA ATAGCTTATG
1851  GGGAAACTTT ATAGATATAC GCTCGATCAA TCAGCTTATA GAAACCAAGT
1901  CCAGTGGGGA GCCTTTTGAG CGTGAGCTAT GGCTTTCAGG AATTGCGAAT
1951  TTCTTCTATA GAGATTCTAT GCCCACCCGC CATGGTTTCC GCCATATCAG
2001  CGGGGGTTAT GCACTAGGGA TCACAGCAAC AACTCCTGCC GAGGATCAGC
2051  TTACTTTTGC CTTCTGCCAG CTCTTTGCTA GAGATCGCAA TCATATTACA
2101  GGTAAGAACC ACGGAGATAC TTACGGTGCC TCTTTGTATT TCCACCATAC
2151  AGAAGGGCTC TTCGACATCG CCAATTTCCT CTGGGGAAAA GCAACCCGAG
2201  CTCCCTGGGT GCTCTCTGAG ATCTCCCAGA TCATTCCTTT ATCGTTCGAT
2251  GCTAAATTCA GTTATCTCCA TACAGACAAC CACATGAAGA CATATTATAC
2301  CGATAACTCT ATCATCAAGG GTTCTTGGAG AAACGATGCC TTCTGTGCAG
2351  ATCTTGGAGC TAGCCTGCCT TTTGTTATTT CCGTTCCGTA TCTTCTGAAA
2401  GAAGTCGAAC CTTTTGTCAA AGTACAGTAT ATCTATGCGC ATCAGCAAGA
2451  CTTCTACGAG CGTCATGCTG AAGGACGCGC TTTCAATAAA AGCGAGCTTA
2501  TCAACGTAGA GATTCCTATA GGCGTCACCT TCGAAAGAGA CTCAAAATCA
2551  GAAAAGGGAA CTTACGATCT TACTCTTATG TATATACTCG ATGCTTACCG
2601  ACGCAATCCT AAATGTCAAA CTTCCCTAAT AGCTAGCGAT GCTAACTGGA
2651  TGGCCTATGG TACCAACCTC GCACGACAAG GTTTTTCTGT TCGTGCTGCG
2701  AACCATTTCC AAGTGAACCC CCACATGGAA ATCTTCGGTC AATTCGCTTT
2751  TGAAGTACGA AGTTCTTCAC GAAATTATAA TACAAACCTA GGCTCTAAGT
2801  TTTGTTTCTA G
```

The PSORT algorithm predicts inner membrane (0.187).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 77A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 77B) and for FACS analysis.

The cp6728 protein was also identified in the 2D-PAGE experiment.

These experiments show that cp6728 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 78

The following *C.pneumoniae* protein (PID 4376847) was expressed <SEQ ID 155; cp6847>:

```
  1  MFVMKKLVRL CVVLLSLLPN VLFSSDLLRE EGIKKMMDKL IEYHVDAQEV
 51  STDILSRSLS SYIQSFDPHK SYLSNQEVAV FLQSPETKKR LLKNYKAGNF
101  AIYRNINQLI HESILRARQW RNEWVKNPKE LVLEASSYQI SKQPMQWSKS
151  LDEVKQRQRA LLLSYLSLHL AGASSSRYEG KEEQLAALCL RQIENHENVY
201  LGINDHGVAM DRDEEAYQFH IRVVKALAHS LDAHTAYFSK DEALAMRIQL
251  EKGMCGIGVV LKEDIDGVVV REIIPGGPAA KSGDLQLGDI IYRVDGKDIE
301  HLSFRGVLDC LRGGHGSTVV LDIHRGESDH TIALRREKIL LEDRRVDVSY
351  EPYGDGVIGK VTLHSFYEGE NQVSSEQDLR RAIQGLKEKN LLGLVLDIRE
401  NTGGFLSQAI KVSGLFMTNG VVVVSRYADG TMKCYRTVSP KKFYDGPLAI
451  LVSKSSASAA EIVAQTLQDY GVALVVGDEQ TYGKGTIQHQ TITGDASQDD
501  CFKVTVGKYY SPSGKSTQLQ GVKSDILIPS LYAEDRLGER FLEHPLPADC
551  CDNVLHDPLT DLDTQTRPWF QKYYLPNLQK QETLWREMLP QLTKNSEQRL
601  SENSNFQAFL SQIKSSEKTD LSYGSNDLQL EESINILKDM ILLQQCRK*
```

A predicted signal peptide is highlighted.

The cp6847 nucleotide sequence <SEQ ID 156> is:

```
   1  ATGTTCGTAA TGAAAAAACT TGTCCGTCTA TGCGTAGTTC TTCTTTCTTT
  51  ACTTCCGAAT GTATTATTTT CTTCGGATCT TTTACGAGAA GAGGGCATCA
 101  AAAAGATGAT GGACAAGCTG ATCGAGTATC ATGTCGATGC TCAAGAGGTT
 151  TCTACGGATA TACTCTCGCG TTCTTTATCT AGTTACATTC AATCTTTTGA
 201  TCCTCATAAA TCTTATCTTT CAAACCAAGA GGTTGCAGTT TTTCTACAGT
 251  CTCCGGAAAC AAAGAAACGT CTCTTAAAGA ATTATAAGGC AGGCAACTTT
 301  GCTATTTATC GCAACATCAA TCAATTAATT CATGAGAGTA TTCTTCGTGC
 351  CAGGCAGTGG AGAAACGAAT GGGTTAAGAA TCCAAAAGAG CTTGTATTGG
 401  AGGCATCCTC ATATCAGATA TCGAAGCAAC CTATGCAATG GAGCAAATCT
 451  TTAGACGAAG TGAAGCAGAG ACAACGCGCT CTACTCCTTT CCTATCTTTC
 501  TTTACATCTT GCTGGAGCTT CTTCCTCTCG TTATGAGGGT AAAGAAGAGC
 551  AGCTTGCTGC TCTGTGTCTA CGTCAAATCG AGAACCATGA GAATGTATAT
 601  TTAGGTATCA ACGATCATGG TGTTGCTATG GATCGGGATG AAGAAGCCTA
 651  CCAATTCCAT ATCCGTGTTG TTAAAGCTTT AGCTCATAGC TTAGATGCAC
 701  ATACGGCGTA TTTCAGTAAG GACGAAGCGT TGGCGATGCG AATCCAACTA
 751  GAAAAAGGCA TGTGTGGAAT TGGTGTTGTT CTGAAGGAAG ATATTGATGG
 801  AGTTGTTGTT AGAGAAATCA TTCCTGGGGG ACCTGCGGCT AAATCTGGGG
 851  ATCTTCAGCT TGGAGATATC ATCTATCGGG TGGATGGCAA GGATATCGAG
 901  CATCTTTCTT TCCGCGGTGT TTTAGATTGT TTACGTGGAG GTCATGGCTC
 951  TACTGTAGTC TTAGATATCC ATCGTGGGGA GAGCGATCAT ACGATCGCCT
1001  TGAGAAGGGA GAAAATCCTT TTAGAAGACC GTCGTGTGGA TGTTTCCTAT
1051  GAGCCTTATG GAGATGGTGT GATTGGGAAA GTTACGTTAC ATTCTTTTTA
1101  TGAAGGAGAA AATCAGGTTT CTAGTGAACA AGATCTACGT CGAGCGATTC
1151  AGGGATTAAA GGAGAAGAAC CTTCTTGGAT TAGTTTTAGA TATCCGAGAA
1201  AATACGGGTG GATTTTTATC TCAAGCGATC AAAGTTTCTG GTTTATTTAT
1251  GACCAATGGC GTTGTGGTTG TATCTCGCTA TGCTGATGGT ACCATGAAGT
1301  GCTACCGCAC AGTATCTCCT AAAAAATTCT ATGATGGTCC TTTGGCTATT
1351  TTAGTATCTA AAAGTTCCGC ATCAGCAGCG GAGATTGTAG CACAAACTCT
1401  CCAAGATTAT GGAGTTGCTT TAGTTGTTGG AGATGAGCAG ACCTATGGGA
1451  AGGGAACGAT TCAGCATCAA ACAATTACTG GAGATGCCTC TCAGGACGAT
1501  TGTTTTAAGG TTACTGTAGG GAAATATTAT TCCCCTTCTG GGAAATCGAC
1551  TCAACTTCAG GGAGTAAAAT CCGATATTTT AATTCCTTCT CTCTATGCTG
1601  AAGATCGTCT AGGAGAGCGT TTTCTAGAGC ATCCCTTACC TGCAGATTGC
1651  TGTGATAATG TACTTCACGA TCCTCTCACG GACTTGGATA CTCAAACACG
1701  TCCTTGGTTT CAAAAATACT ATCTTCCTAA TCTACAAAAG CAAGAGACTC
1751  TTTGGAGAGA GATGCTACCT CAGCTTACGA AAAACAGTGA GCAAAGGCTT
1801  TCTGAGAATT CGAATTTTCA GGCATTTTTG TCGCAGATAA AATCATCTGA
1851  AAAAACGGAC CTATCCTATG GTTCCAATGA TTTACAATTG GAAGAGTCGA
1901  TAAACATTTT GAAGGACATG ATTTTATTAC AACAGTGTAG AAAATAA
```

The PSORT algorithm predicts periplasmic (0.932).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 78A). The recombinant protein was used to immunise miee, whose sera were used in a Western blot (Figure 78B) and for FACS analysis.

These experiments show that cp6847 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 79

The following *C.pneumoniae* protein (PID 4376969) was expressed <SEQ ID 157; cp6969>:

```
  1  MRLFSLGTIY LFFSLALSSC CGYSILNSPY HLSSLGKSLL QERIFIAPIK
 51  EDPHGQLCSA LTYELSKRSF AISGRSSCAG YTLKVELLNG IDKNIGFTYA
101  PNKLGDKTHR HFIVSNEGRL SLSAKVQLIN NDTQEVLIDQ CVARESVDFD
151  FEPDLGTANA HEFALGQFEM HSEAIKSARR ILSIRLAETI AQQVYYDLF*
```

A predicted signal peptide is highlighted.

The cp6969 nucleotide sequence <SEQ ID 158> is:

```
  1  ATGAGATTGT TTTCTTTAGG CACGATTTAT CTTTTTTTTT CTCTAGCACT
 51  TTCGTCATGC TGTGGTTACT CTATTTTAAA CAGCCCGTAT CACTTATCGT
101  CTTTAGGTAA GTCTTTATTA CAGGAAAGAA TTTTCATTGC TCCCATAAAA
```

```
151  GAAGATCCTC ATGGTCAGCT CTGCTCAGCT CTAACTTATG AGCTTAGTAA
201  GCGTTCTTTT GCTATCTCTG GAAGGAGTTC TTGCGCAGGC TATACTCTTA
251  AAGTAGAGCT TCTGAATGGT ATTGACAAGA ATATAGGTTT TACGTATGCC
301  CCAAATAAAC TCGGAGATAA GACTCACAGG CATTTTATAG TCTCTAATGA
351  AGGCAGACTA TCACTATCTG CAAAAGTACA GCTTATCAAT AATGACACTC
401  AAGAAGTCCT TATAGACCAA TGTGTTGCTC GAGAGTCTGT AGACTTTGAC
451  TTTGAGCCTG ACTTAGGAAC AGCAAACGCT CATGAATTTG CTTTAGGCCA
501  ATTTGAAATG CATAGTGAAG CCATAAAAAG TGCTCGCCGT ATACTATCTA
551  TACGCCTAGC CGAGACGATT GCTCAACAGG TATACTATGA CCTTTTTTGA
```

The PSORT algorithm predicts inner membrane (0.126).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 79A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 79B) and for FACS analysis.

These experiments show that cp6969 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 80

The following *C.pneumoniae* protein (PID 4377109) was expressed <SEQ ID 159; cp7109>:

```
  1  MKKTCCQNYR SIGVVFSVVL FVLTTQTLFA GHFIDIGTSG LYSWARGVSG
 51  DGRVVVGYEG GNAFKYVDGE KFLLEGLVPR SEALVFKASY DGSVIIGISD
101  QDPSCRAVKW VNGALVDLGI FSEGMQSFAE GVSSDGKTIV GCLYSDDTET
151  NFAVKWDETG MVVLPNLPED RHSCAWDASE DGSVIVGDAM GSEEIAKAVY
201  WKDGEQHLLS NIPGAKRSSA HAVSKDGSFI VGEFISEENE VHAFVYHNGV
251  IKDIGTLGGD YSVATGVSRD GKVIVGHSTR TDGEYRAFKY VDGRMIDLGT
301  LGGSASFAFG VSDDGKTIVG KFETELGECH AFIYLDD*
```

A predicted signal peptide is highlighted.

The cp7109 nucleotide sequence <SEQ ID 160> is:

```
   1  ATGAAAAAGA CATGTTGCCA AAATTACAGA TCGATAGGCG TTGTGTTCTC
  51  TGTGGTACTT TTCGTTCTTA CAACACAGAC GCTGTTTGCA GGACATTTTA
 101  TTGATATTGG AACTTCTGGA TTATATTCTT GGGCTCGAGG TGTATCTGGA
 151  GATGGCCGCG TTGTCGTAGG TTATGAAGGT GGCAATGCAT TTAAATATGT
 201  TGATGGTGAG AAATTTCTGT TAGAAGGTTT GGTCCCGAGA TCCGAGGCCT
 251  TGGTATTTAA AGCTTCTTAT GATGGCTCTG TAATTATAGG AATCTCGGAT
 301  CAAGATCCGT CTTGCCGCGC TGTGAAGTGG GTAAACGGTG CACTTGTTGA
 351  TCTTGGAATA TTTTCTGAGG GAATGCAATC TTTTGCAGAG GGTGTTTCCA
 401  GTGATGGAAA GACGATTGTA GGGTGCCTAT ATAGTGATGA TACAGAGACA
 451  AACTTTGCTG TGAAGTGGGA TGAAACAGGA ATGGTTGTTC TCCCTAACTT
 501  ACCAGAAGAT CGACATTCTT GCGCTTGGGA TGCCTCTGAA GATGGCTCTG
 551  TGATTGTAGG GGACGCCATG GGTAGCGAGG AAATTGCCAA GGCAGTGTAC
 601  TGGAAGGACG GTGAACAACA TCTGCTTTCT AATATCCCAG GAGCTAAAAG
 651  ATCGTCAGCA CATGCAGTTT CTAAAGATGG ATCTTTTATC GTAGGCGAGT
 701  TCATCAGTGA AGAAAATGAA GTTCATGCCT TTGTTTATCA CAACGGTGTT
 751  ATCAAAGATA TCGGGACTTT AGGAGGAGAT TACTCTGTAG CAACTGGAGT
 801  TTCTAGGGAT GGTAAGGTCA TCGTGGGTCA TTCTACAAGA ACAGATGGTG
 851  AATACCGTGC ATTTAAATAT GTGGATGGAA GAATGATAGA TTTGGGGACT
 901  TTAGGAGGTT CAGCATCTTT TGCTTTTGGT GTTTCTGACG ATGGCAAAAC
 951  AATCGTAGGA AAATTTGAAA CAGAGCTAGG AGAATGTCAT GCCTTTATCT
1001  ACCTTGATGA TTAG
```

The PSORT algorithm predicts outer membrane (0.887).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 80A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 80B) and for FACS analysis.

These experiments show that cp7109 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 81

The following *C.pneumoniae* protein (PID 4377110) was expressed <SEQ ID 161; cp7110>:

```
  1  MAAIKQILRS MLSQSSLWMV LFSLYSLSGY CYVITDKPED DFHSSSAVKW
 51  DHWGKTTLSR LSNKKASAKA VSGTGATTVG FIKDTWSRTY AVRWNYWGTK
101  ELPTSSWVKK SKATGISSDG SIIAGIVENE LSQSFAVTWK NNEMYLLPST
151  WAVQSKAYGI SSDGSVIVGS AKDAWSRTFA VKWTGHEAQV LPVGWAVKSV
201  ANSVSANGSI IVGSVQDASG ILYAVKWEGN TITHLGTLGG YSAIAKAVSN
251  NGKVIVGRSE TYYGEVHAFC HKNGVMSDLG TLGGSYSAAK GVSATGKVIV
301  GMSTTANGKL HAFKYVGGRM IDLGEYSWKE ACANAVSIDG EIIVGVQSE*
```

A predicted signal peptide is highlighted.

The cp7110 nueleotide sequencc <SEQ ID 162> is:

```
   1  ATGGCAGCTA TAAAACAAAT TTTACGTTCT ATGCTATCTC AGAGTAGCTT
  51  ATGGATGGTC CTATTTTCAT TATATTCTCT ATCTGGTTAT TGCTATGTAA
 101  TTACAGACAA ACCAGAAGAT GACTTCCATT CTTCATCCGC AGTAAAATGG
 151  GATCATTGGG GAAAGACAAC TCTCTCAAGA TTATCAAATA AAAAAGCCTC
 201  TGCAAAAGCT GTTTCAGGAA CTGGTGCTAC AACTGTCGGC TTTATAAAAG
 251  ACACTTGGTC TCGAACATAC GCAGTAAGAT GGAATTATTG GGGGACCAAA
 301  GAACTCCCTA CCAGCTCATG GGTAAAAAAA TCAAAAGCAA CAGGAATCTC
 351  CTCTGATGGG TCTATAATCG CGGGGATTGT CGAGAATGAG CTTTCTCAAA
 401  GTTTCGCAGT CACATGGAAA AACAATGAAA TGTATTTGCT CCCTTCCACA
 451  TGGGCAGTGC AATCTAAAGC GTATGGAATT TCTTCTGATG GCTCTGTTAT
 501  TGTAGGGAGT GCTAAGGATG CTTGGTCGCG AACTTTCGCT GTGAAGTGGA
 551  CGGGACACGA GGCTCAGGTG TTACCAGTAG GCTGGGCTGT CAAATCTGTA
 601  GCGAATTCTG TATCTGCCAA TGGATCTATA ATTGTAGGGT CTGTACAAGA
 651  CGCCTCTGGA ATTCTTTATG CTGTAAAGTG GGAAGGGAAC ACTATTACAC
 701  ATCTAGGAAC TTTAGGAGGC TATTCTGCCA TTGCAAAAGC TGTATCCAAT
 751  AATGGCAAGG TCATTGTAGG GAGATCCGAA ACATATTATG GAGAGGTCCA
 801  TGCTTTCTGT CATAAGAATG GCGTCATGTC AGACCTCGGC ACCCTCGGAG
 851  GATCTTATTC TGCAGCTAAG GGAGTCTCTG CAACTGGAAA AGTTATTGTC
 901  GGTATGTCCA CAACAGCAAA TGGGAAATTG CATGCCTTTA AATATGTCGG
 951  TGGAAGAATG ATCGACTTAG GAGAGTATAG CTGGAAAGAA GCCTGTGCAA
1001  ACGCTGTTTC TATTGATGGA GAAATTATTG TTGGAGTCCA ATCAGAATAA
```

The PSORT algorithm predicts outer membrane (0.827).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 81A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 81B) and for FACS analysis.

These experiments show that cp7110 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Figure 191 shows a schematic representation of the structural relationships between of cp7105, cp7106, cp7107, cp7108, cp7109 and cp7110, each of which is identified herein. These six proteins may be grouped in a new family of related outer membrane-associated proteins. These proteins have a repeat structure in common (*cf.* the pmp family).

Example 82

The following *C.pneumoniae* protein (PID 4377127) was expressed <SEQ ID 163; cp7127>:

```
  1  MVFFRNSLLH LVALSGMLCC SSGVALTIAE KMASLEHSGR GADDYEGMAS
```

51 FNANMREYSL QLSKLYEEAR KLRASGTEDE ALWKDLIRRI GEVRGYLREI
101 EELWAAEIRE KGGNLEDYAL WNHPETTIYN LVTDYGTEDS IYLIPQEIGA
151 IKIATLSKFV VPKESFEDCL TQILSRLGIG VRQVNSWIKE LYMMRKEGCS
201 VAGVFSSRKD LEALPETAYI GFVLNSNVDA HTNQHVLKKF INPETTHVDV
251 IAGRVWIFGS AGEVGELLKI YNFVQSESIR QEYRVIPLTK IDPGEMISIL
301 NAAFREDLTK DVSEESLGLR VVPLQYQGRS LFLSGTAALV QQALTLIREL
351 EEGIENPTDK TVFWYNVKHS DPQELAALLS QVHDVFSGEN KASVGAADGC
401 GSQLNASIQI DTTVSSSAKD GSVKYGNFIA DSKTGTLIMV VEKEVLPRIQ
451 MLLKKLDVPK KMVRIEVLLF ERKLAHEQKS GLNLLRLGEE VCKKGCSPSV
501 SWAGGTGILE FLFKGSTGSS IVPGYDLAYQ FLMAQEDVRI NASPSVVTMN
551 QTPARIAVVD EMSIAVSSDK DKAQYNRAQY GIMIKMLPVI NVGEEDGKSY
601 ITLETDITFD TTGKNHDDRP DVTRRNITNK VRIADGETVI IGGLRCKQMS
651 DSHDGIPFLG DIPGIGKLFG MSSTSDSLTE MFVFITPKIL ENPVEQQERK
701 EEALLSSRPG EREEYYQALA ASEAAARAAH KKLEMFPASG VSLSQVERQE
751 YDGC*

A predicted signal peptide is highlighted.

The cp7127 nucleotide sequence <SEQ ID 164> is:

1 ATGGTTTTTT TCCGTAATTC TTTACTGCAT TTAGTTGCCC TATCCGGAAT
51 GCTCTGTTGT TCTTCTGGAG TGGCTTTAAC GATAGCCGAG AAGATGGCTT
101 CTTTAGAGCA CTCGGGGAGA GGAGCAGACG ATTATGAGGG GATGGCTTCG
151 TTTAATGCCA ATATGAGGGA GTATAGCCTT CAGCTGAGCA AGTTGTATGA
201 GGAAGCACGA AAGCTACGCG CTTCTGGAAC TGAGGATGAA GCTCTGTGGA
251 AGGACTTAAT TCGACGGATT GGTGAGGTGC GAGGCTATCT TCGAGAGATC
301 GAGGAGCTTT GGGCTGCAGA AATTCGTGAG AAAGGGGGCA ATCTCGAGGA
351 CTACGCCCTC TGGAATCACC CAGAGACTAC GATTTACAAT CTTGTTACCG
401 ATTACGGAAC CGAAGACTCT ATTTATTTGA TTCCTCAAGA AATCGGAGCG
451 ATTAAAATCG CAACCTTATC GAAATTTGTA GTTCCTAAAG AGTCTTTCGA
501 AGACTGTCTC ACTCAGATCC TATCTCGCTT AGGTATTGGC GTGCGTCAGG
551 TCAATTCTTG GATTAAGGAA CTTTATATGA TGCGTAAGGA GGGCTGCAGT
601 GTTGCTGGAG TTTTTTCCTC CAGAAAAGAT TTAGAGGCGC TCCCAGAAAC
651 AGCCTATATT GGTTTTGTAT TGAATTCGAA CGTAGATGCG CATACCAATC
701 AACATGTCTT AAAAAAGTTC ATTAACCCTG AAACAACGCA TGTAGATGTG
751 ATTGCAGGAC GTGTGTGGAT TTTTGGTTCT GCGGGGGAAG TCGGCGAGCT
801 TCTGAAGATT TATAATTTTG TGCAGTCGGA GAGCATACGT CAAGAGTATC
851 GGGTGATTCC CTTAACTAAG ATCGATCCAG GGGAGATGAT TTCCATTCTC
901 AACGCAGCAT TTCGTGAGGA TCTGACTAAA GATGTTAGTG AAGAATCTTT
951 AGGCCTTCGT GTAGTTCCTT TACAGTATCA AGGGCGTTCG TTGTTTTTAA
1001 GTGGAACCGC GGCGTTAGTG CAGCAAGCGC TGACTCTCAT TCGAGAGCTT
1051 GAAGAAGGGA TTGAGAACCC TACGGATAAA ACAGTATTTT GGTATAACGT
1101 CAAGCACTCC GATCCCCAAG AGTTGGCGGC ATTGCTTTCC CAAGTCCATG
1151 ATGTCTTCTC TGGCGAGAAT AAGGCGAGTG TCGGAGCTGC AGATGGATGT
1201 GGGTCGCAAT TAAATGCCTC GATCCAAATT GATACTACAG TAAGTTCTTC
1251 TGCGAAAGAT GGCTCAGTGA AGTACGGAAA CTTCATCGCG GATTCTAAGA
1301 CAGGAACTCT GATTATGGTG GTTGAGAAAG AAGTTCTTCC ACGTATTCAG
1351 ATGCTACTTA AGAAACTAGA TGTCCCTAAA AAGATGGTCC GTATCGAGGT
1401 GCTGTTATTT GAAAGAAAAT TGGCACATGA GCAGAAATCT GGGTTAAATC
1451 TTCTACGTCT TGGTGAGGAA GTTTGTAAAA AAGGGTGCAG TCCTTCTGTG
1501 TCTTGGGCCG GGGGTACTGG CATACTAGAA TTTTTATTTA AAGGAAGTAC
1551 GGGATCTTCG ATAGTTCCTG GTTATGATCT CGCCTATCAA TTTTTAATGG
1601 CTCAAGAGGA CGTTCGGATT AATGCGAGTC CTTCTGTAGT TACTATGAAC
1651 CAAACCCCAG CACGGATTGC TGTTGTTGAT GAAATGTCAA TAGCGGTGTC
1701 TTCAGATAAA GATAAAGCGC AATACAATCG TGCGCAGTAC GGTATCATGA
1751 TAAAAATGCT CCCCGTAATT AATGTGGGAG AGGAAGACGG AAAAAGTTAC
1801 ATTACTTTAG AGACAGACAT CACCTTTGAT ACTACGGGAA AAAATCATGA
1851 TGATCGTCCT GATGTTACAA GGCGTAATAT TACTAATAAG GTGCGCATTG
1901 CTGACGGAGA GACTGTGATT ATTGGAGGTT TGCGTTGCAA ACAGATGTCA
1951 GATTCTCATG ATGGCATTCC TTTCCTTGGA GACATTCCTG GTATAGGGAA
2001 GTTATTTGGA ATGAGTTCCA CATCAGACAG TCTCACGGAG ATGTTTGTAT
2051 TTATCACTCC GAAGATCCTA GAAAATCCTG TAGAGCAACA AGAACGTAAA
2101 GAAGAAGCTT TACTCTCTTC GCGCCCTGGA GAGAGAGAAG AATACTATCA
2151 GGCTTTAGCA GCTAGTGAGG CTGCAGCACG AGCAGCTCAT AAAAAATTAG
2201 AGATGTTCCC GGCATCAGGA GTATCTTTAT CTCAGGTAGA GAGGCAAGAA
2251 TACGATGGCT GCTAG

The PSORT algorithm predicts periplasmic (0.920).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 82A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 82B) and for FACS analysis.

These experiments show that cp7127 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 83

The following *C.pneumoniae* protein (PID 4377133) was expressed <SEQ ID 165; cp7133>:

```
  1 MQPFIFTLLC LTSLVSLVAF DAANARKRCA CAQTIERGEN FFSIKRSACA
 51 EIEYQEKSRH ASAIERISKD KGKVTPKQIA KVATKKKQRY RLLQVPFSRP
101 PNNSRYNLYA LLSEPPECYS DTASWYAIFI RLLRRAYVDT GNVPPGSEYA
151 IANALISNKQ EILERGAQLG PDVIETLTLP EEQAEIFYKM LKGSSNSQSL
201 LNFLHYEEKS LGHCKLNLIF MDPLLLEAVL DHPDAYRETS LLRDGIWEAV
251 KRQEHAIQEH GQAAALELFK TRTDFRLELR DKMQLLLSRY DLLPLLNKKM
301 FDYTLGSAGD YLFLVDPDTK AISRCRCPSK SIKL
```

A predicted signal peptide is highlighted.

The cp7133 nucleotide sequence <SEQ ID 166> is:

```
   1 ATGCAACCTT TTATCTTTAC TTTACTGTGC TTGACATCTT TGGTTTCTTT
  51 AGTCGCCTTT GATGCTGCGA ATGCTCGTAA ACGTTGTGCC TGTGCTCAAA
 101 CTATAGAACG TGGAGAGAAC TTCTTTTCCA TAAAACGCTC TGCTTGTGCT
 151 GAAATCGAAT ATCAAGAAAA ATCTCGCCAC GCCTCAGCAA TTGAAAGAAT
 201 CTCAAAAGAT AAAGGCAAAG TCACTCCAAA GCAGATTGCG AAAGTAGCTA
 251 CTAAGAAAAA GCAAAGATAC CGTTTATTGC AGGTTCCTTT TTCAAGGCCT
 301 CCGAATAACT CAAGGTATAA CCTCTATGCT TTGCTTAGTG AACCTCCCGA
 351 ATGCTATAGC GATACAGCAT CATGGTATGC TATTTTTATT CGGTTACTTC
 401 GACGTGCTTA TGTAGACACG GGAAATGTAC CTCCTGGATC TGAGTATGCC
 451 ATCGCTAATG CTTTGATAAG TAACAAACAA GAGATTTTAG AGAGGGGAGC
 501 GCAGCTTGGA CCCGATGTTA TTGAAACTCT AACATTGCCT GAGGAACAAG
 551 CCGAGATTTT TTATAAAATG CTCAAAGGGT CGTCAAACTC TCAGTCGCTA
 601 CTGAATTTTC TGCATTATGA AGAGAAAAGC TTAGGCCACT GTAAGCTAAA
 651 TCTGATCTTC ATGGATCCCC TACTGTTAGA AGCTGTTCTA GATCATCCCG
 701 ATGCTTATAG GGAAACGTCG CTCCTGCGCG ATGGCATTTG GGAAGCGGTG
 751 AAGCGTCAAG AACATGCCAT CCAAGAACAT GGCCAGGCAG CTGCTTTGGA
 801 GCTTTTTAAA ACACGCACCG ACTTCCGCCT GGAGCTGCGA GATAAGATGC
 851 AGTTACTTCT AAGTCGATAC GATTTGCTCC CCTTATTAAA TAAAAAAATG
 901 TTCGACTACA CCTTAGGAAG TGCCGGAGAT TACTTATTTT TGGTAGACCC
 951 AGATACTAAG GCAATTTCTC GATGTCGCTG CCCTTCAAAG AGTATTAAAT
1001 TATAA
```

The PSORT algorithm predicts outer membrane (0.92).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 83A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 83B) and for FACS analysis.

These experiments show that cp7133 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 84

The following *C.pneumoniae* protein (PID 4377222) was expressed <SEQ ID 167; cp7222>:

```
  1 MNRRDMVITA VVVNAILLVA LFVTSKRIGV KDYDEGFRNF ASSKVTQAVV
 51 SEEKVIEKPV VAEVPSRPIA KETLAAQFIE SKPVIVTTPP VPVVSETPEV
```

```
101  PTVAVPPQPV RETVKEEQAP YATVVVKKGD FLERIARANH TTVAKLMQIN
151  DLTTTQLKIG QVIKVPTSQD VSNEKTPQTQ TANPENYYIV QEGDSPWTIA
201  LRNHIRLDDL LKMNDLDEYK ARRLKPGDQL RIR*
```

A predicted signal peptide is highlighted.

The cp7222 nucleotide sequence <SEQ ID 168> is:

```
  1  ATGAATCGTA GAGACATGGT AATAACAGCT GTCGTAGTGA ATGCTATATT
 51  GCTTGTGGCT CTTTTCGTCA CATCAAAGCG TATTGGCGTC AAGGACTATG
101  ACGAGGGATT CCGTAATTTT GCTTCTAGCA AGGTTACACA AGCAGTAGTT
151  TCAGAAGAAA AAGTCATAGA AAAGCCTGTA GTCGCAGAAG TGCCTAGCCG
201  TCCTATCGCT AAAGAGACTC TAGCTGCACA GTTTATTGAA AGTAAGCCGG
251  TTATTGTAAC CACACCACCC GTGCCTGTTG TTAGCGAAAC CCCAGAAGTG
301  CCTACTGTGG CAGTTCCGCC TCAGCCTGTT CGTGAGACAG TAAAAGAGGA
351  ACAAGCTCCT TATGCTACTG TTGTAGTGAA AAAAGGAGAT TTTCTCGAAC
401  GCATTGCGAG AGCAAATCAT ACTACCGTTG CAAAATTGAT GCAGATCAAT
451  GATCTTACCA CCACCCAACT TAAAATTGGT CAGGTCATCA AAGTCCCTAC
501  GTCTCAAGAT GTCAGCAACG AAAAAACTCC TCAAACACAG ACCGCAAACC
551  CTGAAAATTA TTATATCGTC CAAGAAGGGG ATAGCCCGTG GACAATAGCA
601  TTGCGTAACC ATATTCGATT GGATGATTTG CTAAAAATGA ATGATCTCGA
651  TGAATATAAA GCCCGGCGCC TTAAGCCTGG AGATCAGTTG CGCATACGTT
701  GA
```

The PSORT algorithm predicts periplasmic (0.935).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 84A) and also in his-tagged form. The recombinant proteins were used to immunise miee, whose sera were used in a Western blot (Figure 84B) and for FACS analysis.

These experiments show that cp7222 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 85

The following *C.pneumoniae* protein (PID 4377225) was expressed <SEQ ID 169; cp7225>:

```
  1  MKGTPQYHFI GIGGIGMSAL AHILLDRGYE VSGSDLYESY TIESLKAKGA
 51  RCFSGHDSSH VPHDAVVVYS SSIAPDNVEY LTAIQRSSRL LHRAELLSQL
101  MEGYESILVS GSHGKTGTSS LIRAIFQEAQ KDPSYAIGGL AANCLNGYSG
151  SSKIFVAEAD ESDGSLKHYT PRAVVITNID NEHLNNYAGN LDNLVQVIQD
201  FSRKVTDLNK VFYNGDCPIL KGNVQGISYG YSPECQLHIV SYNQKAWQSH
251  FSFTFLGQEY QDIELNLPGQ HNAANAAAAC GVALTFGIDI NIIRKALKKF
301  SGVHRRLERK NISESFLFLE DYAHHPVEVA HTLRSVRDAV GLRRVIAIFQ
351  PHRFSRLEEC LQTFPKAFQE ADEVILTDVY SAGESPRESI ILSDLAEQIR
401  KSSYVHCCYV PHGDIVDYLR NYIRIHDVCV SLGAGNIYTI GEALKDFNPK
451  KLSIGLVCGG KSCEHDISLL SAQHVSKYIS PEFYDVSYFI INRQGLWRTG
501  KDFPHLIEET QGDSPLSSEI ASALAKVDCL FPVLHGPFGE DGTIQGFFEI
551  LGKPYAGPSL SLAATAMDKL LTKRIASAVG VPVVPYQPLN LCFWKRNPEL
601  CIQNLIETFS FPMIVKTAHL GSSIGIFLVR DKEELQEKIS EAFLYDTDVF
651  VEESRLGSRE IEVSCIGHSS SWYCMAGPNE RCGASGFIDY QEKYGFDGID
701  CAKISFDLQL SQESLDCVRE LAERVYRAMQ GKGSARIDFF LDEEGNYWLS
751  EVNPIPGMTA ASPFLQAFVH AGWTQEQIVD HFIIDALHKF DKQQTIEQAF
801  TKEQDLVKR*
```

The cp7225 nucleotide sequence <SEQ ID 170> is:

```
  1  ATGAAGGGAA CTCCTCAGTA TCATTTTATC GGTATCGGTG GTATAGGAAT
 51  GAGCGCTTTA GCTCATATTT TGCTTGATCG TGGCTATGAG GTCTCTGGAA
101  GCGACTTATA TGAAAGCTAT ACGATCGAAA GCCTGAAAGC TAAAGGTGCG
151  AGGTGTTTCT CAGGCCATGA TTCCTCCCAT GTTCCTCATG ATGCCGTCGT
201  TGTTTATAGC TCAAGTATAG CCCCTGATAA TGTAGAGTAT CTTACCGCTA
251  TTCAAAGATC ATCACGTCTT CTTCATAGAG CAGAGCTCTT GAGTCAGCTT
301  ATGGAGGGTT ATGAAAGCAT TCTGGTTTCA GGAAGCCATG GGAAGACAGG
351  GACCTCATCT CTAATTCGAG CGATTTTCCA GGAAGCTCAG AAAGATCCCT
```

```
 401  CCTATGCTAT TGGAGGACTC GCTGCAAACT GCCTGAATGG GTATTCTGGA
 451  TCATCGAAAA TCTTCGTTGC CGAAGCCGAT GAAAGTGATG GGTCTTTAAA
 501  GCACTACACT CCCCGTGCAG TAGTCATTAC AAATATAGAT AATGAACATT
 551  TGAATAATTA CGCTGGGAAT CTTGATAACC TGGTTCAGGT AATCCAGGAC
 601  TTCTCTAGAA AAGTAACAGA TCTCAATAAG GTATTCTATA ACGGGGATTG
 651  TCCTATTTTG AAAGGAAATG TCCAAGGGAT TTCTTATGGA TATTCACCAG
 701  AATGTCAATT GCATATCGTT TCCTATAATC AAAAGGCATG GCAATCTCAC
 751  TTTTCCTTTA CCTTTTTAGG CCAGGAGTAT CAAGACATTG AGCTCAATCT
 801  CCCTGGACAA CATAACGCTG CAAATGCAGC AGCAGCCTGT GGAGTTGCTC
 851  TTACCTTTGG CATAGACATA AACATCATTC GAAAAGCTCT CAAAAAATTC
 901  TCGGGAGTTC ATCGACGTCT AGAAAGAAAA AATATATCCG AAAGCTTTCT
 951  TTTCTTAGAA GATTATGCTC ATCATCCTGT AGAGGTTGCA CATACCCTGC
1001  GCTCTGTGCG TGATGCTGTG GGTTTGCGAA GAGTCATCGC AATTTTTCAA
1051  CCACATCGAT TCTCTCGTTT AGAAGAGTGC TTACAAACCT TCCCCAAAGC
1101  TTTCCAAGAA GCTGATGAAG TCATACTTAC AGATGTCTAT AGTGCCGGAG
1151  AAAGTCCTAG AGAGTCTATC ATTCTTTCCG ACCTTGCGGA ACAGATTCGT
1201  AAGTCTTCTT ATGTCCATTG TTGTTATGTT CCCCATGGAG ACATCGTAGA
1251  TTATCTACGA AACTACATTC GCATTCATGA TGTCTGTGTT TCTCTAGGAG
1301  CTGGAAATAT CTATACTATT GGAGAGGCTT TAAAAGACTT TAACCCTAAA
1351  AAATTATCCA TAGGACTCGT CTGTGGAGGG AAATCTTGCG AACACGATAT
1401  TTCTCTACTT TCTGCTCAAC ATGTCTCTAA ATATATTTCT CCTGAATTCT
1451  ATGATGTGAG TTACTTCATC ATAAATCGTC AGGGCTTATG GAGAACAGGA
1501  AAGGATTTTC CTCATCTTAT TGAAGAGACT CAAGGGGATT CGCCACTTTC
1551  TTCTGAAATC GCTTCAGCTT TAGCAAAAGT CGACTGTTTG TTTCCCGTGC
1601  TCCATGGCCC ATTTGGAGAG GATGGTACGA TCCAGGGATT TTTTGAAATC
1651  TTAGGAAAAC CTTATGCCGG ACCCTCACTA TCTTTAGCAG CAACTGCAAT
1701  GGATAAGCTG TTAACAAAAC GAATTGCATC AGCAGTGGGT GTTCCTGTAG
1751  TCCCTTACCA ACCTTTAAAT CTCTGTTTCT GGAAACGCAA TCCAGAACTA
1801  TGTATTCAGA ATCTTATAGA GACATTTTCT TTCCCTATGA TTGTAAAAAC
1851  TGCACATTTG GGATCTAGTA TTGGGATATT TTTAGTCCGT GATAAAGAGG
1901  AATTACAAGA AAAGATCTCA GAAGCATTTC TATATGACAC GGATGTGTTT
1951  GTGGAGGAAA GTCGCTTAGG GTCTCGTGAA ATCGAAGTGT CCTGTATCGG
2001  CCATTCTTCT AGCTGGTATT GTATGGCAGG GCCTAATGAA CGCTGTGGTG
2051  CTAGTGGGTT TATTGATTAT CAAGAGAAAT ATGGATTTGA TGGCATAGAT
2101  TGCGCAAAGA TCTCTTTTGA TTTACAGCTC TCACAAGAAT CTTTAGATTG
2151  TGTTAGAGAA CTTGCAGAGC GTGTCTACCG AGCAATGCAA GGAAAAGGTT
2201  CAGCTCGAAT AGATTTTTTC TTGGATGAAG AGGGGAATTA TTGGTTGTCA
2251  GAGGTCAATC CTATTCCAGG AATGACAGCA GCTAGCCCAT TTTTACAAGC
2301  TTTTGTTCAC GCAGGATGGA CGCAAGAACA AATTGTAGAT CACTTTATTA
2351  TAGATGCTCT ACATAAGTTT GATAAGCAGC AGACTATCGA ACAGGCATTC
2401  ACTAAAGAAC AAGATTTAGT TAAAAGATAA
```

The PSORT algorithm predicts inner membrane (0.16).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 85A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 85B) and for FACS analysis.

These experiments show that cp7225 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 86

The following *C.pneumoniae* protein (PID 4377248) was expressed <SEQ ID 171; cp7248>:

```
  1  MKFWLQGCAF VGCLLLTLPC CAARRRASGE NLQQTRPIAA ANLQWESYAE
 51  ALEHSKQDHK PICLFFTGSD WCMWCIKMQD QILQSSEFKH FAGVHLHMVE
101  VDFPQKNHQP EEQRQKNQEL KAQYKVTGFP ELVFIDAEGK QLARMGFEPG
151  GGAAYVSKVK SALKLR*
```

A predicted signal peptide is highlighted.

The cp7248 nucleotide sequence <SEQ ID 172> is:

```
  1  ATGAAATTTT GGTTGCAAGG ATGTGCTTTT GTCGGTTGTC TGCTATTGAC
```

```
  51  TTTACCTTGT TGTGCTGCAC GAAGACGTGC TTCTGGAGAA AATTTGCAAC
 101  AAACTCGTCC TATAGCAGCT GCAAATCTAC AATGGGAGAG CTATGCAGAA
 151  GCTCTTGAAC ATTCTAAACA AGATCACAAA CCTATTTGTC TTTTCTTTAC
 201  AGGATCAGAC TGGTGTATGT GGTGCATAAA AATGCAAGAC CAGATTTTGC
 251  AAAGCTCTGA GTTTAAGCAT TTTGCGGGTG TGCATCTGCA TATGGTTGAA
 301  GTTGATTTCC CCCAAAAGAA TCATCAACCT GAAGAGCAGC GCCAAAAAAA
 351  TCAAGAACTG AAAGCTCAAT ATAAAGTTAC AGGATTCCCC GAACTGGTCT
 401  TCATAGATGC AGAAGGAAAA CAGCTTGCTC GCATGGGATT TGAGCCTGGT
 451  GGTGGAGCTG CTTACGTAAG CAAGGTGAAG TCTGCTCTTA AACTACGTTA
 501  A
```

The PSORT algorithm prediets periplasmic (0.932).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 86A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 86B) and for FACS analysis.

The ep7248 protein was also identified in the 2D-PAGE experiment.

These experiments show that cp7248 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 87

The following *C.pneumoniae* protein (PID 4377249) was expressed <SEQ ID 173; cp7249>:

```
   1  MIPSPTPINF RDDTILETDP KPSLIMFSSK KTEIASERRK AHPTLFKVLG
  51  TIWNIVKFII SIILFLPLAL LWVLKKTCQF FILPSSIISQ SMSKTAVAIR
 101  RMTFLSHIKQ LLSLKEISAA DRVVIQYDDL VVDSLAIKIP HALPHRWILY
 151  SQGNSGLMEN LFDRGDSSLH QLAKATGSNL LVFNYPGIMS SKGEAKRENL
 201  VKSYQACVRY LRDEETGPKA NQIIAFGYSL GTSVQAAALD REVTDGSDGT
 251  SWIVVKDRGP RSLADVANQI CKPIASAIIK LVGWNIDSVK PSERLRCPEI
 301  FIYNSNHDQE LISDGLFERE NCVATPFLEL PEVKTSGTKI PIPERDLLHL
 351  NPLSPNVVDR LAAVISNYLD SENRKSQQPD *
```

The cp7249 nucleotide sequence <SEQ ID 174> is:

```
   1  ATGATCCCAT CCCCTACCCC AATAAACTTT CGTGATGATA CGATTCTAGA
  51  GACGGATCCA AAGCCGTCTT TAATCATGTT CTCTTCAAAA AAAACAGAGA
 101  TAGCTTCTGA AAGACGGAAG GCCCATCCCA CCTTATTTAA AGTTCTAGGA
 151  ACGATTTGGA ATATTGTGAA GTTTATTATC TCAATCATTC TGTTCCTTCC
 201  CTTAGCGTTA TTGTGGGTAC TCAAGAAAAC CTGTCAGTTT TTCATTCTCC
 251  CATCTTCTAT CATATCTCAG AGCATGTCAA AAACAGCTGT GGCAATTCGG
 301  CGAATGACCT TTCTGTCCCA TATTAAACAA CTCCTAAGCC TTAAGGAAAT
 351  CTCAGCTGCC GATCGTGTGG TTATACAATA TGACGATTTG GTGGTTGATA
 401  GCTTAGCTAT AAAGATACCT CATGCTCTTC CCCACAGGTG GATTCTTTAT
 451  TCTCAAGGAA ACTCTGGATT GATGGAAAAC CTGTTCGATC GGGGCGATTC
 501  CTCTCTACAC CAGCTAGCCA AAGCAACCGG CTCGAATCTT CTTGTGTTCA
 551  ACTATCCTGG AATTATGTCC AGCAAAGGAG AAGCGAAACG AGAAAATCTG
 601  GTTAAATCGT ATCAGGCATG CGTACGCTAC CTACGAGATG AAGAGACAGG
 651  TCCTAAAGCC AATCAAATCA TAGCTTTCGG ATACTCTTTG GGAACTAGTG
 701  TCCAAGCTGC TGCTCTAGAT CGTGAGGTCA CTGATGGCAG TGATGGAACT
 751  TCATGGATTG TTGTAAAAGA TCGGGGCCCT CGCTCTCTAG CAGATGTCGC
 801  GAATCAAATT TGTAAGCCCA TAGCTTCCGC GATTATAAAA CTCGTTGGTT
 851  GGAACATAGA CTCTGTGAAA CCTAGCGAAA GATTGCGTTG TCCCGAAATT
 901  TTCATTTACA ACTCTAATCA TGATCAAGAA CTCATTAGCG ACGGCCTCTT
 951  CGAAAGAGAA AATTGCGTAG CAACACCTTT TCTAGAGCTT CCTGAAGTAA
1001  AAACCTCGGG GACTAAAATT CCTATACCCG AAAGGGATCT TCTCCATCTA
1051  AATCCTCTCA GTCCAAATGT AGTAGACAGA TTAGCAGCAG TGATCTCTAA
1101  TTATTTAGAT TCTGAAAACA GAAAGTCTCA GCAACCTGAT TAA
```

The PSORT algorithm predicts inner membrane (0.571).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 87A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 87B) and for FACS analysis.

These experiments show that cp7249 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 88

The following *C.pneumoniae* protein (PID 4377261) was expressed <SEQ ID 175; cp7261>:

```
  1  MLPISILLFY VILGCLSAYI ADKKKRNVIG WFFAGAFFGF IGLVVLLLLP
 51  SRRNALEKPQ NDPFDNSDLF DDLKKSLAGN DEIPSSGDLQ EIVIDTEKWF
101  YLNKDRENVG PISFEELVVL LKGKTYPEEI WVWKKGMKDW QRVKDVPSLQ
151  QALKEASK*
```

The cp7261 nucleotide sequenee <SEQ ID 176> is:

```
  1  ATGCTCCCTA TTTCGATTTT ATTATTTTAT GTGATTCTAG GTTGTCTATC
 51  TGCCTACATA GCAGATAAGA AAAAACGAAA TGTTATTGGC TGGTTTTTTG
101  CAGGAGCATT TTTTGGATTT ATTGGTCTAG TTGTCCTTCT TCTTCTTCCT
151  TCTCGTCGAA ACGCTTTAGA AAAGCCACAA AACGATCCTT TTGATAACTC
201  CGATCTTTTT GATGATTTGA AAAAAAGTTT AGCAGGTAAT GACGAGATAC
251  CCTCATCGGG AGATCTTCAA GAAATCGTTA TCGATACAGA GAAGTGGTTT
301  TATTTAAATA AAGATAGAGA AAACGTAGGT CCGATATCTT TTGAGGAGTT
351  GGTCGTACTT TTAAAGGGAA AAACGTATCC AGAAGAAATT TGGGTATGGA
401  AAAAGGGAAT GAAAGATTGG CAACGAGTGA AGGATGTTCC ATCACTACAA
451  CAGGCTTTGA AAGAAGCATC AAAATAA
```

The PSORT algorithm predicts inner membrane (0.848).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 88A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 88B) and for FACS analysis.

These experiments show that cp7261 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 89

The following *C.pneumoniae* protein (PID 4377305) was expressed <SEQ ID 177; cp7305>:

```
  1  MEVYSFHPAV RTSFQHRVMA ALDAWFFLGG HRLKVVSLDS CNSGWAYQEL
 51  VSISTTEKVL KLLSYLLVPI VIIALLIRCL LHSNFRIDVE KERWLKIREL
101  GIDIESCKLP SSYVNQVSSF IWFEKDKSKR PRIDVDYHTL HSKDWVVFPI
151  VFQKIPKTSR FSYWFSQKET RKRDYVRNML DHVIGYLTSE GGEWLQYISK
201  TSYQSATSLD PERVLQYCLT DNQELQGEVQ RLLNEESATK SSGDKEVLLS
251  HVSDIICQCW WPKFLEVIQS PAFIEELVEE VSGKLNLDFL CLEKANTLDQ
301  ELRNSLLRAV VHHGSEGVDI KKVGAGLIIY TEAIQLQIPF SRS*
```

The cp7305 nucleotide sequence <SEQ ID 178> is:

```
  1  ATGGAAGTTT ATAGTTTTCA CCCTGCGGTA AGGACTTCGT TTCAGCACCG
 51  TGTAATGGCA GCACTAGATG CTTGGTTTTT TCTAGGAGGG CACCGTTTAA
101  AAGTAGTTTC TCTAGATAGT TGTAACTCAG GTTGGGCGTA TCAAGAACTT
151  GTGTCTATTT CAACGACAGA AAAAGTCTTG AAACTACTCT CTTACCTACT
201  CGTACCGATT GTCATAATAG CTCTGTTAAT TCGTTGTCTT TTACATAGCA
251  ATTTTAGGAT AGACGTAGAG AAGGAACGTT GGTTAAAAAT AAGGGAGTTA
301  GGAATTGATA TAGAAAGCTG CAAACTCCCC AGTTCTTATG TAAACCAGGT
351  TTCCTCGTTT ATTTGGTTTG AAAAAGATAA ATCCAAACGG CCACGTATTG
401  ATGTAGATTA TCATACGCTA CATAGCAAAG ACTGGGTAGT TTTCCCTATC
```

```
 451  GTTTTTCAGA AAATTCCAAA GACCTCGCGT TTCAGTTATT GGTTCTCACA
 501  AAAAGAAACA AGGAAGAGGG ATTATGTGAG AAATATGCTG GACCACGTCA
 551  TTGGTTATCT AACGTCAGAA GGTGGGGAGT GGTTGCAGTA TATATCGAAA
 601  ACCTCTTATC AAAGCGCTAC TTCCTTGGAT CCTGAAAGAG TTCTTCAATA
 651  TTGCTTAACT GATAACCAGG AGCTCCAGGG AGAAGTGCAA CGTTTGCTTA
 701  ATGAGGAGAG TGCGACCAAA AGCTCTGGGG ATAAGGAAGT TTTGTTAAGT
 751  CATGTATCTG ACATTATTTG CCAGTGTTGG TGGCCAAAGT TTCTTGAAGT
 801  TATACAATCT CCGGCCTTTA TTGAAGAATT AGTAGAAGAA GTGAGTGGTA
 851  AACTTAATTT AGATTTTTTA TGCCTAGAAA AGGCTAATAC ATTAGATCAG
 901  GAGTTGAGAA ACAGTCTTCT AAGAGCAGTC GTACACCACG GTTCTGAAGG
 951  AGTTGATATT AAGAAAGTTG GTGCCGGCCT CATTATTTAT ACGGAAGCTA
1001  TTCAATTACA GATTCCCTTC TCAAGGAGTT AA
```

The PSORT algorithm prediets inner membrane (0.508).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 89A) and also as a double GST/his fusion. The recombinant proteins were used to immunise miee, whose sera were used in a Western blot (Figure 89B) and for FACS analysis.

These experiments show that cp7305 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequenee alone.

Example 90

The following *C.pneumoniae* protein (PID 4377347) was expressed <SEQ ID 179; cp7347>:

```
   1  MKKGKLGAIV FGLLFTSSVA GFSKDLTKDN AYQDLNVIEH LISLKYAPLP
  51  WKELLFGWDL SQQTQQARLQ LVLEEKPTTN YCQKVLSNYV RSLNDYHAGI
 101  TFYRTESAYI PYVLKLSEDG HVFVVDVQTS QGDIYLGDEI LEVDGMGIRE
 151  AIESLRFGRG SATDYSAAVR SLTSRSAAFG DAVPSGIAML KLRRPSGLIR
 201  STPVRWRYTP EHIGDFSLVA PLIPEHKPQL PTQSCVLFRS GVNSQSSSSS
 251  LFSSYMVPYF WEELRVQNKQ RFDSNHHIGS RNGFLPTFGP ILWEQDKGPY
 301  RSYIFKAKDS QGNPHRIGFL RISSYVWTDL EGLEEDHKDS PWELFGEIID
 351  HLEKETDALI IDQTHNPGGS VFYLYSLLSM LTDHPLDTPK HRMIFTQDEV
 401  SSALHWQDLL EDVFTDEQAV AVLGETMEGY CMDMHAVASL QNFSQSVLSS
 451  WVSGDINLSK PMPLLGFAQV RPHPKHQYTK PLFMLIDEDD FSCGDLAPAI
 501  LKDNGRATLI GKPTAGAGGF VFQVTFPNRS GIKGLSLTGS LAVRKDGEFI
 551  ENLGVAPHID LGFTSRDLQT SRFTDYVEAV KTIVLTSLSE NAKKSEEQTS
 601  PQETPEVIRV SYPTTTSAS*
```

A predicted signal peptide is highlighted.

The cp7347 nucleotide sequence <SEQ ID 180> is:

```
   1  ATGAAAAAAG GGAAATTAGG AGCCATAGTT TTTGGCCTTC TATTTACAAG
  51  TAGTGTTGCT GGTTTTTCTA AGGATTTGAC TAAAGACAAC GCTTATCAAG
 101  ATTTAAATGT CATAGAGCAT TTAATATCGT TAAAATATGC TCCTTTACCA
 151  TGGAAGGAAC TATTATTTGG TTGGGATTTA TCTCAGCAAA CACAGCAAGC
 201  TCGCTTGCAA CTGGTCTTAG AAGAAAAACC AACAACCAAC TACTGCCAGA
 251  AGGTACTCTC TAACTACGTG AGATCATTAA ACGATTATCA TGCAGGGATT
 301  ACGTTTTATC GTACTGAAAG TGCGTATATC CCTTACGTAT TGAAGTTAAG
 351  TGAAGATGGT CATGTCTTTG TAGTCGACGT ACAGACTAGC CAAGGGGATA
 401  TTTACTTAGG GGATGAAATC CTTGAAGTAG ATGGAATGGG GATTCGTGAG
 451  GCTATCGAAA GCCTTCGCTT TGGACGAGGG AGTGCCACAG ACTATTCTGC
 501  TGCAGTTCGT TCCTTGACAT CGCGTTCCGC CGCTTTTGGA GATGCGGTTC
 551  CTTCAGGAAT TGCCATGTTG AAACTTCGCC GACCCAGTGG TTTGATCCGT
 601  TCGACACCGG TCCGTTGGCG TTATACTCCA GAGCATATCG GAGATTTTTC
 651  TTTAGTTGCT CCTTTGATTC CTGAACATAA ACCTCAATTA CCTACACAAA
 701  GTTGTGTGCT ATTCCGTTCC GGGGTAAATT CACAGTCTTC TAGTAGCTCT
 751  TTATTCAGTT CCTACATGGT GCCTTATTTC TGGGAAGAAT TGCGGGTTCA
 801  AAATAAGCAG CGTTTTGACA GTAATCACCA TATAGGGAGC CGTAATGGAT
 851  TTTTACCTAC GTTTGGTCCT ATTCTTTGGG AACAAGACAA GGGGCCCTAT
 901  CGTTCCTATA TCTTTAAAGC AAAAGATTCT CAGGGCAATC CCCATCGCAT
 951  AGGATTTTTA AGAATTTCTT CTTATGTTTG GACTGATTTA GAAGGACTTG
1001  AAGAGGATCA TAAGGATAGT CCTTGGGAGC TCTTTGGAGA GATCATCGAT
```

```
1051 CATTTGGAAA AAGAGACTGA TGCTTTGATT ATTGATCAGA CCCATAATCC
1101 TGGAGGCAGT GTTTTCTATC TCTATTCGTT ACTATCTATG TTAACAGATC
1151 ATCCTTTAGA TACTCCTAAA CATAGAATGA TTTTCACTCA GGATGAAGTC
1201 AGCTCGGCTT TGCACTGGCA AGATCTACTA GAAGATGTCT TCACAGATGA
1251 GCAGGCAGTT GCCGTGCTAG GGGAAACTAT GGAAGGATAT TGCATGGATA
1301 TGCATGCTGT AGCCTCTCTT CAAAACTTCT CTCAGAGTGT CCTTTCTTCC
1351 TGGGTTTCAG GTGATATTAA CCTTTCAAAA CCTATGCCTT TGCTAGGATT
1401 TGCACAGGTT CGACCTCATC CTAAACATCA ATATACTAAA CCTTTGTTTA
1451 TGTTGATAGA CGAGGATGAC TTCTCTTGTG GAGATTTAGC GCCTGCAATT
1501 TTGAAGGATA ATGGCCGCGC TACTCTCATT GGAAAGCCAA CAGCAGGAGC
1551 TGGAGGTTTT GTATTCCAAG TCACTTTCCC TAACCGTTCT GGAATTAAAG
1601 GTCTTTCTTT AACAGGATCT TTAGCTGTTA GGAAAGATGG TGAGTTTATT
1651 GAAAACTTAG GAGTGGCTCC TCATATTGAT TTAGGATTTA CCTCCAGGGA
1701 TTTGCAAACT TCCAGGTTTA CTGATTACGT TGAGGCAGTG AAAACTATAG
1751 TTTTAACTTC TTTGTCTGAG AACGCTAAGA AGAGTGAAGA GCAGACTTCT
1801 CCGCAAGAGA CGCCTGAAGT TATTCGAGTC TCTTATCCCA CAACGACTTC
1851 TGCTTCGTAA
```

The PSORT algorithm prediets periplasmic space (0.2497).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 90A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 90B) and for FACS analysis.

These experiments show that cp7347 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 91

The following *C.pneumoniae* protein (PID 4377353) was expressed <SEQ ID 181; cp7353>:

```
  1 MNMPVPSAVP SANITLKEDS STVSTASGIL KTATGEVLVS CTALEGSSST
 51 DALISLALGQ IILATQQELL LQSTNVHQLL FLPPEVVELE IQVVDLLVQL
101 EHAETITSEP QETQTQSRSE QTLPQQSSSK QSALSPRSLK PEISDSKQQQ
151 ALQTPKDSAV RKHSEAPSPE TQARASLSQA SSSSQRSLPP QESAPERTLL
201 EQQKASSFSP LSQFSAEKQK EALTTSKSHE LYKERDQDRQ QREQHDRKHD
251 QEEDAESKKK KKKRGLGVEA VAEEPGENLD IAALIFSDQM RPPAEETSKK
301 ETTFKKKLPS PMSVFSRFIP SKNPLSVGSS IHGPIQTPKV ENVFLRFMKL
351 MARILGQAEA EANELYMRVK QRTDDVDTLT VLISKINNEK KDIDWSENEE
401 MKALLNRAKE IGVTIDKEKY TWTEEEKRLL KENVQMRKEN MEKITQMERT
451 DMQRHLQEIS QCHQARSNVL KLLKELMDTF IYNLRP*
```

The cp7353 nucleotide sequence <SEQ ID 182> is:

```
   1 ATGAATATGC CTGTTCCTTC TGCAGTTCCC TCTGCAAATA TAACTCTAAA
  51 AGAAGACAGC TCAACAGTTT CCACAGCCTC TGGAATATTA AAGACTGCAA
 101 CAGGTGAAGT CTTAGTCTCT TGTACAGCGC TAGAAGGAAG CTCTTCTACA
 151 GATGCTTTAA TTAGCTTAGC TTTAGGACAA ATCATTCTTG CGACCCAACA
 201 AGAACTGCTC TTACAAAGCA CAAATGTTCA TCAACTCCTC TTCCTCCCTC
 251 CTGAAGTTGT AGAATTAGAA ATCCAAGTTG TTGACTTGCT AGTGCAATTG
 301 GAACATGCAG AGACAATCAC AAGTGAACCA CAAGAAACAC AAACGCAAAG
 351 TAGGAGTGAG CAGACCCTCC CTCAACAAAG CAGCAGTAAA CAATCTGCTC
 401 TCTCCCCACG CTCCTTAAAA CCTGAAATTT CTGATTCTAA ACAACAGCAA
 451 GCTCTTCAAA CACCAAAAGA CTCTGCTGTA AGAAAACACA GCGAAGCACC
 501 GTCACCTGAG ACACAAGCTC GCGCTTCCTT ATCTCAGGCA AGCTCAAGTT
 551 CTCAGAGATC CTTACCTCCG CAAGAAAGTG CGCCAGAAAG AACACTATTA
 601 GAACAACAAA AAGCAAGCTC CTTCTCTCCT CTATCCCAGT TCTCTGCAGA
 651 GAAACAAAAA GAGGCCCTGA CGACCTCAAA ATCTCATGAA CTCTATAAAG
 701 AACGCGATCA AGATCGCCAA CAAAGAGAGC AGCACGACAG AAAGCACGAT
 751 CAGGAAGAAG ACGCTGAATC TAAAAAGAAA AAGAAGAAAC GTGGTCTCGG
 801 TGTAGAGGCA GTCGCTGAGG AACCCGGAGA AAATCTAGAT ATTGCCGCTT
 851 TAATCTTCTC AGATCAAATG CGACCTCCTG CTGAAGAAAC TTCTAAAAAA
 901 GAAACGACAT TCAAAAAGAA GCTACCTTCT CCAATGTCTG TGTTTAGCAG
 951 ATTCATCCCT AGTAAGAATC CGTTATCTGT AGGCTCTTCA ATACACGGGC
1001 CTATACAAAC TCCAAAAGTA GAAAATGTGT TCTTAAGGTT CATGAAGCTC
```

```
1051  ATGGCAAGAA TCTTAGGCCA AGCCGAAGCC GAAGCTAATG AACTCTACAT
1101  GCGAGTCAAA CAACGTACCG ATGATGTAGA CACACTCACA GTCCTTATCT
1151  CTAAGATCAA TAATGAAAAG AAAGACATTG ATTGGAGTGA AAATGAAGAG
1201  ATGAAAGCTC TTTTAAATCG AGCTAAAGAG ATTGGAGTCA CTATAGACAA
1251  AGAAAAATAT ACTTGGACAG AAGAGGAAAA AAGACTTCTA AAAGAGAATG
1301  TCCAAATGCG CAAAGAGAAT ATGGAGAAAA TCACTCAAAT GGAAAGGACG
1351  GACATGCAAA GGCACCTCCA AGAGATTTCT CAATGTCATC AAGCGCGCTC
1401  TAATGTATTG AAGTTATTGA AAGAACTTAT GGACACCTTC ATTTACAACC
1451  TACGCCCCTA A
```

The PSORT algorithm predicts cytoplasm (0.1308).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 91A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 91B) and for FACS analysis.

These experiments show that cp7353 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 92

The following *C.pneumoniae* protein (PID 4377408) was expressed <SEQ ID 183; cp7408>:

```
  1  MLKIQKKRMC VSVVITVGAI VGFFNSADAA PKKKKIPIQI LYSFTKVSSY
 51  LKNEDASTIF CVDVDRGLLQ HRYLGSPGWQ ETRRRQLFKS LENQSYGNER
101  LGEETLAIDI FRNKECLESE IPEQMEAILA NSSALVLGIS SFGITGIPAT
151  LHSLLRQNLS FQKRSIASES FLLKIDSAPS DASVFYKGVL FRGETAIVDA
201  LSQLFAQLDL SPKKIIFLGE DPEVVQAVGS ACIGWGMNFL GLVYYPAQES
251  LFSYVHPYST ATELQEAQGL QVISDEVAQL TLNALPKMN*
```

The cp7408 nucleotide sequence <SEQ ID 184> is:

```
  1  ATGTTGAAAA TCCAGAAAAA AAGAATGTGT GTCAGCGTAG TCATCACGGT
 51  AGGCGCCATA GTGGGGTTTT TCAATTCTGC AGACGCAGCA CCAAAGAAAA
101  AGAAGATCCC TATACAGATT CTCTACTCCT TTACTAAAGT CTCTTCCTAT
151  TTAAAAAACG AAGACGCAAG TACTATATTT TGCGTCGATG TGGATCGTGG
201  ACTTCTCCAG CATCGGTATT TAGGTAGTCC AGGATGGCAG GAAACCAGAC
251  GTCGGCAGTT ATTTAAATCC TTAGAAAATC AATCATACGG CAACGAACGT
301  TTAGGAGAAG AAACTCTTGC TATTGATATT TTCAGGAACA AAGAGTGCTT
351  GGAGAGCGAG ATCCCAGAGC AGATGGAAGC TATCCTTGCA AATTCCTCGG
401  CCTTGGTCTT AGGCATCTCT TCTTTTGGGA TCACAGGAAT TCCTGCGACT
451  TTGCATAGTT TGCTTCGACA GAATCTATCT TTCCAAAAAC GCTCTATAGC
501  ATCGGAGAGC TTCCTTTTAA AGATCGATAG TGCCCCCTCA GATGCCTCTG
551  TTTTTTATAA AGGCGTGCTT TTCCGCGGAG AGACTGCGAT CGTGGATGCG
601  TTAAGCCAAT TATTTGCCCA GCTCGATCTT TCTCCTAAAA AAATTATCTT
651  TCTAGGAGAA GACCCTGAGG TCGTTCAAGC TGTTGGGTCT GCTTGTATAG
701  GTTGGGGCAT GAACTTTTTA GGCCTGGTAT ACTATCCTGC TCAAGAAAGC
751  CTTTTTTCTT ATGTTCATCC TTACTCTACA GCAACGGAGC TCCAAGAAGC
801  ACAGGGTTTA CAAGTAATTT CAGATGAAGT CGCACAGCTT ACTTTAAACG
851  CTCTTCCGAA AATGAATTAA
```

The PSORT algorithm predicts inner membrane (0.123).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 92A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 92B) and for FACS analysis.

These experiments show that cp7408 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 93

The following *C.pneumoniae* protein (PID 4376424) was expressed <SEQ ID 185; cp6424>:

```
  1  MMHNIVVLSE EPGRSAFLGR TAFFPNKYPI AQGGVGIPST IGNLFTIWYC
 51  FYFYRAATPQ SDHPDGCGFI LLERLKELGA GFFYCDLRES NTTGFTLFFE
101  GSNKGVLKNH LFIRDE*
```

The cp6424 nucleotide sequence <SEQ ID 186> is:

```
  1  ATGATGCACA ATATTGTTGT TCTTAGTGAG GAACCTGGAC GAAGCGCTTT
 51  TCTTGGTAGG ACGGCATTTT TCCCTAATAA GTATCCAATA GCTCAGGGTG
101  GTGTTGGAAT ACCATCTACA ATAGGCAATC TCTTTACTAT ATGGTACTGT
151  TTCTATTTTT ATAGAGCTGC AACTCCACAA TCTGATCATC CTGACGGATG
201  TGGCTTTATT CTACTAGAAA GGCTTAAGGA GCTCGGTGCA GGGTTCTTTT
251  ATTGTGATCT TCGTGAGTCC AATACCACTG GCTTTACTCT TTTTTTTGAA
301  GGCTCCAATA AAGGTGTGTT AAAGAATCAC TTGTTTATTA GAGATGAGTA
351  A
```

The PSORT algorithm predicts cytoplasm (0.2502).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 93A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in Western blots (Figure 93B) and for FACS analyses (Figure 93C; GST-fusion).

These experiments show that cp6424 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 94

The following *C.pneumoniae* protein (PID 4376449) was expressed <SEQ ID 187; cp6449>:

```
  1  VASETYPSQI LHAQREVRDA YFNQADCHPA RANQILEAKK ICLLDVYHTN
 51  HYSVFTFCVD NYPNLRFTFV SSKNNEMNGL SNPLDNVLVE AMVRRTHARN
101  LLAACKIRNI EVPRVVGLDL RSGILISKLE LKQPQFQSLT EDFVNHSTNQ
151  EEARVHQKHV LLISLILLCK QAVLESFQEK KRSS*
```

The cp6449 nucleotide sequence <SEQ ID 188> is:

```
  1  GTGGCGTCTG AAACGTATCC TTCTCAGATA TTGCACGCTC AGAGGGAAGT
 51  ACGTGATGCC TATTTTAATC AAGCGGATTG CCATCCTGCT CGGGCTAATC
101  AGATTCTCGA GGCTAAGAAA ATCTGTTTAT TAGATGTTTA TCATACTAAT
151  CATTATTCCG TATTTACTTT TTGTGTAGAT AATTATCCGA ATCTCCGCTT
201  TACATTTGTA TCTTCAAAAA ACAATGAGAT GAATGGCTTA TCTAATCCTC
251  TAGATAATGT TCTTGTAGAG GCTATGGTAC GTAGAACACA TGCAAGAAAC
301  CTACTTGCAG CGTGTAAAAT TCGAAATATT GAGGTTCCAA GGGTTGTTGG
351  GCTTGACCTA AGATCTGGGA TACTCATTTC GAAACTAGAA TTGAAGCAAC
401  CTCAGTTCCA AAGTTTAACA GAAGACTTCG TAAATCATTC CACAAATCAG
451  GAAGAAGCTC GCGTCCATCA AAAGCATGTG TTGCTAATTT CTTTAATTTT
501  ACTTTGCAAG CAGGCCGTTC TGGAATCATT CCAGGAAAAA AAGCGATCCT
551  CTTAA
```

The PSORT algorithm predicts inner membrane (0.2084).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 94A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in Western blots (Figure 94B) and for FACS analyses (Figure 94C; GST-fusion).

These experiments show that cp6449 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 95

The following *C.pneumoniae* protein (PID 4376495) was expressed <SEQ ID 189; cp6495>:

```
MRELNAFELTQPEEYRNRWVLMPCLKCRFCRTQHAKVWSYRCVHEASLYEKNCFLTLTYDDKHLPQYGSLVKLHLQLFLKR
LRKMISPHKIRYFECGAYGTKLQRPHYHLLLS
```

The cp6495 nucleotide sequence <SEQ ID 190> is:

```
TTGCGAGAATTAAATGCTTTTGAATTAACTCAACCTGAAGAGTATCGAAACCGTTGGGTTTTGATGCCTTGTCTTAAGTGT
CGTTTTTGTAGAACGCAACATGCAAAAGTCTGGTCTTATCGTTGTGTCCATGAAGCTTCTTTGTATGAGAAAAATTGTTTT
CTTACTTTGACTTATGATGATAAGCATTTACCTCAGTATGGTTCGTTGGTAAAGCTGCATTTACAGCTGTTTCTTAAGAGA
TTAAGAAAGATGATTTCTCCTCATAAAATTCGTTATTTTGAATGTGGTGCGTATGGAACCAAATTACAAAGACCTCATTAT
CATCTACTTTTATCATGA
```

The PSORT algorithm predicts cytoplasmic (0.280).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 95A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 95B) and for FACS analysis (Figure 95C).

These experiments show that cp6495 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 96

The following *C.pneumoniae* protein (PID 4376506) was expressed <SEQ ID 191; cp6506>:

```
  1  MRRFLFLILS SLPLVAFSAD NFTILEEKQS PLSRVSIIFA LPGVTPVSFD
 51  GNCPIPWFSH SKKTLEGQRI YYSGDSFGKY FVVSALWPNK VSSAVVACNM
101  ILKHRVDLIL IIGSCYSRSQ DSRFGSVLVS KGYINYDADV RPFFERFEIP
151  DIKKSVFATS EVHREAILRG GEEFISTHKQ EIEELLKTHG YLKSTTKTEH
201  TLMEGLVATG ESFAMSRNYF LSLQKLYPEI HGFDSVSGAV SQVCYEYSIP
251  CLGVNILLPH PLESRSNEDW KHLQSEASKI YMDTLLKSVL KELCSSH*
```

The cp6506 nucleotide sequence <SEQ ID 192> is:

```
  1  ATGCGTCGTT TTCTGTTTCT TATTCTTAGC TCTCTTCCTT TGGTCGCATT
 51  CTCTGCTGAT AATTTCACTA TTCTAGAAGA AAAACAGAGT CCTTTAAGTC
101  GTGTAAGTAT TATTTTTGCT TTACCTGGGG TTACTCCCGT TTCTTTTGAT
151  GGTAATTGTC CTATTCCTTG GTTTTCTCAT AGTAAAAAGA CTCTAGAGGG
201  ACAGAGAATT TATTACTCTG GCGACTCCTT TGGGAAATAC TTTGTAGTTT
251  CTGCTCTTTG GCCTAATAAA GTTTCTTCAG CTGTTGTGGC TTGTAATATG
301  ATTCTTAAAC ATCGAGTGGA TCTTATTCTA ATTATAGGCT CGTGTTACTC
351  TAGGTCTCAA GATAGCCGTT TTGGCAGCGT CTTAGTTTCT AAAGGCTACA
401  TTAATTATGA TGCAGATGTG AGGCCTTTCT TTGAAAGATT TGAGATTCCA
451  GACATTAAAA AGAGTGTTTT TGCAACCAGT GAGGTTCATC GGGAGGCAAT
501  TCTTCGTGGA GGCGAAGAGT TTATTTCTAC CCATAAACAA GAAATCGAAG
551  AGCTTTTGAA GACTCATGGG TATTTGAAAT CAACAACCAA AACGGAGCAC
601  ACCTTAATGG AAGGTTTGGT TGCTACAGGC GAGTCTTTCG CGATGTCGCG
651  AAACTATTTT CTTTCCTTAC AAAAATTGTA TCCAGAGATT CATGGTTTTG
701  ATAGTGTCAG CGGCGCTGTT TCTCAGGTAT GCTATGAATA TAGCATTCCT
751  TGTTTAGGTG TGAATATCCT TCTCCCTCAT CCTTTAGAAT CACGGAGTAA
801  CGAGGATTGG AAGCATCTTC AAAGTGAGGC AAGTAAAATT TATATGGATA
851  CCTTGCTCAA GAGTGTATTA AAAGAACTCT GTTCTTCTCA TTAA
```

The PSORT algorithm predicts periplasmic space (0.571).

The protein was expressed in *E.coli* and purified as his-tag (Figure 96A) and GST-fusion (Figure 96B) products. The GST-fusion protein was used to immunise mice, whose sera were used in a Western blot (Figure 96C) and for FACS analysis (Figure 96D).

These experiments show that cp6506 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 97

The following *C.pneumoniae* protein (PID 4376882) was expressed <SEQ ID 193; cp6882>:

```
  1  MSLLNLPSSQ DSASEDSTSQ SQIFDPIRNR ELVSTPEEKV RQRLLSFLMH
 51  KLNYPKKLII IEKELKTLFP LLMRKGTLIP KRRPDILIIT PPTYTDAQGN
101  THNLGDPKPL LLIECKALAV NQNALKQLLS YNYSIGATCI AMAGKHSQVS
151  ALFNPKTQTL DFYPGLPEYS QLLNYFISLN L*
```

The cp6882 nucleotide sequence <SEQ ID 194> is:

```
  1  ATGTCCTTAT TGAACCTTCC CTCAAGCCAG GATTCTGCAT CTGAGGACTC
 51  CACATCGCAA TCTCAAATCT TCGATCCCAT TAGAAATCGG GAGTTAGTTT
101  CTACTCCCGA AGAAAAAGTC CGCCAAAGGT TGCTCTCCTT CCTAATGCAT
151  AAGCTGAACT ACCCTAAGAA ACTCATCATC ATAGAAAAAG AACTCAAAAC
201  TCTTTTTCCT CTGCTTATGC GTAAAGGAAC CCTAATCCCA AAACGCCGCC
251  CAGATATTCT CATCATCACT CCCCCCACAT ACACAGACGC ACAGGGAAAC
301  ACTCACAACC TAGGCGACCC AAAACCCCTG CTACTTATCG AATGTAAGGC
351  CTTAGCCGTA AACCAAAATG CACTCAAACA ACTCCTTAGC TATAACTACT
401  CTATCGGAGC CACCTGCATT GCTATGGCAG GGAAACACTC TCAAGTGTCA
451  GCTCTCTTCA ATCCAAAAAC ACAAACTCTT GATTTTTATC CTGGCCTCCC
501  AGAGTATTCC CAACTCCTAA ACTACTTTAT TTCTTTAAAC TTATAG
```

The PSORT algorithm predicts cytoplasm (0.362).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 97A). The protein was used to immunise mice, whose sera were used in a Western blot (Figure 97B) and for FACS analysis (Figure 97C).

These experiments show that cp6882 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 98

The following *C.pneumoniae* protein (PID 4376979) was expressed <SEQ ID 195; cp6979>:

```
  1  MSVNPSGNSK NDLWITGAHD QHPDVKESGV TSANLGSHRV TASGGRQGLL
 51  ARIKEAVTGF FSRMSFFRSG APRGSQQPSA PSADTVRSPL PGGDARATEG
101  AGRNLIKKGY QPGMKVTIPQ VPGGGAQRSS GSTTLKPTRP APPPPKTGGT
151  NAKRPATHGK GPAPQPPKTG GTNAKRAATH GKGPAPQPPK GILKQPGQSG
201  TSGKKRVSWS DED*
```

The cp6979 nucleotide sequence <SEQ ID 196> is:

```
  1  ATGTCTGTTA ATCCATCAGG AAATTCCAAG AACGATCTCT GGATTACGGG
 51  AGCTCATGAT CAGCATCCCG ATGTTAAAGA ATCCGGGGTT ACAAGTGCTA
101  ACCTAGGAAG TCATAGAGTG ACTGCCTCAG GAGGACGCCA AGGGTTATTA
151  GCACGAATCA AAGAAGCAGT AACCGGGTTT TTTAGTCGGA TGAGCTTCTT
201  CAGATCGGGA GCTCCAAGAG GTAGCCAACA ACCCTCTGCT CCATCTGCAG
251  ATACTGTACG TAGCCCGTTG CCGGGAGGGG ATGCTCGCGC TACCGAGGGA
301  GCTGGTAGGA ACTTAATTAA AAAAGGGTAC CAACCAGGGA TGAAAGTCAC
351  TATCCCACAG GTTCCTGGAG GAGGGGCCCA ACGTTCATCA GGTAGCACGA
401  CACTAAAGCC TACGCGTCCG GCACCCCCAC CTCCTAAAAC GGGTGGAACT
451  AATGCAAAAC GTCCGGCAAC GCACGGGAAG GGTCCAGCAC CCCAGCCTCC
501  TAAAACAGGT GGGACCAATG CTAAGCGCGC AGCAACGCAT GGGAAAGGTC
551  CAGCACCTCA ACCTCCTAAG GGCATTTTGA AACAGCCTGG GCAGTCTGGG
601  ACTTCAGGAA AGAAGCGTGT CAGCTGGTCT GACGAAGATT AA
```

The PSORT algorithm predicts cytoplasm (0.360).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 98A). The GST-fusion protein was used to immunise mice, whose sera were used in a Western blot (Figure 98B) and for FACS analysis (Figure 98C).

These experiments show that cp6979 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 99

The following *C.pneumoniae* protein (PID 4377028) was expressed <SEQ ID 197; cp7028>:

```
  1 MLLGFLCDCP CASWQCAAVA NCYDSVFMSR PEHKPNIPYI TKATRRGLRM
 51 KTLAYLASLK DARQLAYDFL KDPGSLARLA KALIAPKEAL QEGNLFFYGC
101 SNIEDILEEM RRPHRILLLG FSYCQKPKAC PEGRFNDACR YDPSHPTCAS
151 CSIGTMMRLN ARRYTTVIIP TFIDIAKHLH TLKKRYPGYQ ILFAVTACEL
201 SLKMFGDYAS VMNLKGVGIR LTGRICNTFK AFKLAERGVK PGVTILEEDG
251 FEVLARILTE YSSAPFPRDF CEIH*
```

The cp7028 nucleotide sequence <SEQ ID 198> is:

```
  1 ATGCTTCTAG GGTTTTTGTG TGACTGCCCC TGTGCTTCGT GGCAGTGTGC
 51 GGCCGTTGCT AATTGTTATG ATTCCGTATT TATGTCTAGA CCAGAGCACA
101 AACCTAATAT TCCTTATATT ACTAAAGCTA CAAGACGGGG TCTGCGTATG
151 AAGACGCTTG CTTATCTGGC CTCTTTAAAA GATGCTAGAC AGCTTGCCTA
201 TGATTTTCTG AAAGATCCTG GTTCTTTAGC TCGGTTAGCT AAGGCTTTGA
251 TAGCTCCTAA GGAGGCCTTA CAGGAGGGCA ACCTATTTTT TTATGGCTGT
301 AGTAATATTG AGGATATTTT AGAGGAGATG CGTCGTCCTC ATAGAATCCT
351 TTTGTTAGGA TTTTCTTATT GTCAAAAGCC TAAGGCATGT CCTGAAGGGC
401 GTTTCAATGA TGCTTGTCGG TATGATCCTT CACATCCTAC ATGTGCCTCA
451 TGTTCTATAG GGACCATGAT GCGGCTGAAT GCTCGTAGAT ACACTACTGT
501 GATCATCCCT ACATTTATAG ATATCGCAAA ACATTTACAC ACTTTAAAAA
551 AGCGCTACCC TGGATATCAA ATTCTCTTTG CAGTTACTGC TTGTGAACTT
601 TCCTTAAAAA TGTTTGGAGA TTATGCCTCC GTAATGAACT TAAAGGGTGT
651 GGGCATCAGA CTCACAGGAC GTATTTGCAA TACATTTAAG GCATTTAAAT
701 TAGCTGAGCG AGGAGTCAAA CCAGGAGTCA CTATCCTAGA AGAAGATGGC
751 TTTGAGGTAT TAGCAAGGAT TCTTACAGAA TACAGTAGCG CTCCTTTCCC
801 TAGAGACTTT TGTGAGATCC ATTAG
```

The PSORT algorithm predicts cytoplasm (0.1453).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 99A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 99B) and for FACS analysis (Figure 99C).

These experiments show that cp7028 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 100

The following *C.pneumoniae* protein (PID 4377355) was expressed <SEQ ID 199; cp7355>:

```
  1 MKKVVTLSII FFATYCASEL SAVTVVAVPL SEAPGKIQVR PVVGLQFQEE
 51 QGSVPYSFYY PYDYGYYYPE TYGYTKNTGQ ESRECYTRFE DGTIFYECD*
```

The cp7355 nucleotide sequence <SEQ ID 200> is:

```
  1 ATGAAGAAAG TCGTAACACT ATCCATTATA TTTTTCGCAA CGTATTGTGC
 51 ATCAGAGCTT AGTGCTGTAA CTGTAGTGGC TGTGCCTTTA TCAGAGGCTC
101 CAGGGAAGAT TCAAGTTCGT CCCGTCGTTG GTCTGCAATT TCAAGAAGAA
151 CAGGGTTCTG TGCCCTATAG TTTTTATTAT CCTTATGACT ATGGGTATTA
201 CTATCCAGAG ACTTATGGCT ATACTAAAAA TACAGGTCAA GAAAGTCGCG
```

```
251  AATGTTATAC CCGATTTGAA GATGGCACAA TTTTTTATGA ATGCGATTAG
```

The PSORT algorithm predicts inner membrane (0.143).

The protein was expressed in *E.coli* and purified as a GST-fusion (Figure 100A) and a his-tag product. The proteins were used to immunise mice, whose sera were used in a Western blot (Figure 100B) and for FACS analysis (Figure 100C).

These experiments show that cp7355 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 101

The following *C.pneumoniae* protein (PID 4377380) was expressed <SEQ ID 201; cp7380>:

```
  1  VHYCERTLDP KYILKIALKL RQSLSLFFQN SQSLQRAYST PYSYYRIILQ
 51  KENKEKQALA RHKCISILEF FKNLLFVHLL SLSKNQREGC STDMAVVSTP
101  FFNRNLWYRL LSSRFSLWKS YCPRFFLDYL EAFGLLSDFL DHQAVIKFFE
151  LETHFSYYPV SGFVAPHQYL SLLQDRYFPI ASVMRTLDKD NFSLTPDLIH
201  DLLGHVPWLL HPSFSEFFIN MGRLFTKVIE KVQALPSKKQ RIQTLQSNLI
251  AIVRCFWFTV ESGLIENHEG RKAYGAVLIS SPQELGHAFI DNVRVLPLEL
301  DQIIRLPFNT STPQETLFSI RHFDELVELT SKLEWMLDQG LLESIPLYNQ
351  EKYLSGFEVL CQ*
```

The cp7380 nucleotide sequence <SEQ ID 202> is:

```
   1  GTGCACTACT GCGAGAGAAC CCTGGACCCA AAGTATATTC TGAAGATTGC
  51  TCTAAAGCTG AGACAATCAC TTTCCCTGTT CTTCCAGAAC AGCCAATCAC
 101  TCCAACGTGC ATACTCGACC CCATATTCCT ACTACCGAAT CATTCTACAA
 151  AAGGAAAATA AAGAGAAGCA AGCTTTAGCT CGACACAAAT GCATTTCTAT
 201  TTTAGAATTT TTCAAAAACT TACTCTTTGT TCATCTTCTG TCATTATCAA
 251  AGAATCAAAG GGAAGGTTGC TCCACTGATA TGGCTGTTGT AAGCACTCCC
 301  TTTTTTAATC GGAATTTATG GTATCGACTC CTTTCCTCAC GGTTTTCTCT
 351  ATGGAAAAGC TATTGTCCAA GATTTTTTCT TGATTACTTA GAAGCTTTCG
 401  GTCTCCTTTC TGATTTCTTA GACCATCAAG CAGTCATTAA ATTCTTCGAA
 451  TTAGAAACAC ATTTTTCCTA TTATCCCGTT TCAGGATTTG TAGCTCCCCA
 501  TCAATACTTG TCTCTGTTGC AGGACCGTTA CTTTCCCATT GCCTCTGTAA
 551  TGCGAACTCT CGATAAAGAT AATTTCTCCT TAACTCCTGA TCTCATCCAT
 601  GACCTTTTAG GGCACGTGCC TTGGCTTCTA CATCCCTCAT TTTCTGAATT
 651  TTTCATAAAC ATGGGAAGAC TCTTCACTAA AGTCATAGAA AAAGTACAAG
 701  CTCTTCCTAG TAAAAAACAA CGCATACAAA CCCTACAAAG CAATCTGATC
 751  GCTATTGTAC GCTGCTTTTG GTTTACTGTT GAAAGCGGAC TTATTGAAAA
 801  CCATGAAGGA AGAAAAGCAT ATGGAGCCGT TCTTATCAGT TCTCCTCAGG
 851  AACTTGGACA CGCTTTCATT GATAACGTAC GTGTTCTCCC TTTAGAATTG
 901  GATCAGATTA TTCGTCTTCC CTTCAATACA TCAACTCCAC AAGAGACTTT
 951  ATTTTCAATA AGACATTTTG ATGAACTGGT AGAACTCACT TCAAAATTAG
1001  AATGGATGCT CGACCAAGGT CTGTTAGAAT CAATTCCCCT TTACAATCAA
1051  GAGAAATATC TTTCTGGTTT TGAGGTACTT TGCCAATGA
```

The PSORT algorithm predicts inner membrane (0.1362).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 101A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 101B) and for FACS analysis (Figure 101C).

These experiments show that cp7380 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 102

The following *C.pneumoniae* protein (PID 4376904) was expressed <SEQ ID 203; cp6904>:

```
  1  MMNYEDAKLR GQAVAILYQI GAIKFGKHIL ASGEETPLYV DMRLVISSPE
 51  VLQTVATLIW RLRPSFNSSL LCGVPYTALT LATSISLKYN IPMVLRRKEL
101  QNVDPSDAIK VEGLFTPGQT CLVINDMVSS GKSIIETAVA LEENGLVVRE
151  ALVFLDRRKE ACQPLGPQGI KVSSVFTVPT LIKALIAYGK LSSGDLTLAN
201  KISEILEIES *
```

The cp6904 nucleotide sequence <SEQ ID 204> is:

```
  1  ATGATGAACT ACGAAGATGC AAAATTACGC GGTCAAGCTG TAGCAATTCT
 51  ATACCAAATC GGAGCTATAA AGTTCGGAAA ACATATTCTC GCTAGCGGAG
101  AAGAAACTCC TCTGTATGTA GATATGCGTC TTGTGATCTC CTCTCCAGAA
151  GTTCTCCAGA CAGTGGCAAC TCTTATTTGG CGCCTCCGCC CCTCATTCAA
201  TAGTAGCTTA CTCTGCGGAG TCCCTTATAC TGCTCTAACC CTAGCAACCT
251  CGATCTCTTT AAAATATAAC ATCCCTATGG TATTGCGAAG GAAGGAATTA
301  CAGAATGTAG ACCCCTCGGA CGCTATTAAA GTAGAAGGGT TATTTACTCC
351  AGGACAAACT TGTTTAGTCA TCAATGATAT GGTTTCCTCA GGAAAATCTA
401  TAATAGAGAC AGCAGTCGCA CTGGAAGAAA ATGGTCTGGT AGTTCGTGAA
451  GCATTGGTAT TCTTAGATCG TAGAAAAGAA GCGTGTCAAC CACTTGGTCC
501  ACAGGGAATA AAAGTCAGTT CGGTATTTAC TGTACCCACT CTGATAAAAG
551  CTTTGATCGC TTATGGGAAG CTAAGCAGTG GTGATCTAAC CCTGGCAAAC
601  AAAATTTCCG AAATTCTAGA AATTGAATCT TAA
```

The PSORT algorithm predicts cytoplasm (0.0358).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 102A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 102B) and for FACS analysis.

The cp6904 protein was also identified in the 2D-PAGE experiment.

These experiments show that cp6904 is a surface-exposed and immunoaecessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 103

The following *C.pneumoniae* protein (PID 4376964) was expressed <SEQ ID 205; cp6964>:

```
  1  MKKLIALIGI FLVPIKGNTN KEHDAHATVL KAARAKYNLF FVQDVFPVHE
 51  VIEPISPDCL VHYEGWV*
```

The cp6964 nucleotide sequence <SEQ ID 206> is:

```
  1  ATGAAAAAAT TGATTGCTTT GATAGGGATA TTTCTTGTTC CAATAAAAGG
 51  AAATACCAAT AAGGAACACG ACGCTCACGC GACTGTTTTA AAAGCGGCCA
101  GAGCAAAGTA TAATTTGTTC TTTGTTCAGG ATGTTTTCCC TGTACACGAA
151  GTTATCGAGC CTATTTCTCC CGATTGCCTG GTACATTATG AAGGGTGGGT
201  TTGA
```

The PSORT algorithm predicts inner membrane (0.091).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 103A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 103B) and for FACS analysis (Figure 103C).

These experiments show that cp6964 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 104

The following *C.pneumoniae* protein (PID 4377387) was expressed <SEQ ID 207; cp7387>:

```
  1  LNFAKIDHNH LYLTCLGDLG VACPILSTDC LPNYSEKASH EVLVYSKFRC
 51  ISGEPSRLAT SGNDTYYSIV SLPIGLRYEV TSPSGRHDFN IDMHVAPKIG
101  AVLSHGTREA KEIPGSSKDY AFFSLTARES LMISEKLAMT FQVSEVIQNC
151  YSQCTKVTKT NLKEQYRHLS HNTGFELSVK SAF*
```

The cp7387 nucleotide sequence <SEQ ID 208> is:

```
  1  TTGAATTTTG CAAAGATTGA TCACAATCAT CTCTACCTTA CATGTTTGGG
 51  AGATCTTGGT GTAGCTTGTC CTATACTTTC TACAGATTGT CTACCTAATT
101  ATAGCGAGAA AGCATCTCAT GAGGTTCTTG TTTATAGTAA ATTTAGATGC
151  ATTTCTGGAG AGCCATCTCG ACTTGCAACT TCAGGAAATG ACACATATTA
201  TTCTATAGTA AGTTTACCTA TAGGACTCCG TTACGAAGTG ACTTCACCAT
251  CAGGACGTCA TGATTTCAAT ATTGATATGC ATGTAGCTCC AAAGATAGGT
301  GCAGTACTCT CTCATGGAAC ACGAGAGGCT AAAGAGATCC CAGGATCTTC
351  AAAAGACTAT GCATTTTTTA GCTTGACTGC TAGAGAAAGT TTAATGATTT
401  CTGAAAAGCT TGCGATGACT TTCCAAGTTA GCGAAGTTAT TCAGAATTGT
451  TATTCACAAT GTACTAAAGT AACGAAAACT AATTTAAAAG AACAGTATAG
501  GCACTTATCC CACAATACAG GGTTTGAGTT AAGCGTCAAG TCTGCATTCT
551  AA
```

The PSORT algorithm predicts inner membrane (0.043).

The protein was expressed in *E.coli* and purified as a his-tagged-fusion product (Figure 104A) and also as a GST-fusion (Figure 104B). The recombinant proteins were used to immunise mice, whose sera were used in a Western blot and for FACS analysis (Figure 104C; his-tagged).

These experiments show that cp7387 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 105

The following *C.pneumoniae* protein (PID 4376281) was expressed <SEQ ID 209; cp6281>:

```
  1  MFLQFFHPIV FSDQSLSFLP YLGKSSGIIE KCSNIVEHYL HLGGDTSVII
 51  TGVSGATFLS VDHALPISKS EKIIKILSYI LILPLILALF IKIVLRIILF
101  FKYRGLILDV KKEDLKKTLT PDQENLSLPL PSPTTLKKIH ALHILVRSGK
151  TYNELIQEGF SFTKITDLGQ APSPKQDIGF SYNSLLPNFY FHSLVSVPNI
201  SGEERALNYH KEQQEEMAVK LKTMQACSFV FRSLHLPSMQ TKDKKAGFGL
251  LTFFPWKIYP L*
```

The cp6281 nucleotide sequence <SEQ ID 210> is:

```
  1  ATGTTTCTTC AGTTTTTTCA TCCTATAGTC TTCTCGGATC AGTCCTTATC
 51  TTTTCTTCCT TACCTAGGAA AAAGCTCTGG CATTATTGAA AAATGTTCCA
101  ATATCGTTGA ACACTATTTA CATTTGGGAG GAGACACTTC TGTTATCATC
151  ACAGGAGTTT CTGGAGCTAC CTTTCTATCT GTTGATCATG CCCTCCCAAT
201  CTCGAAATCT GAAAAAATAA TAAAAATTCT CTCCTATATT TTAATTCTTC
251  CTCTGATTCT AGCTCTCTTT ATTAAGATCG TTTTACGCAT TATCTTATTC
301  TTCAAGTATC GTGGTCTAAT CCTAGATGTT AAGAAGGAGG ATTTGAAAAA
351  AACACTTACA CCTGACCAAG AAAACCTCAG TCTTCCTTTA CCATCTCCTA
401  CAACATTAAA GAAAATTCAT GCGCTACACA TTTTAGTGCG TTCTGGAAAA
451  ACCTATAACG AGCTTATACA AGAAGGGTTT TCTTTCACTA AAATCACAGA
501  TCTTGGTCAA GCTCCTTCAC CAAAGCAAGA TATTGGCTTC TCTTATAATT
551  CCCTTCTCCC TAACTTCTAT TTTCATTCCT TGGTATCTGT TCCAAATATT
601  TCAGGCGAGG AACGGGCTCT TAATTATCAT AAAGAACAAC AAGAGGAAAT
651  GGCTGTTAAA TTAAAAACAA TGCAAGCGTG TTCTTTTGTC TTCCGATCCC
701  TGCATTTACC TTCAATGCAA ACGAAGGACA AAAAGGCTGG ATTTGGACTA
751  CTGACGTTTT TCCCTTGGAA AATCTACCCC CTATAA
```

The PSORT algorithm predicts inner membrane (0.5373).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 105A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 105B) and for FACS analysis.

These experiments show that cp6281 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 106 and
Example 107

The following *C.pneumoniae* protein (PID 4376306) was expressed <SEQ ID 211; cp6306>:

```
  1  MGNHETYIHP GVLPSSHAQD VSRSTVYPSR SFIMRRMLMG WNFNRVPSKS
 51  SEQLMDGHRI PLIFFGKHHP TISILNVNRF SWLSIFYNGE RGF*
```

The cp6306 nucleotide sequence <SEQ ID 212> is:

```
  1  ATGGGAAACC ATGAGACCTA TATACATCCA GGAGTGCTCC CGAGTAGTCA
 51  TGCTCAGGAT GTTAGCAGAT CTACAGTTTA CCCCAGTCGA AGTTTTATCA
101  TGAGACGTAT GCTCATGGGC TGGAATTTCA ATCGTGTTCC CTCGAAGAGC
151  TCCGAGCAGT TAATGGATGG TCATCGCATA CCTCTTATAT TTTTTGGGAA
201  GCATCATCCT ACTATATCTA TTTTAAATGT CAATAGATTT TCTTGGCTCT
251  CCATTTTTTA CAATGGAGAA AGGGGGTTTT GA
```

The PSORT algorithm predicts cytoplasm (0.167).

The following *C.pneumoniae* protein (PID 4376434) was also expressed <SEQ ID 213; cp6434>:

```
  1  MSESINRSIH LEASTPFFIK LTNLCESRLV KITSLVISLL ALVGAGVTLV
 51  VLFVAGILPL LPVLILEIIL ITVLVLLFCL VLEPYLIEKP SKIKELPKVD
101  ELSVVETDST L*
```

The cp6434 nucleotide sequence <SEQ ID 214> is:

```
  1  ATGTCTGAAA GTATTAACAG AAGCATTCAT TTAGAAGCCT CTACACCATT
 51  TTTTATAAAA TTAACGAATC TCTGTGAAAG TAGATTAGTT AAGATCACTT
101  CTCTTGTTAT TTCTCTATTA GCTTTAGTGG GTGCGGGAGT CACTCTTGTG
151  GTTTTATTTG TAGCTGGGAT CCTTCCTTTA CTTCCTGTAC TCATCTTAGA
201  AATTATTTTA ATAACCGTCC TTGTCTTGCT TTTTTGTTTG GTATTGGAAC
251  CTTATTTAAT AGAAAAACCT AGTAAAATAA AGGAACTACC TAAAGTAGAC
301  GAGCTATCTG TAGTAGAAAC GGACAGTACT CTTTAA
```

The PSORT algorithm predicts inner membrane (0.6859).

The proteins were expressed in *E.coli* and purified as his-tag products (Figure 106A; 6306 = lanes 2-4; 6434 = lanes 8-10). The recombinant proteins were used to immunise mice, whose sera were used in Western blots (Figures 106B & 107) and for FACS analysis.

These experiments show that cp6306 & cp6434 are surface-exposed and immunoaccessible proteins, and that they are useful immunogens. These properties are not evident from the sequences alone.

Example 108

The following *C.pneumoniae* protein (PID 4377400) was expressed <SEQ ID 215; cp7400>:

```
  1  MRVMRFFCLF FLGFLGSFHC VAEDKGVDLF GVWDDNQITE CDDSYMTEGR
 51  EEVEKVVDA
```

The cp7400 nucleotide sequence <SEQ ID 216> is:

```
  1  GTGAGAGTTA TGAGATTTTT TTGTCTATTT TTTCTTGGGT TCCTAGGATC
 51  TTTTCATTGT GTTGCTGAAG ACAAGGGCGT GGATTTATTT GGAGTCTGGG
101  ACGATAACCA AATTACAGAG TGTGACGATA GTTACATGAC AGAGGGTCGT
151  GAAGAGGTTG AAAAGGTAGT GGACGCTTAG
```

The PSORT algorithm predicts periplasmic space (0.924).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 108A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 108B) and for FACS analysis.

These experiments show that cp7400 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 109

The following *C.pneumoniae* protein (PID 4376395) was expressed <SEQ ID 217; cp6395>:

```
   1 MENAMSSSFV YNGPSWILKT SVAQEVFKKH GKGIQVLLST SVMLFIGLGV
  51 CAFIFPQYLI VFVLTIALLM LAISLVLFLL IRSVRSSMVD RLWCSEKGYA
 101 LHQHENGPFL DVKRVQQILL RSPYIKVRAL WPSGDIPEDP SQAAVLLLSP
 151 WTFFSSVDVE ALLPSPQEKE GKYIDPVLPK LSRIERVSLL VFLSAFTLDD
 201 LNEQGVNPLM NNEEFLFFIN KKAREHGIQD LKHEIMSSLE KTGVPLDPSM
 251 SFQVSQAMFS VYRYLRQRDL TTSELRCFHL LSCFKGDVVH CLASFENPKD
 301 LADSDFLEAC KNVEWGEFIS ACEKALLKNP QGISIKDLKQ FLVR*
```

The cp6395 nueleotide sequence <SEQ ID 218> is:

```
   1 ATGGAGAATG CTATGTCATC ATCGTTTGTG TATAATGGGC CTTCGTGGAT
  51 TTTAAAAACG TCAGTAGCTC AGGAGGTATT TAAAAAGCAC GGTAAGGGGA
 101 TTCAGGTTCT CTTAAGTACT TCAGTGATGC TTTTTATAGG TCTTGGAGTC
 151 TGTGCCTTTA TATTTCCTCA ATATCTGATT GTTTTTGTTT TGACTATAGC
 201 TTTGCTTATG CTCGCTATAA GCTTGGTATT GTTTCTCTTA ATACGTTCTG
 251 TACGCTCTTC AATGGTAGAT CGTTTGTGGT GTTCTGAAAA AGGATATGCT
 301 CTTCATCAAC ATGAGAACGG GCCTTTTTTG GATGTGAAGC GTGTACAGCA
 351 AATTCTTCTA AGATCACCCT ATATTAAAGT TCGGGCTTTA TGGCCGTCTG
 401 GAGATATCCC TGAGGATCCT TCACAAGCTG CGGTTCTATT ACTTTCTCCT
 451 TGGACTTTCT TTTCATCCGT GGATGTAGAG GCTTTATTAC CGAGTCCTCA
 501 AGAAAAGGAG GGTAAGTATA TAGATCCTGT GCTGCCTAAG TTGTCTAGGA
 551 TAGAGAGAGT CTCACTTTTA GTGTTTTTGA GTGCATTTAC TTTGGATGAC
 601 TTAAACGAAC AGGGAGTCAA TCCTTTGATG AATAATGAGG AATTTTTATT
 651 TTTTATAAAT AAGAAAGCGC GTGAGCATGG GATTCAGGAT TTAAAACACG
 701 AGATTATGTC TTCGTTAGAG AAAACAGGAG TGCCATTAGA CCCCTCAATG
 751 AGTTTTCAAG TTTCACAAGC GATGTTTTCT GTATATCGCT ACTTGAGACA
 801 AAGGGATTTA ACGACTTCAG AATTAAGATG TTTTCACCTC TTAAGTTGTT
 851 TTAAAGGGGA TGTGGTTCAT TGTTTAGCTT CATTTGAAAA CCCTAAAGAT
 901 TTAGCAGATT CTGACTTTTT AGAAGCTTGT AAGAACGTGG AATGGGGTGA
 951 GTTTATTTCG GCATGTGAGA AGGCTCTTTT AAAGAATCCG CAAGGAATTT
1001 CCATTAAGGA TCTAAAACAA TTTTTAGTGA GGTAA
```

The PSORT algorithm predicts inner membrane (0.6307).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 109A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 109B) and for FACS analysis.

These experiments show that cp6395 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 110

The following *C.pneumoniae* protein (PID 4376396) was expressed <SEQ ID 219; cp6396>:

```
   1 MIEFAFVPHT SVTADRIEDR MACRMNKLST LAITSLCVLI SSVCIMIGIL
  51 CISGTVGTYA FVVGIIFSVL ALVACVFFLY FFYFSSEEFK CASSQEFRFL
 101 PIPAVVSALR SYEYISQDAI NDVIKDTMQL STLSSLLDPE AFFLEFPYFN
 151 SLIVNHSMKE ADRLSREAFL ILLGEITWKD CETKILPWLK DPNITPDDFW
 201 KLLKDHFDLK DFKKRIATWI RKAYPEIRLP KKHCLDKSIY KGCCKFLLLS
```

```
251  ENDVQYQRLL HKVCYFSGEF PAMVLGLGSE VPMVLGLPKV PKDLTWEMFM
301  ENMPVLLQSK REGHWKISLE DVASL*
```

The cp6396 nucleotide sequence <SEQ ID 220> is:

```
  1  ATGATCGAGT TTGCTTTTGT TCCTCATACC TCCGTGACAG CGGATCGGAT
 51  TGAGGATCGC ATGGCCTGTC GCATGAACAA GTTGTCTACT TTAGCAATTA
101  CAAGTCTTTG TGTATTGATC AGTTCAGTTT GTATTATGAT TGGGATTTTA
151  TGCATTTCTG GAACGGTTGG GACCTATGCA TTTGTTGTAG GAATTATTTT
201  TTCTGTGCTT GCTTTGGTAG CATGTGTTTT CTTTCTTTAT TTCTTTTATT
251  TTTCTTCTGA GGAATTTAAG TGTGCTTCTT CGCAGGAGTT TCGTTTTTTG
301  CCTATACCAG CTGTGGTTTC TGCATTGCGT TCCTATGAAT ACATTTCTCA
351  GGACGCTATC AATGACGTTA TAAAAGATAC GATGCAGTTG TCTACCCTTT
401  CTTCTCTTTT AGATCCCGAA GCTTTTTTCT TAGAATTTCC TTATTTTAAC
451  TCTTTGATAG TGAATCATTC GATGAAGGAA GCGGATCGTT TGTCTCGAGA
501  GGCTTTTTTG ATTTTATTAG GTGAGATTAC TTGGAAGGAT TGTGAAACAA
551  AAATTTTGCC ATGGTTGAAA GATCCTAATA TCACTCCTGA TGATTTCTGG
601  AAGCTATTAA AAGACCATTT CGATTTAAAG GACTTTAAGA AGAGGATCGC
651  CACTTGGATA CGGAAGGCCT ATCCAGAAAT TAGATTACCG AAGAAGCATT
701  GTTTAGATAA GTCTATCTAT AAGGGGTGTT GTAAGTTTTT ATTACTTTCT
751  GAGAATGATG TGCAATATCA GAGGTTATTA CATAAGGTCT GTTATTTCTC
801  TGGGGAGTTT CCTGCCATGG TTTTAGGTTT GGGAAGTGAA GTGCCTATGG
851  TGTTAGGACT CCCTAAGGTT CCCAAGGATC TTACCTGGGA GATGTTTATG
901  GAAAATATGC CTGTTCTTCT GCAAAGCAAA AGAGAGGGGC ATTGGAAAAT
951  CTCCTTGGAA GACGTAGCCT CTCTTTAA
```

The PSORT algorithm predicts inner membrane (0.6095).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 110A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 110B) and for FACS analysis.

These experiments show that cp6396 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequenee alone.

Example 111

The following *C.pneumoniae* protein (PID 4376408) was expressed <SEQ ID 221; cp6408>:

```
  1  MNTSLKRPLK SHFDVVGSFL RPEHLKKTRE SLKEGSISLD QLMQIEDIAI
 51  QDLIKKQKAA GLSFITDGEF RRATWHYDFM WGFHGVGHHR ATEGVFFDGE
101  RAMIDDTYLT DKISVSHHPF VDHFKFVKAL EDEFTTAKQT LPAPAQFLKQ
151  MIFPNNIEVT RKFYPTNQEL IEDIVAGYRK VIRDLYDAGC RYLQLDDCTR
201  GGLVDPRVCS WYGIDEKGLQ DLIQQYLLIN NLVIADRPDD LVVNLHVCRG
251  NYHSKFFASG SYDFIAKPLF EQTNVDGYYL EFDHERSGDF SPLTFISGEK
301  TVCLGLVTSK TPTLENKDEV IARIHQAADY LPLERLSLSP QCGFASCEIG
351  NKLTEEEQWA KVALVKEISE EVWK*
```

The cp6408 nucleotide sequence <SEQ ID 222> is:

```
  1  ATGAATACTT CACTAAAAAG ACCTCTGAAA TCTCATTTTG ATGTTGTCGG
 51  TAGTTTTTTG CGTCCTGAGC ATTTAAAAAA AACTAGAGAA AGCCTTAAAG
101  AAGGCTCTAT TTCTCTAGAT CAACTCATGC AAATTGAGGA TATCGCTATC
151  CAAGATTTGA TCAAAAAACA AAAAGCAGCA GGTCTTTCTT TTATTACTGA
201  TGGAGAATTC CGCAGAGCTA CGTGGCATTA CGACTTCATG TGGGGTTTTC
251  ATGGCGTAGG TCACCACAGA GCTACAGAAG GAGTTTTCTT TGATGGAGAA
301  CGCGCTATGA TCGATGATAC CTATCTGACA GACAAGATCT CTGTATCTCA
351  CCACCCATTT GTGGATCACT TTAAATTTGT AAAAGCTCTA GAAGATGAAT
401  TTACGACTGC AAAGCAAACT CTTCCTGCAC CGGCACAGTT TTTAAAGCAG
451  ATGATCTTCC CTAATAATAT AGAGGTCACA CGTAAATTCT ATCCTACAAA
501  TCAGGAGCTA ATTGAAGATA TTGTTGCAGG TTATCGTAAA GTCATTCGCG
551  ATCTTTATGA TGCTGGCTGC CGCTATCTCC AATTAGATGA CTGTACTCGG
601  GGAGGTTTAG TAGACCCTCG AGTCTGTTCG TGGTATGGTA TCGATGAAAA
651  AGGTCTTCAA GATCTGATTC AACAATATCT TCTGATTAAT AATCTTGTAA
701  TTGCAGATCG TCCCGATGAT CTAGTCGTTA ATTTACATGT ATGCCGTGGG
```

```
 751  AACTACCACT CAAAATTCTT TGCTAGTGGT AGTTATGACT TTATTGCAAA
 801  GCCCCTATTC GAACAAACAA ATGTAGACGG CTACTATTTA GAGTTTGATC
 851  ATGAGCGTTC TGGAGACTTC TCTCCTCTCA CCTTCATTTC TGGAGAAAAA
 901  ACTGTCTGCT TAGGTCTTGT TACCAGCAAA ACCCCTACAC TTGAAAATAA
 951  GGATGAGGTC ATTGCTCGCA TACATCAAGC AGCAGACTAC CTGCCCTTGG
1001  AAAGACTCTC TCTAAGTCCA CAGTGTGGTT TTGCTTCATG TGAAATAGGA
1051  AATAAATTAA CAGAAGAAGA GCAATGGGCT AAAGTTGCTC TAGTAAAAGA
1101  AATTTCCGAA GAAGTTTGGA AATAA
```

The PSORT algorithm predicts cytoplasm (0.2171).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 111A) and also as a his-tagged product. The his-tag protein was used to immunise mice, whose sera were used in a Western blot (Figure 111B) and for FACS analysis.

These experiments show that cp6408 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 112

The following *C.pneumoniae* protein (PID 4376430) was expressed <SEQ ID 223; cp6430>:

```
  1  MKLYSISSDV DTPWIFQLMS KVDSYLFLGG NRIKVVSIVM QEPNLIIGKV
 51  ENVRISTIVK ILKILSFLIF PLILIALALH YFLHAKYANH LLVSKILERA
101  PQYVPIPGRS GDTASHYKLT TLVPVSQKNL QAMGSNPLEV EAALRTTKPS
151  FFCVPAKYRQ IIISSHGIRF SLDLEQLADD INLDSVSWPT EYLNSTMDFC
201  SKADKRVIQN VQNLRTGTYI NSVGKRSLLK FMLQHLFIDG ITQENPEALP
251  NNTSGRLTLF PSVRYIYSHF TPQNPTIWPQ VFFRQGPLDE DRGGGFEILE
301  QLQELGVRFP ICPSQGPDNP NFQGFQGIRI YWEDSYQPNK EV*
```

The cp6430 nucleotide sequence <SEQ ID 224> is:

```
   1  ATGAAACTTT ATAGCATCTC TTCAGATGTA GATACACCTT GGATATTTCA
  51  GCTTATGTCA AAGGTAGATT CTTATCTTTT CTTAGGCGGG AATAGAATCA
 101  AGGTTGTATC TATAGTTATG CAAGAACCTA ACTTAATTAT TGGAAAAGTA
 151  GAAAACGTTC GGATCTCCAC AATAGTGAAA ATATTAAAGA TTTTATCCTT
 201  CTTAATCTTC CCTCTGATTT TAATCGCTTT AGCCCTACAC TATTTTCTAC
 251  ATGCTAAATA TGCTAATCAC TTACTTGTAT CTAAGATTTT AGAAAGAGCT
 301  CCTCAGTATG TGCCTATTCC TGGTCGTTCA GGAGACACGG CGTCTCATTA
 351  TAAATTAACA ACATTGGTTC CAGTATCCCA AAAAAATCTA CAAGCTATGG
 401  GATCAAATCC TCTAGAAGTT GAAGCGGCTC TTCGAACTAC AAAACCCTCT
 451  TTTTTCTGTG TACCTGCAAA ATACCGTCAG ATTATAATTT CAAGTCACGG
 501  CATTCGCTTT TCTTTAGATC TTGAACAACT TGCTGATGAC ATTAATTTAG
 551  ATTCGGTTTC CTGGCCTACG GAGTATCTTA ACTCTACTAT GGATTTTTGC
 601  AGCAAGGCAG ATAAACGTGT TATACAGAAT GTACAAAATC TGCGGACAGG
 651  AACTTACATA AATTCTGTAG GAAAGCGTAG CCTTTTAAAA TTCATGTTAC
 701  AGCACCTATT TATTGATGGG ATCACACAAG AAAACCCTGA AGCCCTTCCT
 751  AACAATACAT CTGGAAGACT GACTCTATTC CCTAGTGTTC GTTATATCTA
 801  TTCTCATTTT ACTCCACAAA ATCCTACAAT ATGGCCGCAA GTCTTTTTCA
 851  GACAAGGTCC TCTAGATGAA GATCGAGGAG GAGGATTTGA GATCTTAGAG
 901  CAATTACAAG AGTTAGGAGT TAGGTTTCCA ATTTGCCCCT CTCAAGGACC
 951  AGACAATCCT AATTTTCAAG GTTTTCAAGG GATTCGTATC TATTGGGAAG
1001  ATTCCTATCA ACCCAATAAG GAGGTTTAA
```

The PSORT algorithm predicts inner membrane (0.5140).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 112A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 112B) and for FACS analysis.

These experiments show that cp6430 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 113

The following *C.pneumoniae* protein (PID 4376439) was expressed <SEQ ID 225; cp6439>:

```
  1  MSYDTLFKNL EKEDSVHKIC NEIFALVPRL NTIACTEAII KNLPKADIHV
 51  HLPGTITPQL AWILGVKNGF LKWSYNSWTN HRLLSPKNPH KQYSNIFRNF
101  QDICHEKDPD LSVLQYNILN YDFNSFDRVM ATVQGHRFPP GGIQNEEDLL
151  LIFNNYLQQC LDDTIVYTEV QQNIRLAHVL YPSLPEKHAR MKFYQILYRA
201  SQTFSKHGIT LRFLNCFNKT FAPQINTQEP AQEAVQWLQE VDSTFPGLFV
251  GIQSAGSESA PGACPKRLAS GYRNAYDSGF GCEAHAGEGI ETRTIFSSAK
301  VNPEGLIEIT RVTFSSLKRK QPSSLPIRVT CQLG*
```

The cp6439 nucleotide sequence <SEQ ID 226> is:

```
   1  ATGTCTTATG ATACGTTATT CAAGAATCTT GAAAAGGAAG ATTCTGTACA
  51  TAAGATATGC AATGAGATCT TTGCATTAGT ACCACGACTC AATACAATCG
 101  CTTGCACCGA AGCTATCATC AAAAACCTCC CCAAAGCAGA TATCCATGTA
 151  CACCTTCCTG GGACCATAAC ACCTCAATTA GCTTGGATTT TAGGTGTGAA
 201  AAATGGGTTC TTAAAATGGT CTTATAATTC TTGGACCAAT CATCGATTAC
 251  TTTCTCCTAA GAATCCTCAT AAACAATACT CCAATATTTT CCGAAACTTT
 301  CAAGATATCT GTCACGAAAA GGATCCGGAT TTAAGTGTAT TACAATATAA
 351  TATCTTAAAT TACGATTTTA ATAGCTTTGA TAGAGTGATG GCTACAGTAC
 401  AAGGACATCG CTTTCCTCCT GGAGGAATCC AAAATGAAGA AGACCTTCTT
 451  CTCATTTTCA ATAACTATCT CCAGCAATGT CTGGACGATA CTATCGTGTA
 501  TACTGAAGTA CAACAAAATA TCCGCCTTGC CCATGTTTTG TATCCTTCAT
 551  TACCTGAAAA GCACGCGCGT ATGAAGTTTT ATCAAATCTT GTATCGTGCT
 601  TCGCAAACGT TTTCAAAACA CGGGATTACT TTACGATTTT TAAACTGCTT
 651  CAATAAAACA TTTGCTCCAC AAATAAACAC ACAAGAACCT GCCCAAGAAG
 701  CTGTTCAATG GCTCCAAGAG GTTGATTCTA CATTTCCTGG TCTATTTGTA
 751  GGGATACAAT CCGCAGGATC AGAATCTGCG CCCGGAGCCT GTCCTAAGCG
 801  ATTAGCTTCT GGATATAGAA ATGCTTATGA CTCAGGGTTT GGTTGTGAAG
 851  CTCATGCTGG AGAAGGCATA GAGACCCGGA CTATTTTTTC GTCAGCTAAG
 901  GTAAATCCAG AGGGATTGAT CGAGATAACC CGAGTGACTT TCTCGTCTCT
 951  TAAACGAAAA CAGCCATCTA GTTTACCCAT AAGAGTTACT TGCCAGTTAG
1001  GATAA
```

The PSORT algorithm predicts cytoplasm (0.1628).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 113A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 113B) and for FACS analysis.

These experiments show that cp6439 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 114

The following *C.pneumoniae* protein (PID 4376440) was expressed <SEQ ID 227; cp6440>:

```
  1  LQSARRHLNT IFILDFGSQY TYVLAKQVRK LFVYCEVLPW NISVQCLKER
 51  APLGIILSGG PHSVYENKAP HLDPEIYKLG IPILAICYGM QLMARDFGGT
101  VSPGVGEFGY TPIHLYPCEL FKHIVDCESL DTEIRMSHRD HVTTIPEGFN
151  VIASTSQCSI SGIENTKQRL YGLQFHPEVS DSTPTGNKIL ETFVQEICSA
201  PTLWNPLYIQ QDLVSKIQDT VIEVFDEVAQ SLDVQWLAQG TIYSDVIESS
251  RSGHASEVIK SHHNVGGLPK NLKLKLVEPL RYLFKDEVRI LGEALGLSSY
301  LLDRHPFPGP GLTIRVIGEI LPEYLAILRR ADLIFIEELR KAKLYDKISQ
351  AFALFLPIKS VSVKGDCRSY GYTIALRAVE STDFMTGRWA YLPCDVLSSC
401  SSRIINEIPE VSRVVYDISD KPPATIEWE*
```

The cp6440 nucleotide sequence <SEQ ID 228> is:

```
   1  TTGCAGAGTG CAAGGAGACA TTTGAACACC ATATTTATTC TAGATTTTGG
  51  ATCTCAATAT ACTTATGTAT TAGCAAAGCA AGTGCGGAAG TTATTTGTAT
 101  ATTGCGAAGT TCTTCCCTGG AATATCTCTG TGCAATGTTT AAAAGAAAGA
 151  GCGCCTTTGG GGATCATTCT CTCAGGAGGT CCTCACTCTG TCTATGAAAA
```

```
 201  CAAGGCTCCA CATTTAGATC CTGAAATCTA TAAACTTGGC ATTCCAATTC
 251  TAGCTATTTG CTATGGCATG CAGCTTATGG CTAGAGATTT TGGAGGGACT
 301  GTAAGCCCTG GTGTAGGAGA ATTTGGATAT ACGCCCATCC ATCTGTATCC
 351  TTGTGAGCTC TTCAAACACA TCGTCGACTG CGAATCTCTA GACACAGAGA
 401  TTCGGATGAG CCATCGGGAT CATGTTACGA CAATTCCTGA AGGATTTAAT
 451  GTAATCGCAT CCACCTCACA ATGCTCGATC TCAGGAATAG AAAATACCAA
 501  ACAACGGTTG TACGGGCTGC AATTTCATCC CGAGGTTTCT GACTCCACTC
 551  CAACGGGAAA TAAGATTCTA GAAACTTTTG TTCAAGAGAT CTGTTCTGCT
 601  CCCACACTAT GGAATCCCTT GTATATTCAG CAAGACCTTG TAAGTAAAAT
 651  TCAAGATACC GTTATTGAAG TATTTGATGA AGTCGCTCAG TCATTAGACG
 701  TACAATGGTT AGCTCAAGGA ACCATCTACT CAGATGTTAT TGAGTCCTCA
 751  CGCTCTGGAC ATGCCTCCGA AGTAATAAAA TCACATCATA ATGTAGGGGG
 801  GCTTCCAAAA AATCTTAAGC TGAAGTTAGT CGAGCCCTTA CGTTATTTAT
 851  TTAAAGATGA AGTTCGAATT TTAGGAGAAG CCCTAGGACT TTCTAGCTAT
 901  CTCTTGGACA GGCATCCTTT TCCTGGACCT GGCTTGACAA TTCGTGTGAT
 951  TGGAGAGATC CTTCCTGAAT ATCTAGCCAT TTTACGACGG GCGGACCTCA
1001  TCTTTATAGA AGAGCTTAGG AAAGCAAAAC TCTACGATAA AATAAGCCAA
1051  GCCTTTGCTC TATTTCTTCC TATAAAATCA GTATCTGTAA AAGGAGATTG
1101  TAGAAGCTAT GGTTATACCA TAGCATTACG TGCTGTAGAA TCTACAGATT
1151  TCATGACAGG ACGATGGGCC TACCTTCCAT GCGATGTTCT CAGTTCTTGC
1201  TCATCGCGAA TTATTAATGA AATACCCGAG GTAAGCCGAG TGGTCTATGA
1251  TATTTCTGAC AAGCCACCAG CAACTATAGA ATGGGAATAG
```

The PSORT algorithm predicts cytoplasm (0.0481).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 114A) and also as a his-tagged product. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 114B) and for FACS analysis.

These experiments show that cp6440 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequenee alone.

Example 115

The following *C.pneumoniae* protein (PID 4376475) was expressed <SEQ ID 229; cp6475>:

```
  1  MNTYTFSPTL QKSFSLFLLE KLDSYFFFGG TRTQILVITP TNIRLAAKKR
 51  GCKVSTIEKI IKILSFILLP LVIIAFILRY FLHKKFDKQF LCIPKVISNE
101  DEALLGSRPQ AVEKAVREIS PAFFSIPRKY QLIRIDTPKD DAPSILFPIG
151  IEIILKDLCI DTLKQSNLFL KREMDFLGHP EEKALFDSIC SIEKDQEWMS
201  LESKKLLITH FLKYLFVSGI EQLNPGFNPE NGRGYFSEIS TAKIHFHQHG
251  RYGPIRSSGP IMKEI*
```

The cp6475 nucleotide sequence <SEQ ID 230> is:

```
  1  ATGAATACCT ATACCTTCTC TCCTACACTT CAGAAAAGCT TCAGCCTATT
 51  TCTTTTAGAA AAATTAGACT CTTACTTTTT CTTTGGAGGG ACTCGTACAC
101  AAATCTTAGT CATCACACCA ACCAATATTA GATTAGCAGC TAAAAAAAGA
151  GGGTGTAAGG TTTCTACTAT AGAAAAGATA ATCAAGATCC TCTCTTTTAT
201  CCTGCTGCCC CTAGTTATCA TTGCCTTTAT ACTTCGCTAT TTCTTACATA
251  AGAAATTCGA TAAACAGTTC TTGTGTATCC CAAAAGTCAT TTCTAACGAA
301  GACGAAGCTC TTCTTGGATC TAGACCACAA GCAGTTGAAA AAGCAGTTCG
351  AGAAATATCT CCAGCCTTCT TCTCTATACC AAGAAAATAC CAACTTATTA
401  GAATCGACAC TCCTAAAGAT GACGCTCCCT CAATCCTTTT CCCTATAGGC
451  ATAGAGATCA TTCTCAAAGA TTTATGTATT GATACACTCA AGCAATCTAA
501  TCTTTTCCTT AAAAGAGAAA TGGATTTCTT AGGTCATCCA GAAGAAAAAG
551  CATTATTCGA CTCGATATGT TCTATAGAAA AAGATCAAGA ATGGATGAGC
601  TTGGAAAGTA AAAAACTTTT AATCACGCAC TTCCTAAAGT ATCTCTTTGT
651  CTCTGGAATC GAACAACTAA ATCCAGGCTT TAACCCAGAG AATGGGCGTG
701  GGTATTTTTC AGAAATAAGT ACAGCAAAGA TCCATTTTCA TCAGCACGGT
751  CGATATGGGC CAATCCGTTC TTCGGGACCC ATCATGAAGG AAATATAA
```

The PSORT algorithm predicts inner membrane (0.5373).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 115A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 115B) and for FACS analysis.

These experiments show that cp6475 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 116

The following *C.pneumoniae* protein (PID 4376482) was expressed <SEQ ID 231; cp6482>:

```
  1 MLVELEALKR EFAHLKDQKP TSDQEITSLY QCLDHLEFVL LGLGQDKFLK
 51 ATEDEDVLFE SQKAIDAWNA LLTKARDVLG LGDIGAIYQT IEFLGAYLSK
101 VNRRAFCIAS EIHFLKTAIR DLNAYYLLDF RWPLCKIEEF VDWGNDCVEI
151 AKRKLCTFEK ETKELNESLL REEHAMEKCS IQDLQRKLSD IIIELHDVSL
201 FCFSKTPSQE EYQKDCLYQS RLRYLLLLYE YTLLCKTSTD FQEQARAKEE
251 FIREKFSLLE LEKGIKQTKE LEFAIAKSKL ERGCLVMRKY EAAAKHSLDS
301 MFEEETVKSP RKDTE*
```

The cp6482 nucleotide sequence <SEQ ID 232> is:

```
  1 ATGCTAGTAG AGTTAGAGGC TCTTAAAAGA GAGTTTGCGC ATTTAAAAGA
 51 CCAGAAGCCG ACAAGTGACC AAGAGATCAC TTCACTTTAT CAATGTTTGG
101 ATCATCTTGA ATTCGTTTTA CTCGGGCTGG GCCAGGACAA ATTTTTAAAG
151 GCTACGGAAG ATGAAGATGT GCTTTTTGAG TCTCAAAAAG CAATCGATGC
201 GTGGAATGCT TTATTGACAA AAGCCAGAGA TGTTTTAGGT CTTGGGGACA
251 TAGGTGCTAT CTATCAGACT ATAGAATTCT TGGGTGCCTA TTTATCAAAA
301 GTGAATCGGA GGGCTTTTTG TATTGCTTCG GAGATACATT TTCTAAAAAC
351 AGCAATCCGA GATTTGAATG CATATTACCT GTTAGATTTT AGATGGCCTC
401 TTTGCAAGAT AGAAGAGTTT GTGGATTGGG GGAATGATTG TGTTGAAATA
451 GCAAAGAGGA AGCTATGCAC TTTTGAAAAA GAAACCAAGG AGCTCAATGA
501 GAGCCTTCTT AGAGAGGAGC ATGCGATGGA GAAATGCTCG ATTCAAGATC
551 TGCAAAGGAA ACTTAGCGAC ATTATTATTG AATTGCATGA TGTTTCTCTT
601 TTTTGTTTTT CTAAGACTCC CAGTCAAGAG GAGTATCAAA AGGATTGTTT
651 GTATCAATCA CGATTGAGGT ACTTATTGTT GCTGTATGAG TATACATTGT
701 TATGTAAGAC ATCCACAGAT TTTCAAGAGC AGGCTAGGGC TAAAGAGGAG
751 TTCATTAGGG AGAAATTCAG CCTTCTAGAG CTCGAAAAGG GAATAAAACA
801 AACTAAAGAG CTTGAGTTTG CAATTGCTAA AAGTAAGTTA GAACGGGGCT
851 GTTTAGTTAT GAGGAAGTAT GAAGCTGCCG CTAAACATAG TTTAGATTCT
901 ATGTTCGAAG AAGAAACTGT GAAGTCGCCG CGGAAAGACA CAGAATAA
```

The PSORT algorithm predicts eytoplasm (0.4607).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 116A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 116B) and for FACS analysis.

These experiments show that cp6482 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 117

The following *C.pneumoniae* protein (PID 4376486) was expressed <SEQ ID 233; cp6486>:

```
  1 VVVVALFILG IFFLSGSLAF LVHTSCGVLL GAALPILCIG LVLLAVALIV
 51 FLCHKHKTRQ DLDYYDQDLD SLVIHKKEIP NDISELRVTF EKLQNLFQFH
101 TKDFSDLSQE LQGKFINCME KWLTLEDEVT KFLIVRDRFL ETRRNFTTFG
151 EQVKGIQSNI FDLHEEKSSL YLELYRLRKD LQVLLNFFLL PPGILKVDYD
201 EIEAIKGLFI RLTSRLDKLD VKAQERKKFI NEMSREFKEV EKAFDIVDRA
251 TKKLMDRAKK ESPARLFMGR TESLLEMKKN EEALKNQGLD PENLSHPELF
301 SPYQQLLILN YLNSEIVLHH YEFLISGTVT SGLTLEECEN RMRAASTGLN
```

```
351  ALLVRKLQFR GAIKSAYFEK LTEIEKELRS LQDVIKSLEL ELIHKIKDIV
401  TEET*
```

The cp6486 nucleotide sequence <SEQ ID 234> is:

```
   1  GTGGTGGTTG TCGCTTTATT TATCCTTGGG ATTTTCTTTT TATCTGGTTC
  51  TCTTGCATTC CTTGTTCATA CGTCTTGCGG AGTTCTTTTA GGAGCGGCGC
 101  TTCCCATACT TTGCATAGGT CTTGTTTTAT TGGCTGTAGC TCTTATTGTT
 151  TTCTTATGTC ACAAACACAA GACTCGTCAA GATTTAGATT ATTATGATCA
 201  AGATTTAGAT TCTTTGGTGA TTCATAAGAA AGAGATCCCC AATGACATCT
 251  CTGAGTTGCG GGTAACATTT GAAAAGTTGC AAAATCTGTT TCAGTTCCAT
 301  ACGAAAGATT TCTCTGATCT AAGCCAAGAG CTTCAGGGTA AATTTATCAA
 351  TTGCATGGAG AAATGGCTAA CTTTAGAAGA CGAAGTGACT AAATTTCTTA
 401  TTGTTCGAGA TAGATTTTTA GAAACCAGAA GAAATTTTAC CACTTTTGGA
 451  GAACAGGTTA AAGGGATCCA AAGCAATATT TTTGATTTGC ATGAGGAAAA
 501  GTCTTCATTA TATTTAGAAT TGTATAGGCT TAGGAAAGAC CTCCAAGTTC
 551  TATTAAATTT TTTTCTGCTC CCCCCAGGTA TACTCAAGGT AGATTATGAT
 601  GAAATTGAGG CTATCAAAGG TCTGTTTATA AGATTAACCT CTAGATTAGA
 651  TAAGCTTGAT GTGAAAGCTC AGGAACGTAA GAAGTTCATT AATGAAATGA
 701  GTAGGGAATT TAAAGAAGTA GAGAAAGCTT TTGATATTGT CGATAGGGCA
 751  ACAAAAAAGC TTATGGATAG AGCCAAGAAA GAAAGTCCGG CACGTCTTTT
 801  CATGGGTAGA ACTGAGTCTC TCTTAGAAAT GAAAAAAAAT GAAGAAGCCC
 851  TTAAAAATCA GGGGCTAGAT CCTGAAAATC TTTCCCATCC TGAACTTTTT
 901  AGTCCGTATC AACAGCTTTT AATTTTGAAT TATTTAAATA GCGAAATAGT
 951  TCTGCATCAT TATGAGTTCC TTATTTCTGG AACAGTAACT TCTGGCCTAA
1001  CTCTTGAAGA ATGTGAAAAT CGAATGAGGG CGGCTTCTAC TGGGTTGAAC
1051  GCCCTTCTGG TGCGTAAGCT CCAGTTCAGA GGTGCTATAA AATCTGCGTA
1101  TTTTGAAAAA CTCACAGAGA TTGAAAAAGA GTTACGATCA CTTCAAGACG
1151  TAATAAAGTC ATTGGAACTA GAACTGATCC ATAAGATAAA AGATATAGTG
1201  ACAGAAGAAA CTTAG
```

The PSORT algorithm predicts inner membrane (0.7474).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 117A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 117B) and for FACS analysis.

These experiments show that cp6486 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 118

The following *C.pneumoniae* protein (PID 4376526) was expressed <SEQ ID 235; cp6526>:

```
  1  MSPFKKIVNR LLCYISFQKE SRTLPIIIRE PRMTTKSLGS FNSVISKNKI
 51  HFISLGCSRN LVDSEVMLGI LLKAGYESTN EIEDADYLIL NTCAFLKSAR
101  DEAKDYLDHL IDVKKENAKI IVTGCMTSNH KDELKPWMSH IHYLLGSGDV
151  ENILSAIESR ESGEKISAKS YIEMGEVPRQ LSTPKHYAYL KVAEGCRKRC
201  AFCIIPSIKG KLRSKPLDQI LKEFRILVNK SVKEIILIAQ DLGDYGKDLS
251  TDRSSQLESL LHELLKEPGD YWLRMLYLYP DEVSDGIIDL MQSNPKLLPY
301  VDIPLQHIND RILKQMRRTT SREQILGFLE KLRAKVPQVY IRSSVIVGFP
351  GETQEEFQEL ADFIGEGWID NLGIFLYSQE ANTPAAELPD QIPEKVKESR
401  LKILSQIQKR NVDKHNQKLI GEKIEAVIDN YHPETNLLLT ARFYGQAPEV
451  DPCIIVNEAK LVSHFGERCF IEITGTAGYD LVGRVVKKSQ NQALLKTSKA
501  *
```

The cp6526 nucleotide sequence <SEQ ID 236> is:

```
  1  ATGAGTCCTT TTAAGAAAAT AGTAAATCGC TTACTATGCT ATATTTCTTT
 51  TCAAAAAGAA TCAAGAACTC TCCCAATCAT TATTAGAGAA CCTAGGATGA
101  CAACAAAAAG TTTAGGATCT TTCAATTCAG TTATTTCCAA AAATAAAATT
151  CATTTTATTA GTTTGGGATG CTCTCGGAAC CTTGTAGATA GCGAAGTCAT
201  GCTAGGCATT CTTCTTAAGG CAGGTTACGA GTCTACTAAT GAAATTGAAG
251  ATGCTGACTA TTTAATTTTA AATACCTGTG CGTTTTTAAA AAGTGCTAGA
301  GATGAAGCTA AAGATTATCT AGACCATCTA ATTGATGTAA AAAAAGAGAA
```

```
 351  CGCTAAAATT ATTGTAACTG GATGCATGAC TTCCAACCAC AAAGATGAGC
 401  TTAAACCCTG GATGTCACAC ATCCATTACC TACTAGGTTC TGGGGATGTT
 451  GAGAATATTC TTTCTGCTAT TGAGTCTCGT GAATCTGGAG AAAAAATCTC
 501  TGCAAAGAGT TACATTGAGA TGGGAGAAGT TCCAAGACAG CTTTCCACAC
 551  CAAAACACTA TGCCTATTTA AAAGTTGCTG AGGGCTGTAG AAAACGTTGT
 601  GCTTTTTGTA TTATTCCTTC CATTAAAGGA AAGCTCCGCA GCAAACCTCT
 651  GGATCAAATT CTTAAAGAAT TCCGCATCCT TGTAAACAAG AGTGTGAAAG
 701  AGATTATATT GATAGCTCAA GACCTAGGAG ATTATGGAAA GGATCTCTCT
 751  ACAGACCGCA GTTCGCAGCT AGAATCACTA TTACATGAGT TACTGAAAGA
 801  GCCTGGTGAT TATTGGCTGC GGATGTTGTA TTTATATCCT GATGAAGTGA
 851  GTGATGGCAT TATAGATCTT ATGCAATCTA ATCCCAAACT TCTTCCCTAT
 901  GTAGATATTC CCTTACAGCA CATTAACGAC CGTATTTTAA AGCAAATGCG
 951  AAGAACGACT TCTAGGGAGC AAATCCTAGG ATTCCTAGAA AAATTACGTG
1001  CCAAGGTTCC TCAGGTCTAT ATCCGTTCTT CTGTTATTGT GGGTTTCCCC
1051  GGTGAAACTC AGGAAGAATT CCAGGAGTTA GCTGATTTTA TTGGTGAGGG
1101  TTGGATTGAT AATCTCGGAA TTTTCTTGTA CTCTCAAGAA GCGAATACCC
1151  CGGCAGCAGA ACTCCCTGAC CAGATACCAG AAAAAGTTAA AGAATCGAGG
1201  TTGAAAATTC TATCTCAAAT TCAGAAACGC AATGTGGATA AACATAATCA
1251  GAAGCTCATT GGGGAAAAAA TAGAAGCAGT TATTGATAAC TATCATCCTG
1301  AAACGAATCT TTTACTCACT GCAAGGTTCT ATGGACAAGC TCCTGAAGTG
1351  GACCCTTGTA TTATTGTAAA TGAGGCGAAG CTTGTTTCTC ATTTTGGAGA
1401  AAGATGCTTT ATAGAAATCA CAGGGACTGC TGGTTACGAC CTTGTAGGGC
1451  GTGTTGTAAA AAAATCTCAG AACCAAGCTT TGCTAAAAAC TAGCAAAGCT
1501  TAG
```

The PSORT algorithm predicts cytoplasm (0.1296).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 118A) and also as a his-tagged product. The reeombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 118B) and for FACS analysis.

These experiments show that cp6526 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 119

The following *C.pneumoniae* protein (PID 4376528) was expressed <SEQ ID 237; ep6528>:

```
   1  MKNNINNNEC YFKLDSTVDG DLLAANLKTF DTQAQGISST ETFSVQGNAT
  51  FKDQVSATGL TSGTTYNLNA QNFTSSQISI DFKNNRLSNC ALPKEDCDPV
 101  PANYVRSPEY FFCSKPLIGD FDFNSGESYL PLTGSEYTLY QSRNVNSIFR
 151  FIGWKQSTRE LTVGGNTAIQ FLAAGTYIVS FTVGKRWGWN NGWGGAIYIN
 201  NGLGQVQCES TIYSGGGYAT IGTLGTSIYR ASVDVAPNPN DPNASDRYRA
 251  GIFYLSNGGS SAGIGNYSFS LLYYPDDRG*
```

The cp6528 nucleotide sequence <SEQ ID 238> is:

```
   1  ATGAAAAACA ATATTAATAA TAATGAGTGC TATTTTAAAT TAGACTCAAC
  51  TGTAGATGGT GATTTGTTAG CAGCCAATCT CAAGACCTTT GATACACAGG
 101  CCCAAGGAAT CTCATCGACT GAAACATTTT CTGTTCAGGG GAATGCAACA
 151  TTTAAAGATC AAGTTTCAGC AACTGGATTA ACTTCAGGAA CTACTTATAA
 201  TTTAAATGCA CAAAACTTTA CTTCCTCCCA AATCTCTATA GATTTTAAAA
 251  ATAATCGTCT GAGTAATTGT GCATTGCCAA AAGAAGACTG CGATCCGGTG
 301  CCAGCGAATT ATGTTCGTTC TCCCGAATAT TTTTTCTGTT CCAAGCCTCT
 351  GATCGGAGAT TTTGATTTTA ACTCAGGGGA ATCTTATTTG CCTCTGACTG
 401  GTTCGGAATA TACTCTATAT CAGTCACGTA ATGTAAATAG TATATTTCGT
 451  TTTATAGGAT GGAAGCAAAG TACACGAGAA TTAACTGTAG GGGGAAATAC
 501  TGCGATACAA TTTCTTGCAG CAGGAACCTA TATCGTTTCA TTTACTGTTG
 551  GTAAACGGTG GGGATGGAAT AATGGTTGGG GAGGAGCCAT TTATATCAAT
 601  AATGGTTTAG GACAAGTCCA ATGTGAAAGC ACGATTTATA GTGGTGGAGG
 651  GTATGCAACA ATAGGTACAC TGGGGACCTC AATATATAGA GCCTCTGTAG
 701  ATGTAGCTCC TAATCCTAAT GATCCGAATG CTTCGGATCG CTATAGAGCG
 751  GGTATTTTCT ATCTCAGTAA CGGTGGTTCT AGTGCAGGTA TAGGGAATTA
 801  CTCCTTTTCT CTTCTCTATT ATCCGGACGA TAGAGGGTAG
```

The PSORT algorithm predicts cytoplasm (0.1668).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 119A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 119B) and for FACS analysis.

These experiments show that cp6528 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 120

The following *C.pneumoniae* protein (PID 4376627) was expressed <SEQ ID 239; cp6627>:

```
  1 MKCSPLTLVP HIFLKNDCEC HRSCSLKIRT IARLILGLVL ALVSALSFVF
 51 LAAPISYAIG GTLALAAIVI LIITLVVALL AKSKVLPIPN ELQKIIYNRY
101 PKEVFYFVKT HSLTVNELKI FINCWKSGTD LPPNLHKKAE AFGIDILKSI
151 DLTLFPEFEE ILLQNCPLYW LSHFIDKTES VAGEIGLNKT QKVYGLLGPL
201 AFHKGYTTIF HSYTRPLLTL ISESQYKFLY SKASKNQWDS PSVKKTCEEI
251 FKELPHNMIF RKDVQGISQF LFLFFSHGIT WEQAQMIQLI NPDNWKMLCQ
301 FDKAGGHCSM ATFGGFLNTE TNMFDPVSSN YEPTVNFMTW KELKVLLEKV
351 KESPMHPASA LVQKICVNTT HHQNLLKRWQ FVRNTSSQWT SSLPQYAFHA
401 QTYKLEKKIE SSLPIRSSL*
```

The cp6627 nucleotide sequence <SEQ ID 240> is:

```
   1 ATGAAGTGTA GTCCTTTAAC ACTAGTTCCC CATATATTTT TAAAAAATGA
  51 CTGCGAATGT CATAGATCTT GTTCTTTAAA AATTAGGACA ATTGCCCGAC
 101 TCATTCTTGG GCTTGTTCTA GCTCTTGTTA GCGCACTTTC TTTTGTTTTC
 151 CTTGCTGCGC CGATTAGCTA TGCTATTGGA GGAACTTTAG CTTTAGCCGC
 201 TATCGTAATC TTGATTATAA CGCTAGTCGT AGCACTGCTA GCTAAATCAA
 251 AGGTTCTGCC CATCCCCAAC GAACTTCAGA AGATTATTTA CAATCGCTAT
 301 CCTAAAGAAG TCTTTTATTT CGTGAAAACA CACTCCCTGA CTGTTAACGA
 351 ATTAAAAATA TTTATTAATT GCTGGAAAAG CGGTACAGAC CTGCCTCCGA
 401 ATTTACATAA AAAAGCAGAG GCTTTCGGGA TCGATATTCT AAAATCTATA
 451 GATTTAACCC TGTTTCCAGA GTTCGAAGAG ATTCTTCTTC AAAACTGCCC
 501 GTTATACTGG CTCTCCCATT TTATAGACAA AACTGAATCT GTTGCTGGGG
 551 AAATCGGATT AAATAAAACA CAAAAAGTTT ATGGTTTACT TGGGCCCTTA
 601 GCGTTTCATA AAGGATATAC AACTATTTTC CACTCTTATA CACGCCCTCT
 651 ACTAACATTA ATCTCAGAAT CACAGTATAA GTTCCTATAT AGTAAAGCGT
 701 CTAAGAATCA ATGGGATTCT CCTTCTGTGA AAAAAACCTG CGAAGAAATA
 751 TTCAAGGAAC TCCCCCACAA TATGATTTTC CGGAAGGATG TTCAAGGAAT
 801 CTCACAATTC TTATTTCTTT TCTTTTCTCA TGGTATCACT TGGGAACAGG
 851 CTCAGATGAT TCAACTTATA AATCCTGATA ATTGGAAAAT GTTGTGTCAG
 901 TTTGATAAAG CAGGAGGCCA CTGTTCCATG GCAACATTTG GAGGCTTTTT
 951 GAATACTGAA ACAAATATGT TCGATCCAGT ATCCTCTAAC TATGAACCTA
1001 CAGTGAACTT CATGACGTGG AAAGAATTGA AGGTTTTACT AGAGAAAGTA
1051 AAAGAAAGTC CTATGCACCC AGCGAGTGCT CTTGTTCAGA AGATATGCGT
1101 AAATACAACG CACCATCAAA ATCTGTTAAA ACGATGGCAA TTTGTTCGTA
1151 ATACGAGTTC ACAATGGACA TCAAGCTTAC CTCAGTATGC TTTCCACGCC
1201 CAAACCTACA AACTAGAGAA AAAAATAGAA AGCAGTCTCC CTATACGATC
1251 TTCCCTATAA
```

The PSORT algorithm predicts inner membrane (0.7198).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 120A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 120B) and for FACS analysis.

These experiments show that cp6627 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 121

The following *C.pneumoniae* protein (PID 4376629) was expressed <SEQ ID 241; cp6629>:

```
  1 MSNITSPVIQ NNRSCNYYFE LKNSTTIHIV ISAILLCGAL IAFLCVAAPV
 51 SYILSGALLG LGLLIALIGV ILGIKKITPM ISSKEQVFPQ ELVNRIRAHY
101 PKFVSDFVSE AKPNLKDLIS FIDLLNQLHS EVGSSTNYNV SEELQQKIDT
151 FEGIARLKNE VRTASLKRLE SAASSRPLFP SLPKILQKVF PFFWLGEFIS
201 AGSKVVELHR VKKIGGSLEE DLSDYIKPEM LPTYWLIPLD FRPTNSSILN
251 LHTLVLARVL TRDVFQHLKY AALNGEWNLN HSDLNTMKQQ LFAKYHAAYQ
301 SYKHLSQPSL QEDEFYNLLL CIFKHRYSWK QMSLIKTVPA DLWENLCCLT
351 LDHTGRPQDM EFASLIGTLY TQGLIHKESE AFLSSLTLLS LDQFKTIRRQ
401 STNIAMFLEN LATHNSTFRS LPPITVHPLK RSVFSQPEED ESSLLIG*
```

The cp6629 nucleotide sequence <SEQ ID 242> is:

```
   1 ATGAGTAATA TAACCTCGCC AGTTATTCAA AATAATCGCT CTTGTAATTA
  51 TTATTTTGAA TTAAAGAATT CAACCACTAT TCATATTGTT ATCAGTGCCA
 101 TCTTACTCTG CGGAGCTTTG ATAGCTTTCT TGTGTGTAGC AGCTCCTGTT
 151 TCCTATATTC TAAGTGGCGC ATTGTTAGGA TTAGGATTAT TAATAGCCTT
 201 GATTGGTGTG ATTTTAGGAA TAAAAAAAAT CACGCCTATG ATTTCATCAA
 251 AAGAACAAGT ATTCCCCCAA GAACTCGTAA ATAGAATCAG GGCGCACTAT
 301 CCTAAATTTG TCTCTGATTT TGTTTCAGAA GCTAAACCAA ATCTTAAAGA
 351 TCTCATAAGT TTTATTGATC TTCTAAATCA ATTGCACTCT GAAGTTGGAT
 401 CATCTACAAA TTACAACGTA TCTGAAGAAC TACAACAGAA AATAGATACG
 451 TTCGAGGGTA TCGCACGCTT AAAAAATGAA GTCCGTACTG CTTCTCTTAA
 501 AAGACTTGAA AGCGCTGCTT CTTCCCGTCC CCTCTTCCCC TCTTTACCAA
 551 AAATCTTACA AAAGGTATTT CCATTTTTCT GGTTAGGAGA GTTTATTTCT
 601 GCAGGCAGCA AGGTTGTAGA GCTCCATCGA GTTAAGAAAA TTGGAGGCAG
 651 CCTCGAAGAA GACCTTAGTG ATTATATAAA ACCAGAGATG CTTCCTACCT
 701 ATTGGTTGAT TCCTTTAGAT TTTAGACCAA CAAATTCCTC TATTCTAAAT
 751 CTACACACAT TAGTTTTAGC TAGAGTCTTA ACTCGTGATG TTTTTCAACA
 801 TCTTAAGTAT GCAGCATTAA ATGGCGAGTG GAACCTGAAT CATAGTGATC
 851 TAAATACTAT GAAACAGCAG CTCTTTGCTA AATATCATGC GGCGTATCAA
 901 TCCTATAAAC ATCTATCTCA ACCCTCTCTT CAAGAGGATG AATTCTATAA
 951 CCTGCTCTTG TGTATTTTTA AGCATAGGTA CTCGTGGAAG CAGATGTCCT
1001 TAATAAAAAC AGTCCCGGCT GATTTATGGG AAAACCTCTG TTGCTTGACT
1051 TTAGACCATA CAGGACGACC CCAAGACATG GAATTTGCCT CTCTAATTGG
1101 TACTCTCTAC ACACAAGGCC TAATTCATAA AGAAAGCGAA GCATTTCTTT
1151 CTTCATTGAC ACTCCTTAGT TTAGATCAGT TTAAAACGAT CCGTCGTCAG
1201 TCAACCAATA TAGCGATGTT CCTTGAGAAT TTAGCAACTC ATAATTCCAC
1251 CTTTAGAAGC TTACCACCTA TAACAGTCCA TCCACTCAAG AGAAGCGTCT
1301 TCTCCCAACC TGAAGAAGAC GAGTCCTCCC TGCTGATAGG TTAG
```

The PSORT algorithm predicts inner membrane (0.5776).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 121A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 121B) and for FACS analysis.

These experiments show that cp6629 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 122

The following *C.pneumoniae* protein (PID 4376732) was expressed <SEQ ID 243; cp6732>:

```
  1 MEMMSPFQQP EQCHFDVVGS FLRPESLTRA RSDFEEGRIV YEQMRVVEDA
 51 AIRNLIKKQT EAGLIFFTDG EFRRYSWDFD FMWGFHGVDR RRDSNDPEIG
101 VYLKDKISVS KHPFIEHFEF VKTFEKGNAK AKQTIPSPSQ FFHEMIFAPN
151 LKNTRKFYPT NQELIDDIVF YYRQVIQDLY AAGCRNLQLD DCAWCRLLDI
201 RAPSWYGVDS HDRLQEILEQ FLWIHNLVMK DRPEDLFVSL HVCRGDYQAE
251 FFSRRAYDSI EEPLFAKTDV DSYHYYWALD DKYSGGAEPL AYVSGEKHVC
301 LGLISSNHSC IEDRDAVVSR IYEAASYIPL ERLSLSPQCG FASCEGDHRM
```

```
351  TEEEQWKKIA FVKEIAKEIW G*
```

The cp6732 nucleotide sequence <SEQ ID 244> is:

```
   1  ATGGAAATGA TGAGCCCATT CCAACAACCT GAGCAATGTC ATTTTGATGT
  51  TGTGGGAAGT TTCTTACGTC CTGAAAGTCT TACACGAGCA CGCTCTGATT
 101  TTGAAGAAGG AAGAATTGTC TATGAGCAGA TGCGAGTTGT CGAAGATGCT
 151  GCTATTCGTA ATCTCATAAA AAAGCAAACA GAAGCAGGTC TTATCTTTTT
 201  TACTGATGGG GAATTCCGTA GGTATAGTTG GGATTTCGAC TTTATGTGGG
 251  GATTCCATGG CGTGGATCGT CGCAGGGACT CTAATGACCC TGAAATTGGA
 301  GTGTATCTTA AAGATAAAAT CTCCGTATCA AAACATCCGT TTATAGAACA
 351  TTTCGAGTTT GTCAAAACTT TTGAGAAGGG AAATGCAAAA GCAAAACAAA
 401  CGATTCCTTC TCCATCACAA TTTTTCCATG AGATGATTTT TGCTCCTAAT
 451  CTGAAAAATA CTCGGAAGTT TTATCCTACG AATCAAGAGC TAATTGATGA
 501  TATTGTCTTT TATTATCGCC AAGTCATCCA AGATCTTTAT GCTGCAGGTT
 551  GTCGTAATTT GCAGTTGGAC GATTGTGCTT GGTGTCGCCT CTTGGATATA
 601  CGAGCGCCTT CTTGGTATGG TGTTGATTCT CATGACAGGT TGCAGGAAAT
 651  TTTAGAACAG TTTTTATGGA TCCATAATTT AGTGATGAAG GATAGACCCG
 701  AGGATCTTTT TGTAAGTCTG CATGTCTGTC GTGGTGATTA TCAGGCCGAG
 751  TTTTTCTCTA GACGAGCTTA TGATTCTATA GAGGAGCCTT TATTTGCTAA
 801  GACCGATGTG GATAGTTATC ACTATTATTG GGCTCTTGAT GATAAGTATT
 851  CAGGAGGTGC TGAGCCTTTA GCTTACGTCT CTGGAGAGAA ACACGTCTGC
 901  TTGGGATTGA TCTCCAGCAA CCATTCTTGT ATTGAAGATC GAGATGCTGT
 951  GGTTTCTCGT ATTTATGAAG CTGCGAGCTA CATTCCCTTA GAGAGACTTT
1001  CTTTGAGCCC GCAATGTGGG TTTGCTTCTT GTGAGGGAGA CCATAGAATG
1051  ACTGAAGAAG AACAGTGGAA GAAGATCGCC TTTGTGAAAG AGATTGCTAA
1101  AGAGATCTGG GGATAA
```

The PSORT algorithm predicts cytoplasm (0.2196).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 122A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 122B) and for FACS analysis.

These experiments show that cp6732 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 123

The following *C.pneumoniae* protein (PID 4376738) was expressed <SEQ ID 245; cp6738>:

```
  1  VWLRFLLLVS YDEKEKDVVV VCNHSEPNIL GLPPEAVSQL IEELSDEGYS
 51  YLNVVRCDLS GETTVQQRLL LNADEGRSMT VVISELPEGH PDIRNLQLAS
101  ERIFVSREKE AADAYASGCK VVAFDDEHLP WVSSHIAYAE EIREKQEQTM
151  QGSLTEEQLG ALLCNTVSTE KNLAFALDAV IKQSVWRFRN PDLFAYEREA
201  LEASVTDALV SYVSNLDMIP YTSSQGIVIE DSSIVRTSQE HTLIVNCAAF
251  DKLASQIEFL CPSDVLPISG KDPLISDDED EELNPKVSSA ADSKDKT*
```

The cp6738 nucleotide sequence <SEQ ID 246> is:

```
  1  GTGTGGCTGC GCTTTTTACT TTTAGTGTCC TATGATGAGA AGGAGAAAGA
 51  CGTAGTTGTC GTTTGTAATC ATTCTGAACC TAATATCCTC GGCCTGCCTC
101  CTGAAGCAGT CTCTCAGCTT ATTGAAGAGC TTAGCGATGA AGGCTATAGC
151  TATCTGAATG TAGTGCGTTG TGATCTCTCC GGGGAGACTA CGGTTCAACA
201  ACGTCTGCTA TTGAATGCCG ATGAAGGGAG ATCTATGACG GTGGTGATCT
251  CAGAGCTTCC TGAAGGGCAC CCCGATATTC GGAATTTGCA GTTGGCATCC
301  GAAAGAATTT TTGTTTCTCG TGAAAAAGAA GCTGCTGATG CCTATGCTTC
351  AGGATGTAAA GTGGTCGCTT TCGATGATGA GCATCTCCCT TGGGTCTCCA
401  GTCATATTGC CTACGCGGAG GAGATCAGAG AGAAACAAGA ACAAACAATG
451  CAAGGGTCTT TAACTGAAGA GCAGTTAGGA GCACTCCTCT GCAACACAGT
501  CTCCACAGAG AAAAATCTAG CCTTTGCTCT AGACGCCGTG ATAAAACAGT
551  CTGTGTGGAG ATTCCGCAAT CCGGATCTTT TTGCTTATGA GAGAGAAGCT
601  CTAGAGGCTT CAGTAACAGA TGCTTTAGTA TCTTACGTTT CAAATTTAGA
651  CATGATACCG TACACAAGTT CTCAGGGCAT AGTCATAGAA GATAGTAGTA
701  TCGTCCGTAC CTCTCAAGAG CATACACTCA TTGTGAACTG TGCAGCATTC
```

```
751  GATAAGTTAG CGAGCCAAAT AGAGTTCTTA TGCCCCAGTG ACGTGTTGCC
801  CATTTCTGGT AAAGACCCTT TGATTTCTGA TGATGAGGAT GAGGAACTGA
851  ATCCTAAAGT TTCATCTGCT GCAGACTCTA AAGATAAAAC CTAG
```

The PSORT algorithm predicts cytoplasm (0.1587).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 123A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 123B) and for FACS analysis.

These experiments show that cp6738 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 124

The following *C.pneumoniae* protein (PID 4376739) was expressed <SEQ ID 247; cp6739>:

```
  1  MTHCLHGWFS VVRHHFVQAF NFSRPLYSRI THFALGVIKA IPIVGHLVMG
 51  VDWLISHCFE RGVSHPGFPS DIAPILKVEK IAGRDHISRI ENQLKSLRKT
101  IEVEDLDKVH GQYQENPYAD MASSEVLKLD KGVHVSELGK AFSRVRNRIT
151  RSYSYAPTPQ LDSIAIVGID LVSPEEQENL VRLANEVIQL YPKSKTTLYL
201  LIDFNKEWVG DISSDKEKQL RSLGLHSEVQ CLSVLEPQGA EGEDTKHFDL
251  MVGCYGKDSY LREGKILQQA LGTSLGTVPW VNVMHTLPSR YRSRLSLPIN
301  TEKDKTELYK EISRTHHQLH TLGMGLGAQD SGLLLDRQRL HAPLSQGSHC
351  HSYLADLTHE ELKILLFSAF VDAKNISKKE LREVSLNFAN DTSVECGCAF
401  YF*
```

The cp6739 nucleotide sequence <SEQ ID 248> is:

```
   1  ATGACTCATT GCTTACATGG TTGGTTTTCT GTAGTTCGTC ATCACTTTGT
  51  GCAGGCGTTT AATTTCTCAC GTCCTTTATA TTCTCGAATT ACCCACTTCG
 101  CTTTAGGGGT GATTAAGGCC ATCCCCATTG TAGGGCATCT TGTTATGGGA
 151  GTCGATTGGT TGATCTCTCA TTGCTTCGAG AGGGGAGTCT CACACCCTGG
 201  GTTCCCTTCA GATATTGCTC CTATACTGAA AGTAGAAAAG ATCGCGGGCC
 251  GAGATCATAT TTCTAGAATC GAAAATCAGC TAAAGAGCCT TAGGAAAACT
 301  ATCGAGGTTG AAGATCTAGA TAAAGTCCAC GGGCAATATC AAGAGAATCC
 351  TTATGCAGAT ATGGCCTCTA GTGAGGTTCT TAAACTCGAT AAGGGAGTTC
 401  ATGTTAGCGA GCTTGGCAAA GCCTTTTCTA GAGTTCGCAA TCGCATCACC
 451  AGATCCTATA GTTATGCCCC TACTCCTCAG TTGGACTCTA TAGCTATTGT
 501  TGGTATAGAT CTCGTCAGTC CTGAAGAACA AGAGAATTTA GTACGCTTGG
 551  CGAATGAGGT CATTCAACTC TATCCCAAAT CAAAGACAAC TCTATATCTT
 601  CTTATCGATT TTAATAAGGA GTGGGTAGGG GATATCTCCT CTGATAAGGA
 651  AAAACAGCTC CGTTCTCTAG GTCTACATTC TGAAGTTCAG TGTCTTTCCG
 701  TCTTGGAACC TCAGGGTGCC GAGGGCGAAG ATACGAAACA CTTTGACCTT
 751  ATGGTCGGCT GTTATGGGAA GGATTCTTAC TTAAGGGAGG GTAAAATTTT
 801  ACAGCAGGCC CTAGGGACTT CGTTAGGTAC TGTTCCCTGG GTGAATGTTA
 851  TGCACACATT GCCATCTAGG TATAGATCTC GGCTTTCCTT ACCTATAAAT
 901  ACCGAAAAGG ATAAGACAGA GCTTTATAAA GAGATTTCTC GTACACACCA
 951  TCAGTTGCAT ACTTTGGGAA TGGGACTTGG AGCCCAGGAT TCAGGATTGC
1001  TCTTAGACCG GCAACGACTC CATGCTCCTT TATCTCAAGG GTCTCACTGC
1051  CATTCCTATC TTGCAGATCT CACCCATGAA GAGCTGAAAA TTTTGTTATT
1101  TTCAGCATTT GTGGATGCTA AGAACATAAG TAAGAAAGAG CTTCGTGAGG
1151  TATCTCTAAA TTTTGCTAAC GATACTTCCG TAGAGTGTGG CTGCGCTTTT
1201  TACTTTTAG
```

The PSORT algorithm predicts inner membrane (0.2190).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 124A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 124B) and for FACS analysis.

These experiments show that cp6739 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 125

The following *C.pneumoniae* protein (PID 4376741) was expressed <SEQ ID 249; cp6741>:

```
  1  MASCLSAWFS IVREHFYRAF DFSLPFCARI TEFVLGVIKG IPVVGHIIVG
 51  IEWLVSRYLE SFVTKPTFVS DVVSLLKTEK VAGRDHIARV VETLKRQRVA
101  VAPEDEDKVH GKIPVHPFGG IQPVEVLTLY PEVQDATLGL AFSKIRNRVR
151  QAYLQAPRPK LQKIYIIGND MNPFEVDDFL HLARLCNETQ RLYPDATISL
201  YLTASGGRNA MDKKNRKLLS DCELNPKIAC LDFNQGDVVK QATCDCWMVY
251  HGENDQGTLN QIQEELEKSG EETPWIHVGQ KPLSQSLWDF SPFSSLEMKG
301  DKEKALEYSE LEKEQLYSRL VYVGERSSVL SLGFGDSRSG ILMDPKRVHA
351  PLSEGHYCHS YLADLENPGL QKTILAAFLN PKELSSTILQ PISLNLILNS
401  KTYLRQHFGF FERMSRSDRN VVVVVCDSWW GTDWKEEPSF QHFIMELECR
451  GYSHFNIFAF RSNSMCVEER RILNESSQEK AFTMIFCEDS VSQGDIRCLH
501  LASEGMLCGK ECYAVDVYTS GCANFMMEEV LTLERESNLW NRKHGLWKRE
551  VRKQKQEAAL DQDESEIYVC NQLTAQQNFA CS*
```

The cp6741 nucleotide sequence <SEQ ID 250> is:

```
   1  ATGGCTTCTT GTTTATCTGC CTGGTTTTCT ATAGTTCGTG AGCACTTTTA
  51  TCGAGCCTTT GATTTTTCTT TGCCGTTTTG TGCTCGTATT ACGGAATTTG
 101  TATTAGGGGT CATCAAGGGG ATCCCTGTTG TGGGTCACAT TATTGTTGGG
 151  ATAGAGTGGC TCGTTTCTAG GTATTTAGAG AGTTTCGTGA CCAAGCCGAC
 201  ATTTGTCTCT GATGTGGTGA GTCTTCTGAA AACAGAGAAA GTTGCTGGTC
 251  GCGATCACAT TGCTCGTGTA GTGGAGACTT TGAAGAGGCA GAGAGTCGCT
 301  GTGGCTCCTG AAGATGAGGA TAAGGTCCAT GGGAAGATTC CTGTGCATCC
 351  TTTCGGGGGA ATCCAACCTG TAGAAGTTCT CACTCTCTAT CCCGAAGTTC
 401  AAGATGCAAC GTTAGGGCTT GCCTTCTCTA AAATTCGTAA TCGTGTAAGA
 451  CAGGCGTATT TGCAAGCTCC ACGGCCAAAA CTGCAGAAGA TTTACATCAT
 501  AGGAAACGAT ATGAATCCTT TTGAAGTTGA CGACTTCTTG CATCTAGCCC
 551  GTCTCTGTAA TGAAACTCAA AGACTCTATC CTGACGCTAC GATTTCTCTA
 601  TATCTAACAG CTTCTGGTGG TCGCAATGCT ATGGACAAAA AGAATCGGAA
 651  GTTACTTAGT GATTGCGAAC TAAACCCCAA GATTGCTTGT TTGGACTTTA
 701  ATCAGGGTGA TGTAGTCAAA CAAGCAACTT GTGACTGTTG GATGGTGTAT
 751  CATGGGGAGA ATGATCAAGG TACGTTGAAT CAGATTCAGG AAGAGTTAGA
 801  AAAGTCAGGG GAGGAAACCC CTTGGATTCA TGTGGGGCAA AAGCCTCTTT
 851  CACAATCCTT GTGGGATTTC TCTCCATTTT CATCTTTGGA GATGAAGGGA
 901  GATAAAGAGA AAGCTCTAGA GTACTCTGAA TTAGAAAAAG AACAGCTATA
 951  TTCTCGATTG GTATACGTAG GAGAGCGCTC TTCGGTTCTT AGTTTGGGGT
1001  TTGGAGATAG TCGGTCAGGG ATCTTGATGG ACCCAAAACG GGTGCATGCT
1051  CCCTTATCTG AAGGGCATTA TTGTCATTCC TACCTTGCAG ACTTAGAAAA
1101  TCCCGGGTTA CAAAAAACAA TTTTAGCGGC ATTTCTGAAT CCTAAGGAGT
1151  TGAGCAGTAC CATACTGCAA CCTATATCTC TAAATCTTAT CTTAAATAGC
1201  AAAACTTACT TAAGGCAGCA CTTTGGCTTT TTTGAGAGGA TGAGCAGAAG
1251  TGATCGCAAT GTGGTTGTCG TTGTATGTGA TTCTTGGTGG GGTACCGACT
1301  GGAAGGAGGA GCCAAGCTTC CAACACTTTA TTATGGAGCT AGAGTGTCGA
1351  GGGTATTCGC ACTTCAATAT TTTTGCCTTT AGATCTAATA GCATGTGTGT
1401  AGAAGAACGT AGGATCTTAA ATGAAAGTTC TCAAGAGAAA GCCTTTACCA
1451  TGATTTTCTG TGAGGATTCA GTATCTCAAG GAGATATCCG CTGTTTGCAT
1501  TTGGCGTCTG AAGGAATGCT TTGTGGTAAA GAGTGCTATG CTGTCGATGT
1551  CTATACGTCA GGATGCGCGA ACTTTATGAT GGAAGAAGTC TTAACTTTGG
1601  AGCGAGAATC TAATCTGTGG AATAGAAAGC ATGGTCTTTG GAAAAGAGAA
1651  GTTAGAAAAC AGAAACAAGA AGCTGCTTTG GATCAAGACG AGAGCGAGAT
1701  TTACGTTTGT AATCAGCTGA CGGCGCAACA GAACTTCGCT TGTTCTTGA
```

The PSORT algorithm predicts inner membrane (0.2869).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 125A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 125B) and for FACS analysis.

These experiments show that cp6741 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 126

The following *C.pneumoniae* protein (PID 4376742) was expressed <SEQ ID 251; cp6742>:

```
  1 LFVSNFIFFV VMPIPYISSW ISTVRQHFVK AFDFSRPFCS RVTNFALGVI
 51 KAIPIVGHIV MGMEWLVSSC VAGIITRSSF TSDVVQIVKT EKALGRDHIS
101 RVAEILQRER GTITPENQDK VHGKFPVCPF GRLKSEETLK LKPGEREGTL
151 DTVFSPIRTR VTRAYLQAPR PEIRTISIVG SKLKTPQDFS QFVSLANETQ
201 RLHPEALVCL YLTGLNRESQ MCDTTTAEKK QYLHNSGLDS RIQCKDSKED
251 DAGSPENPEL WIGYYSREQQ HNIDGQYIQQ CLGKSADPIP WIHVTEDTKD
301 FYYPPNFTSY SHTRQSTDPT SPPRLPESEG DKDSLYGQLS RSYHHEYMLG
351 LGLKPEDAGL LMDPDRIYAP LSQGHYCHSY LADIENEDLR TLVLSPFLDP
401 GNLSSEDLRP VAFNIARLPL ELDSLFFRLV AGQQEGRNIV TLAHGTPRPE
451 DLDPDSMNIL TRRLQMSGYS YLNIFSYKSR KMIVKERQFF GDRSEGKSFT
501 LILFEDPISA ADFRCLQLAA EGMVAKDLPS VADICASGCS CIQFSEMQSP
551 QAIEYRQWEA RVEDEAGEEA REPVIYSQDQ LSSMLTTQQN FVFSLDAVVK
601 QAIWRFRSKG LLTMERKALG EEFLTAIFSY LGSQERNENM GKRTTEEHEV
651 VISFEELDRM VQVLPAEVPA DSGNDPTRPV PNPDSNPDSS QNEGS*
```

The cp6742 nucleotide sequence <SEQ ID 252> is:

```
   1 TTGTTTGTTT CTAATTTTAT TTTTTTTGTT GTTATGCCAA TTCCCTATAT
  51 TTCTTCTTGG ATTTCTACCG TTCGACAGCA TTTTGTTAAG GCGTTTGATT
 101 TCTCTCGTCC CTTTTGTTCT AGGGTTACGA ATTTTGCTTT AGGGGTCATC
 151 AAGGCCATCC CTATTGTAGG ACATATTGTC ATGGGGATGG AGTGGTTAGT
 201 TTCTTCCTGT GTTGCCGGGA TTATTACTAG GTCCTCCTTT ACCTCAGATG
 251 TCGTTCAGAT TGTAAAGACT GAGAAGGCGT TAGGTCGAGA TCATATATCT
 301 CGAGTGGCGG AGATATTGCA AAGAGAAAGG GGGACCATAA CTCCTGAGAA
 351 TCAAGATAAG GTGCATGGGA AGTTTCCTGT CTGTCCTTTT GGTCGTTTAA
 401 AATCCGAGGA AACTTTAAAA CTTAAGCCGG GAGAAAGAGA GGGAACTTTA
 451 GATACTGTAT TTTCTCCGAT TCGCACGCGC GTGACTCGTG CGTACTTACA
 501 GGCCCCCCGA CCCGAAATAC GTACGATTTC TATTGTGGGT TCGAAACTTA
 551 AAACTCCTCA AGATTTCTCG CAATTTGTGA GTCTCGCGAA TGAAACGCAG
 601 AGACTGCATC CTGAAGCGTT AGTTTGTCTG TATTTGACAG GCTTGAATCG
 651 CGAATCTCAG ATGTGCGATA CAACTACTGC AGAGAAGAAG CAGTACCTAC
 701 ATAACTCAGG TCTCGACTCT AGAATCCAGT GCAAAGACAG TAAAGAAGAC
 751 GACGCTGGCT CTCCTGAAAA TCCCGAACTT TGGATTGGCT ATTATTCACG
 801 AGAGCAACAG CATAATATAG ACGGGCAGTA TATTCAGCAG TGTCTAGGGA
 851 AGAGTGCAGA TCCAATTCCT TGGATTCATG TTACTGAAGA CACAAAGGAT
 901 TTTTATTACC CACCAAACTT TACTTCATAC TCACATACAA GACAATCTAC
 951 AGACCCAACA TCGCCACCAA GACTCCCTGA AAGTGAGGGG GATAAGGATT
1001 CCTTGTACGG ACAACTGAGT CGATCGTATC ACCATGAGTA TATGCTTGGT
1051 TTGGGATTAA AACCAGAGGA TGCAGGACTC CTGATGGACC CGGATAGAAT
1101 CTATGCTCCT CTATCCCAAG GGCATTATTG TCATTCCTAC CTTGCGGATA
1151 TAGAAAATGA GGATCTACGA ACTTTAGTCC TTTCGCCTTT CCTAGATCCT
1201 GGCAATCTTA GTAGCGAGGA TCTTCGTCCT GTAGCATTCA ATATCGCTAG
1251 ATTGCCATTA GAATTGGACT CGTTATTTTT CCGCCTTGTT GCGGGTCAGC
1301 AAGAAGGGAG AAACATAGTT ACCCTTGCCC ACGGAACTCC TCGTCCAGAA
1351 GATCTTGATC CTGACTCAAT GAACATTCTG ACCAGAAGAT TACAAATGTC
1401 TGGATATAGC TATTTGAACA TTTTCTCCTA TAAATCACGG AAAATGATTG
1451 TAAAAGAACG TCAGTTCTTT GGAGATCGTT CTGAAGGGAA GTCTTTCACA
1501 TTGATCTTAT TTGAGGATCC CATTAGTGCA GCAGATTTCC GTTGTTTGCA
1551 GCTAGCTGCA GAAGGTATGG TTGCTAAGGA TCTCCCCAGC GTAGCAGATA
1601 TTTGTGCCTC TGGATGTTCC TGCATTCAGT TTTCTGAGAT GCAGAGTCCT
1651 CAGGCTATTG AATATAGACA ATGGGAGGCA CGTGTCGAAG ATGAAGCAGG
1701 AGAAGAAGCC AGAGAACCAG TAATTTATTC TCAGGATCAA TTGAGCAGCA
1751 TGCTCACTAC ACAACAGAAT TTTGTATTTT CTCTAGATGC TGTGGTAAAA
1801 CAGGCGATCT GGAGATTCCG TTCGAAAGGT CTTCTTACTA TGGAAAGAAA
1851 GGCACTAGGC GAGGAGTTCT TAACTGCGAT ATTTTCCTAT TTAGGGAGTC
1901 AGGAGCGTAA TGAGAATATG GGGAAAAGAA CTACCGAAGA ACATGAGGTC
1951 GTTATCAGCT TCGAAGAGCT AGATCGCATG GTGCAAGTCC TCCCAGCCGA
2001 AGTCCCTGCA GATTCAGGCA ATGATCCTAC GCGTCCCGTT CCTAATCCAG
2051 ATAGTAACCC TGATTCCTCG CAAAATGAAG GCAGTTAG
```

The PSORT algorithm predicts inner membrane (0.2338).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 126A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 126B) and for FACS analysis.

These experiments show that cp6742 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 127

The following *C.pneumoniae* protein (PID 4376744) was expressed <SEQ ID 253; cp6744>:

```
  1 VIQHLLNFAL EETPSISVQY QEQEKLSPCD HSPEIGKKKR WNKLESFSTY
 51 CSLFMSVKDH YKLNLGIQNS LSGWLLDPYR VCAPLSSPYS CPSYLLDLQN
101 KELRRSLLST FLDPKNLTSE TFRSVSINFG NSSFGQRWSE FLSRVLHDEK
151 EKHVAVVCND AKLLEEGLSP EALSLLEEDL RESGYSYLNI LSVSPEGVSK
201 VQERQILRRD LQGRSFTVMI TDLPLGSEDI RSLQLASDRI LVSSSLDAAD
251 ACASGCKVLV YENPNASWAQ ELENFYKQVE RRR*
```

The cp6744 nucleotide sequence <SEQ ID 254> is:

```
  1 GTGATACAAC ATCTTCTAAA CTTTGCTCTA GAAGAGACCC CTTCCATTTC
 51 CGTGCAATAC CAAGAACAAG AGAAGCTCTC TCCGTGCGAT CATTCCCCAG
101 AAATAGGTAA AAAGAAAAGA TGGAATAAGC TGGAATCCTT CTCCACGTAT
151 TGTTCTCTGT TTATGTCTGT TAAGGATCAT TATAAGCTGA ATCTAGGAAT
201 TCAGAATTCC CTGTCAGGGT GGCTTCTGGA TCCCTATAGG GTTTGCGCGC
251 CTTTATCTTC ACCGTACTCG TGTCCTTCCT ATCTTTTAGA TTTGCAAAAC
301 AAAGAGCTAC GTCGTTCCCT TCTGTCAACG TTTCTAGACC CTAAAAATCT
351 CACTAGCGAA ACATTCCGTT CTGTCTCTAT AAACTTTGGC AACTCTTCGT
401 TTGGACAGAG ATGGTCAGAG TTTCTATCTC GTGTTCTGCA CGACGAGAAA
451 GAAAAGCACG TAGCTGTTGT TTGTAATGAT GCAAAACTTC TGGAAGAAGG
501 ATTGTCCCCA GAGGCATTGT CTCTATTAGA AGAAGACTTA AGAGAATCAG
551 GGTATTCGTA TCTAAACATT CTCTCGGTGA GCCCCGAAGG AGTCTCCAAG
601 GTTCAGGAAC GTCAGATTCT AAGGCGAGAT CTCCAAGGAC GGTCCTTTAC
651 TGTCATGATT ACAGATCTTC CTTTAGGTAG CGAAGATATC CGTAGTTTAC
701 AATTAGCCTC GGATAGGATT TTAGTCTCCA GTTCTCTTGA TGCCGCGGAT
751 GCATGTGCTT CGGGATGTAA AGTCTTAGTC TACGAAAATC CAAATGCATC
801 CTGGGCTCAG GAATTGGAGA ACTTCTACAA ACAAGTTGAG AGAAGAAGGT
851 AG
```

The PSORT algorithm predicts cytoplasm (0.3833).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 127A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 127B) and for FACS analysis.

These experiments show that cp6744 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 128

The following *C.pneumoniae* protein (PID 4376745) was expressed <SEQ ID 255; cp6745>:

```
  1 VACPSISSWF TVVRQHFVNA FDFTHPVCSR ITNFALGIIK AIPVLGHIVM
 51 GIEWLISWIP RHTVRHGMFT SDVSSAIKVE QTRGHNCLAP LEAYLSSLRV
101 PISQEDLGKV HGRTPEDPFV DITPTEIVQL LPDEELSTVD EALQGVRSRL
151 TYAYRSVEKP MIQDLALVGF GLRDSADLIN FVRLANGVQN HYPHTKVKLY
201 LAKNLADVWD CEISEEEKGQ LRALGLDPKI ESISLTSAGL PSVPEVATVD
251 FMITCYGKDQ EVQDP*
```

The cp6745 nucleotide sequence <SEQ ID 256> is:

```
  1 GTGGCTTGTC CAAGTATTTC TTCTTGGTTT ACTGTCGTTC GACAGCATTT
 51 TGTAAACGCC TTTGATTTCA CCCATCCCGT TTGTTCTCGG ATTACAAATT
101 TTGCTTTGGG GATCATTAAG GCAATTCCCG TATTAGGACA CATTGTCATG
151 GGAATCGAGT GGTTGATTTC CTGGATTCCC AGACACACCG TTCGTCATGG
201 AATGTTTACT TCTGATGTCT CTAGTGCTAT TAAAGTAGAA CAAACACGGG
251 GTCATAATTG TTTAGCTCCC CTAGAAGCCT ATTTAAGTAG CTTGAGAGTC
301 CCCATTTCCC AAGAAGATCT AGGCAAAGTA CACGGGAGAA CCCCAGAAGA
351 TCCCTTCGTA GATATCACAC CCACAGAAAT TGTCCAACTT CTCCCTGATG
401 AAGAACTCTC TACTGTAGAT GAGGCACTGC AAGGCGTTCG TAGTAGGTTA
451 ACCTATGCCT ATAGGTCCGT AGAGAAACCT ATGATTCAAG ATCTTGCTCT
501 TGTGGGTTTT GGTCTCCGAG ATTCTGCGGA CCTCATAAAT TTCGTGCGTC
551 TTGCTAATGG CGTGCAGAAT CACTATCCCC ATACTAAAGT GAAGCTCTAT
601 TTAGCGAAGA ACTTGGCAGA TGTCTGGGAC TGTGAAATTT CTGAAGAGGA
651 AAAAGGGCAA CTCCGAGCTC TAGGTTTAGA CCCTAAAATA GAGAGTATAT
701 CCCTTACGAG TGCAGGTCTT CCTTCAGTGC CAGAAGTCGC TACTGTCGAT
751 TTTATGATTA CCTGTTACGG GAAAGATCAG GAAGTCCAAG ATCCCTAG
```

The PSORT algorithm predicts inner membrane (0.2253).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 128A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 128B) and for FACS analysis.

These experiments show that cp6745 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 129

The following *C.pneumoniae* protein (PID 4376747) was expressed <SEQ ID 257; cp6747>:

```
  1 MMKQGVGQDA KELYTFLSRG NEHYQPCLWF SLEEELGFLF DEKMLCAPLS
 51 EDHYCHSYLV DLVDQHLKDL ILSMFLDPQN ISAGELLKVS INVGDSFSPL
101 QQKDFLSMVL RDETGKNVVV VFKGVLSLPA TQVCKLVEEL NSKDYSYLNI
151 FSCHGDSSPQ LLFRKELEGT SGRYFTVICA LYLGDTDMRS LQLASERIMV
201 SREFDLVDAY AARCKLLKID HTNWRPGTFS RHADFADAVD VSAGFNSREF
251 KLITQANQGI LESGELPLPS KTFWEGFLAF CDRVTVTRHF IPMLDAAIKQ
301 AVWTHKHPSL IDKECEALDL KTQCLPSIVS YLEYVTNSHE KTSKGPFIQK
351 EIIADCSPLK EALFPGSDED VPSTSEDPSD DHPSDLEDS*
```

The cp6747 nucleotide sequence <SEQ ID 258> is:

```
   1 ATGATGAAAC AAGGAGTCGG GCAGGATGCT AAAGAGCTAT ACACATTTCT
  51 ATCTCGTGGG AATGAGCATT ACCAACCGTG TCTATGGTTC AGTCTCGAAG
 101 AGGAACTCGG ATTCCTTTTC GATGAAAAAA TGCTCTGCGC CCCTCTATCT
 151 GAGGATCACT ATTGCCACTC GTATCTTGTA GATCTAGTGG ATCAACATTT
 201 AAAGGATTTA ATATTATCGA TGTTTTTAGA TCCTCAGAAT ATCTCAGCAG
 251 GAGAACTCCT CAAGGTCTCT ATAAACGTTG GAGATTCTTT TTCTCCTCTA
 301 CAACAGAAAG ATTTCCTCTC GATGGTCTTA CGTGATGAAA CGGGAAAAAA
 351 CGTCGTCGTG GTTTTTAAAG GAGTTCTCTC CTTACCCGCA ACCCAAGTCT
 401 GCAAATTAGT AGAGGAATTG AACTCTAAGG ACTACTCCTA CCTCAATATA
 451 TTTTCTTGTC ACGGAGATAG TAGTCCTCAG CTTTTATTCC GTAAGGAATT
 501 AGAGGGAACT TCAGGGCGTT ATTTTACAGT GATTTGCGCT TTATATCTAG
 551 GGGATACAGA CATGCGTAGT TTACAACTTG CTTCTGAAAG GATCATGGTC
 601 TCTAGAGAGT TTGATCTTGT AGATGCCTAT GCTGCAAGAT GCAAGCTCTT
 651 GAAAATCGAT CATACAAATT GGAGACCTGG AACTTTCAGT CGCCACGCCG
 701 ATTTCGCAGA TGCTGTAGAC GTATCAGCAG GATTTAACTC AAGAGAATTT
 751 AAACTGATTA CGCAGGCGAA TCAAGGGATC CTAGAGTCTG GAGAACTCCC
 801 GCTCCCTTCA AAAACCTTCT GGGAAGGATT CTTAGCATTC TGTGATCGAG
 851 TGACTGTCAC GAGACACTTC ATTCCAATGT TAGACGCCGC TATAAAGCAA
 901 GCGGTATGGA CTCATAAACA TCCCAGCTTG ATAGATAAAG AGTGTGAAGC
 951 CCTAGACTTG AAAACACAGT GCTTGCCATC TATCGTATCG TACCTTGAAT
1001 ATGTCACAAA CTCTCACGAA AAAACATCGA AAGGCCCGTT CATACAAAAA
1051 GAGATTATCG CAGACTGTTC TCCTCTTAAA GAGGCGCTCT TCCCAGGTTC
```

```
1101  TGATGAAGAT GTTCCCTCTA CCTCTGAGGA TCCTTCAGAT GATCATCCTT
1151  CGGATCTTGA AGACTCTTAA
```

The PSORT algorithm predicts inner membrane (0.1447).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 129A) and also as a his-tagged produet. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 129B) and for FACS analysis.

These experiments show that cp6747 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 130

The following *C.pneumoniae* protein (PID 4376756) was expressed <SEQ ID 259; cp6756>:

```
  1  MASGIGGSSG LGKIPPKDNG DRSRSPSPKG ELGSHEISLP PQEHGEEGAS
 51  GSSHIHSSSS FLPEDQESQS SSSAASSPGF FSRVRSGVDR ALKSFGNFFS
101  AESTSQARET RQAFVRLSKT ITADERRDVD SSSAAATEAR VAEDASVSGE
151  NPSQGVPETS SGPEPQRLFS LPSVKKQSGL GRLVQTVRDR IVLPSGAPPT
201  DSEPLSLYEL NLRLSSLRQE LSDIQSNDQL TPEEKAEATV TIQQLIQITE
251  FQCGYMEATQ SSVSLAEARF KGVETSDEIN SLCSELTDPE LQELMSDGDS
301  LQNLLDETAD DLEAALSHTR LSFSLDDNPT PIDNNPTLIS QEEPIYEEIG
351  GAADPQRTRE NWSTRLWNQI REALVSLLGM ILSILGSILH RLRIARHAAA
401  EAVGRCCTCR GEECTSSEED SMSVGSPSEI DETERTGSPH DVPRRNGSPR
451  EDSPLMNALV GWAHKHGAKT KESSESSTPE ISISAPIVRG WSQDSSVSFI
501  VMEDDHIFYD VPRRKDGIYD VPSSPRWSPA RELEEDVFGD YEVPITSAEP
551  SKDKNIYMTP RLATPAIYDL PSRPGSSGSS RSPSSDRVRS SSPNRRGVPL
601  PPVPSPAMSE EGSIYEDMSG ASGAGESDYE DMSRSPSPRG DLDEPIYANT
651  PEDNPFTQRN IDRILQERSG GASASPVEPI YDEIPWIHGR PPATLPRPEN
701  TLTNVSLRVS PGFGPEVRAA LLSESVSAVM VEAESIVPPT EPGDGESEYL
751  EPLGGLVATT KILLQKGWPR GESNA*
```

The cp6756 nucleotide sequence <SEQ ID 260> is:

```
   1  ATGGCATCAG GAATCGGAGG ATCTAGTGGA TTAGGAAAGA TTCCACCTAA
  51  AGATAATGGG GATAGAAGTC GATCGCCCTC TCCTAAGGGA GAACTTGGCA
 101  GCCACGAGAT TTCCCTGCCT CCTCAAGAAC ATGGAGAGGA AGGAGCTTCA
 151  GGATCTTCGC ATATACATAG CAGTTCCTCT TTTCTACCAG AAGATCAGGA
 201  GTCTCAGAGC TCTTCTTCGG CAGCTTCTAG CCCGGGATTT TTTTCTCGCG
 251  TACGTTCTGG GGTAGACAGG GCCTTAAAAT CATTTGGCAA CTTTTTTTCC
 301  GCAGAGTCTA CGAGTCAAGC GCGTGAAACG CGACAAGCTT TTGTTAGATT
 351  ATCAAAAACC ATCACCGCGG ATGAGAGACG GGATGTCGAT TCATCAAGTG
 401  CTGCTGCTAC AGAAGCCCGA GTGGCAGAGG ACGCGAGTGT TTCAGGCGAA
 451  AATCCTTCTC AGGGGGTTCC AGAAACCTCT TCTGGACCAG AACCTCAGCG
 501  TTTATTTTCT CTTCCTTCAG TAAAAAAACA GAGCGGTTTG GGTCGGTTGG
 551  TACAGACAGT TCGCGATCGC ATAGTACTTC CTAGTGGGGC TCCACCTACA
 601  GACAGCGAGC CTTTAAGTCT CTACGAGCTA AACCTCCGTT TGAGTAGTTT
 651  ACGTCAGGAG CTCTCTGACA TACAAAGTAA TGATCAGTTG ACTCCAGAGG
 701  AAAAAGCAGA AGCCACAGTT ACCATACAAC AGCTGATCCA AATTACAGAA
 751  TTCCAATGCG GCTATATGGA GGCAACACAA TCTTCGGTAT CTCTAGCAGA
 801  AGCTCGTTTT AAGGGGGTAG AAACTAGTGA TGAGATCAAT TCCCTCTGTT
 851  CAGAACTGAC AGATCCTGAG CTTCAAGAAC TCATGAGTGA TGGAGACTCT
 901  CTTCAAAACC TATTAGATGA GACTGCCGAC GATTTAGAAG CTGCTTTGTC
 951  CCATACTCGA TTGAGTTTTT CTTTAGACGA TAATCCAACT CCGATAGACA
1001  ATAATCCAAC TCTGATTTCT CAAGAAGAGC CTATTTATGA GGAAATCGGA
1051  GGAGCTGCAG ATCCTCAAAG AACTCGGGAA AACTGGTCTA CAAGATTATG
1101  GAATCAGATT CGCGAGGCTC TGGTTTCTCT TTTAGGAATG ATTTTAAGCA
1151  TTCTAGGGTC CATCTTGCAC AGGTTGCGTA TTGCTCGTCA TGCAGCTGCT
1201  GAAGCAGTGG GTCGTTGTTG CACGTGCCGA GGAGAAGAGT GTACTTCTTC
1251  TGAAGAGGAC TCGATGTCGG TGGGGTCTCC TTCAGAAATT GATGAAACTG
1301  AAAGAACGGG CTCTCCGCAT GACGTTCCAC GCAGAAATGG AAGTCCACGT
1351  GAAGATTCTC CATTGATGAA TGCCTTAGTA GGATGGGCAC ATAAGCACGG
1401  TGCTAAAACC AAGGAGAGTT CAGAATCAAG TACCCCGGAA ATTTCGATTT
1451  CTGCTCCCAT AGTGAGAGGT TGGAGTCAAG ACAGTTCCGT CAGTTTTATT
```

```
1501  GTTATGGAAG ATGATCATAT TTTCTATGAT GTTCCTCGTA GAAAAGATGG
1551  AATCTATGAC GTTCCTAGTT CCCCTAGATG GAGTCCTGCG CGAGAGTTGG
1601  AAGAGGATGT TTTTGGAGAT TATGAAGTTC CTATAACCTC TGCTGAACCA
1651  TCTAAAGACA AGAACATCTA CATGACACCT AGATTAGCAA CTCCTGCTAT
1701  CTATGATCTT CCTTCACGTC CAGGATCGTC TGGAAGCTCA CGTTCTCCGT
1751  CTTCAGATCG CGTACGAAGC AGCTCACCAA ATAGACGGGG TGTGCCTCTT
1801  CCTCCAGTTC CTTCACCTGC TATGAGTGAG GAGGGGAGCA TTTATGAGGA
1851  TATGAGCGGT GCTTCAGGTG CAGGTGAAAG TGATTATGAA GATATGAGCC
1901  GTTCCCCCTC TCCTAGAGGC GACTTGGATG AACCCATATA TGCTAATACT
1951  CCTGAAGATA ATCCATTTAC TCAGAGAAAT ATAGATAGAA TTTTACAGGA
2001  GAGGTCAGGC GGTGCTTCCG CTTCTCCTGT AGAGCCTATT TATGATGAGA
2051  TCCCATGGAT TCATGGCAGG CCCCCTGCTA CACTTCCAAG ACCCGAGAAT
2101  ACATTGACTA ATGTTTCGCT TAGAGTGAGC CCAGGGTTTG GACCAGAAGT
2151  AAGAGCCGCT TTGCTTAGCG AGAGCGTGAG TGCTGTTATG GTCGAAGCAG
2201  AGAGTATTGT TCCTCCAACA GAGCCGGGGG ACGGAGAATC AGAATATCTA
2251  GAGCCCTTAG GGGGACTTGT AGCTACAACG AAAATCTTAC TACAAAAAGG
2301  ATGGCCTCGT GGAGAGTCGA ATGCTTAG
```

The PSORT algorithm predicts inner membrane (0.3994).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 130A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 130B) and for FACS analysis.

These experiments show that cp6756 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 131

The following *C.pneumoniae* protein (PID 4376761) was expressed <SEQ ID 261; cp6761>:

```
  1  MTVAEVKGTF KLVCLGCRVN QYEVQAYRDQ LTILGYQEVL DSEIPADLCI
 51  INTCAVTASA ESSGRHAVRQ LCRQNPTAHI VVTGCLGESD KEFFASLDRQ
101  CTLVSNKEKS RLIEKIFSYD TTFPEFKIHS FEGKSRAFIK VQDGCNSFCS
151  YCIIPYLRGR SVSRPAEKIL AEIAGVVDQG YREVVIAGIN VGDYCDGERS
201  LASLIEQVDR IPGIERIRIS SIDPDDITED LHRAITSSRH TCPSSHLVLQ
251  SGSNSILKRM NRKYSRGDFL DCVEKFRASD PRYAFTTDVI VGFPGESDQD
301  FEDTLRIIED VGFIKVHSFP FSARRRTKAY TFDNQIPNQV IYERKKYLAE
351  VAKRVGQKEM MKRLGETTEV LVEKVTGQVA TGHSPYFEKV SFPVVGTVAI
401  NTLVSVRLDR VEEEGLIGEI V*
```

The cp6761 nucleotide sequence <SEQ ID 262> is:

```
   1  ATGACGGTTG CGGAAGTCAA AGGAACATTT AAGCTGGTCT GTTTAGGCTG
  51  TCGGGTGAAT CAGTATGAGG TCCAAGCATA TCGCGACCAG TTGACTATCT
 101  TAGGTTACCA AGAGGTCCTG GATTCTGAAA TCCCTGCAGA TTTATGCATA
 151  ATCAATACGT GTGCTGTCAC AGCTTCTGCT GAGAGTTCGG GTCGTCATGC
 201  TGTGCGTCAG TTATGTCGTC AGAACCCTAC AGCACATATT GTTGTCACAG
 251  GTTGTTTGGG GGAATCTGAC AAAGAGTTTT TTGCTTCTTT GGATCGGCAA
 301  TGCACACTTG TTTCCAATAA AGAAAAATCC CGACTTATAG AAAAAATTTT
 351  TTCCTATGAT ACGACCTTCC CTGAGTTCAA GATCCATAGT TTTGAGGGAA
 401  AGTCTCGAGC TTTTATTAAA GTTCAAGATG GCTGTAATTC TTTTTGCTCG
 451  TACTGCATTA TTCCTTATTT GCGGGGGCGT TCGGTTTCTC GTCCTGCTGA
 501  GAAGATTTTA GCTGAAATCG CAGGGGTTGT AGACCAAGGA TATCGCGAAG
 551  TTGTAATTGC AGGAATTAAT GTTGGAGATT ATTGCGATGG AGAGCGTTCA
 601  TTAGCCTCTT TGATTGAACA GGTGGACCGG ATTCCTGGAA TTGAGAGGAT
 651  TCGAATTTCC TCTATAGATC CTGATGATAT CACTGAAGAT CTGCACCGTG
 701  CCATCACCTC ATCGCGTCAC ACTTGTCCTT CGTCACACCT TGTTCTTCAA
 751  TCGGGGTCGA ATTCAATTTT AAAGAGAATG AACCGGAAGT ATTCTCGCGG
 801  AGATTTTTTA GATTGTGTAG AGAAGTTCCG TGCTTCTGAT CCTCGCTATG
 851  CCTTTACTAC AGATGTGATT GTCGGATTTC CTGGAGAGAG TGATCAAGAT
 901  TTTGAAGATA CTTTGAGAAT TATTGAAGAT GTAGGCTTTA TTAAAGTGCA
 951  TAGTTTCCCT TTCAGTGCTC GTCGTCGTAC TAAGGCATAT ACTTTTGATA
1001  ATCAGATTCC CAATCAGGTG ATCTATGAGA GGAAGAAGTA TCTTGCTGAG
1051  GTTGCTAAGA GGGTAGGCCA GAAAGAGATG ATGAAGCGTT TAGGAGAGAC
```

```
1101  TACAGAGGTG CTTGTTGAGA AAGTAACGGG GCAGGTTGCT ACGGGTCACT
1151  CTCCTTATTT TGAAAAGGTT TCTTTCCCTG TTGTAGGAAC GGTAGCTATC
1201  AACACTCTAG TTTCTGTGCG TCTTGATAGG GTAGAGGAAG AAGGGCTGAT
1251  TGGGGAGATT GTATGA
```

The PSORT algorithm predicts inner membrane (0.1574).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 131A) and also as a his-tagged product. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 131B) and for FACS analysis.

These experiments show that cp6761 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 132

The following *C.pneumoniae* protein (PID 4376766) was expressed <SEQ ID 263; cp6766>:

```
  1  MATSVPVTSS TSVGEANSSN ERFTERTSRM YYAALVLGAL SCLIFIAMIV
 51  IFPQVGLWAV VLGFALGCLL LSLAIVFAVS GLVLGKTLEP SREATPPEIV
101  AQKEWTTQQD VLGNEYWRSE LISLFLRGDL HESLIVDSKD RSLDIDQSLQ
151  NILKLEPLST TLSLLKKDCV HINIILHLVR QWNLLGVDLS PEVTAHAEEL
201  LLFLIEEQYY SPDILKLIRY GDALQATSPL MDWADSGSFS VDADGVFSCR
251  REECSPEDAL AQFDLLLALE NPDRRFLKDS FLTYIWSSSF FEKFLHRHLE
301  SLQRKLPETA IDVARYEAQI QTFLSRYFQK LDLINAMSLD WGYNCAEGEK
351  CYESANQRLD NLFIAFSSSV PAMKRLFDKY GSVVRVDRRQ IREQILSNTE
401  ILENESGFLC SLYEYPLSYL IDWAVLLDCV RGTEISLEDQ ADYTVCLQGL
451  DSMLSQFASR LQSGQKVLNP RDVLSEQAAV MLVHGLAAQG VSFQGLKALM
501  YLTAVPQRMW LGALPLFESF PVFNRMKEFL GESLGD*
```

The cp6766 nucleotide sequence <SEQ ID 264> is:

```
   1  ATGGCAACCT CTGTTCCTGT AACTTCATCT ACTTCTGTAG GAGAGGCTAA
  51  CTCCTCCAAC GAAAGATTTA CTGAACGAAC ATCGCGAATG TATTACGCAG
 101  CTTTAGTCCT AGGGGCTTTG AGCTGTTTAA TTTTTATTGC TATGATTGTC
 151  ATTTTCCCAC AGGTCGGATT GTGGGCTGTG GTCCTCGGGT TTGCTCTTGG
 201  ATGTTTACTT TTAAGCTTAG CTATCGTTTT TGCTGTCTCC GGTCTCGTTT
 251  TAGGCAAGAC TTTAGAACCT AGTCGAGAAG CGACTCCTCC AGAAATTGTT
 301  GCGCAAAAGG AGTGGACTAC ACAACAAGAT GTCTTAGGGA ATGAGTATTG
 351  GCGTTCCGAG TTGATTTCCT TGTTCTTACG AGGGGATCTC CACGAATCTC
 401  TGATTGTTGA TTCTAAGGAT CGATCTTTAG ATATTGATCA GAGTTTACAA
 451  AATATATTGA AACTTGAGCC CCTATCTACG ACACTTTCGC TGTTAAAGAA
 501  AGATTGTGTC CACATCAATA TCATTTTACA TTTAGTGAGA CAGTGGAACT
 551  TACTGGGAGT GGATCTTAGT CCTGAAGTCA CTGCGCACGC CGAGGAACTT
 601  CTACTCTTTT TGATAGAAGA GCAGTATTAC TCTCCTGATA TTTTGAAATT
 651  GATTCGCTAC GGAGATGCTT TACAAGCAAC GTCTCCTTTG ATGGATTGGG
 701  CAGATTCAGG TTCCTTTAGT GTAGACGCAG ACGGGGTATT TAGCTGTCGC
 751  AGAGAAGAAT GTTCTCCTGA GGATGCTTTG GCGCAATTCG ATCTTCTTTT
 801  GGCGTTGGAA AATCCCGACA GACGCTTCTT AAAGGATTCT TTTCTTACCT
 851  ACATTTGGTC GTCTTCATTT TTTGAGAAGT TTTTACATCG CCATCTAGAG
 901  AGCTTGCAAA GAAAGCTCCC AGAGACAGCG ATCGATGTCG CCCGCTATGA
 951  AGCACAAATA CAAACATTTC TCTCTCGCTA TTTTCAGAAG CTCGATTTGA
1001  TAAACGCAAT GTCCTTAGAT TGGGGATATA ACTGTGCTGA GGGAGAAAAA
1051  TGTTATGAGA GCGCAAATCA AAGATTAGAC AACCTATTTA TTGCTTTTTC
1101  TTCTTCTGTT CCTGCTATGA AGCGGCTCTT TGACAAATAT GGTTCTGTGG
1151  TACGGGTAGA TCGTAGGCAG ATTCGTGAGC AGATTCTTTC GAACACTGAA
1201  ATCTTAGAAA ATGAGTCAGG GTTCCTCTGC AGTTTGTATG AATATCCTTT
1251  ATCCTATTTG ATAGATTGGG CTGTTTTGCT AGACTGTGTT CGCGGTACCG
1301  AAATCTCTCT AGAAGATCAG GCCGATTACA CCGTTTGTTT GCAAGGCTTG
1351  GATTCTATGT TATCTCAATT TGCGAGTCGT TTACAGTCTG GACAAAAAGT
1401  ATTGAATCCT AGAGATGTTT TAAGTGAACA GGCTGCGGTT ATGCTTGTTC
1451  ATGGCTTGGC AGCACAGGGC GTGTCGTTTC AAGGATTGAA AGCTTTGATG
1501  TATTTGACAG CCGTTCCCCA AAGAATGTGG TTAGGAGCAT TGCCTTTATT
1551  TGAATCTTTT CCTGTCTTTA ATCGGATGAA AGAATTTCTT GGGGAATCTC
1601  TGGGAGACTA G
```

The PSORT algorithm predicts inner membrane (0.6158).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 132A) and also as a his-tagged product. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 132B) and for FACS analysis.

These experiments show that cp6766 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 133

The following *C.pneumoniae* protein (PID 4376804) was expressed <SEQ ID 265; cp6804>:

```
  1 MSNQLQPCIS LGCVSYINSF PLSLQLIKRN DIRCVLAPPA DLLNLLIEGK
 51 LDVALTSSLG AISHNLGYVP GFGIAANQRI LSVNLYAAPT FFNSPQPRIA
101 ATLESRSSIG LLKVLCRHLW RIPTPHILRF ITTKVLRQTP ENYDGLLLIG
151 DAALQHPVLP GFVTYDLASG WYDLTKLPFV FALLLHSTSW KEHPLPNLAM
201 EEALQQFESS PEEVLKEAHQ HTGLPPSLLQ EYYALCQYRL GEEHYESFEK
251 FREYYGTLYQ QARL
```

The cp6804 nucleotide sequence <SEQ ID 266> is:

```
  1 ATGTCTAACC AACTCCAGCC ATGTATAAGC TTAGGCTGCG TAAGTTATAT
 51 TAATTCCTTT CCGCTGTCCC TACAACTCAT AAAAAGAAAC GATATTCGCT
101 GTGTTCTTGC TCCCCCTGCA GACCTCCTCA ACTTGCTAAT CGAAGGGAAA
151 CTCGATGTTG CTTTGACCTC ATCCCTAGGA GCTATCTCTC ATAACTTGGG
201 GTATGTCCCC GGCTTTGGAA TTGCAGCAAA CCAACGTATC CTCAGTGTAA
251 ACCTCTATGC AGCTCCCACT TTCTTTAACT CACCGCAACC TCGGATTGCC
301 GCAACTTTAG AAAGTCGCTC CTCTATAGGA CTCTTAAAAG TGCTTTGTCG
351 TCATCTCTGG CGCATCCCAA CTCCTCATAT CCTAAGATTC ATAACTACAA
401 AAGTACTCAG ACAAACCCCT GAAAATTATG ATGGCCTCCT CCTAATCGGA
451 GATGCAGCGC TACAACATCC TGTACTTCCT GGATTTGTAA CCTATGACCT
501 TGCCTCGGGG TGGTATGATC TTACAAAGCT ACCTTTTGTA TTTGCTCTTC
551 TTCTACACAG CACCTCTTGG AAAGAACATC CCCTACCCAA CCTTGCGATG
601 GAAGAAGCCC TCCAACAGTT CGAATCTTCA CCCGAAGAAG TCCTTAAAGA
651 AGCTCATCAA CATACAGGTC TGCCCCCTTC TCTTCTTCAA GAATACTATG
701 CCCTATGCCA GTACCGTCTA GGAGAAGAAC ACTACGAAAG CTTTGAAAAA
751 TTCCGGGAAT ATTATGGAAC CCTCTACCAA CAAGCCCGAC TGTAA
```

The PSORT algorithm predicts inner membrane (0.060).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 133A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 133B) and for FACS analysis.

These experiments show that cp6804 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 134

The following *C.pneumoniae* protein (PID 4376805) was expressed <SEQ ID 267; cp6805>:

```
  1 MSSLLSCGRI EPTRVTCSLK TYLEDTSQNQ LSTRLVRASV IFLCALLIIL
 51 VCVALSSLIP SIMALATSFT VMGLILFVMS LLGDVAIISY LTYSTVTSYR
101 QNKRAFEIHK PARSVYYEGV RHWDLGRSSL GTGEIPIVRT LFSPFQNHGL
151 NHALAAKIFL FMEHFSPEPP NEPLVDWACL IRDFRPHVSS LCFVIEKQGS
201 SLRTKEGNTI CEAFRSDYDA HFAMVDCYRL IHSKLIIEKM GLKNIDIIPS
251 VMVREDYPSR PGEGYREGLL RMYGGKGAL*
```

The cp6805 nucleotide sequence <SEQ ID 268> is:

```
   1  ATGTCATCAC TACTGAGCTG CGGAAGAATA GAGCCGACTC GGGTTACCTG
  51  TAGCTTAAAG ACGTATCTTG AGGATACGAG TCAGAATCAG TTGAGCACAC
 101  GTCTAGTTCG GGCAAGTGTC ATCTTTTTAT GCGCATTGTT GATCATTTTG
 151  GTTTGTGTGG CCCTCTCTAG TTTGATTCCA AGCATTATGG CCTTGGCGAC
 201  CTCTTTTACG GTAATGGGGT TAATTCTTTT TGTGATGTCA CTTCTTGGTG
 251  ACGTTGCAAT TATAAGTTAT CTTACTTATA GCACTGTTAC GAGTTACCGG
 301  CAAAATAAGA GAGCTTTTGA GATTCACAAG CCCGCTCGCT CCGTTTACTA
 351  CGAGGGGGTC CGCCATTGGG ATTTAGGACG ATCATCTTTA GGCACAGGCG
 401  AGATTCCTAT AGTAAGGACG TTATTCTCTC CATTTCAGAA CCATGGTCTT
 451  AACCATGCCT TAGCTGCTAA AATTTTCCTA TTTATGGAGC ATTTCAGCCC
 501  TGAGCCACCG AACGAGCCTT TGGTGGATTG GGCCTGTTTG ATTCGGGATT
 551  TTAGGCCTCA CGTCAGTTCT TTGTGCTTTG TTATTGAAAA ACAAGGGTCA
 601  TCGCTGAGGA CTAAGGAAGG CAATACGATT TGTGAGGCTT TCCGCTCTGA
 651  TTACGACGCC CATTTTGCTA TGGTAGATTG CTACCGGTTG ATCCACTCTA
 701  AGTTGATTAT AGAGAAAATG GGATTGAAGA ATATCGATAT CATTCCGAGT
 751  GTCATGGTTC GTGAAGATTA TCCTAGCCGT CCTGGGGAGG GCTATCGCGA
 801  AGGCCTATTA CGTATGTATG GTGGCAAGGG GGCTCTGTGA
```

The PSORT algorithm predicts inner membrane (0.711).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 134A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 134B) and for FACS analysis.

These experiments show that cp6805 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 135

The following *C.pneumoniae* protein (PID 4376813) was expressed <SEQ ID 269; cp6813>:

```
   1  MSGPSRTESS QVSVLSYVPR DKEIAPKKQF TIAKISTLAI LASLALGALV
  51  AGISLTIVLG NPVFLALLIT TALFSVVTFL VYHQMTSKVS SNWQKVLEQN
 101  FKPLGKAWQE KNVDCYSNEM QFYNNHLNPK FKVAIQTDAS QPFQPTFLTG
 151  LRVIEKNQST GIIFNPVGPT NLIDNTATNL STILYSTLKD KSVWDTCKQR
 201  EGGPAKGEDP FSPTEVRVVK LPNEALDQTF NLNLSSAEKK SILPTFLGHV
 251  CGPKSEELPN QQEYYRQALL AYENCLKAAI ESHAAIVALP LFTSVYEVPP
 301  EEILPKEGTF YWDNQTQAFC KRALLDAIQN TALRYPQRSL LVILQDPFNT
 351  IESQSRSEE*
```

The cp6813 nucleotide sequence <SEQ ID 270> is:

```
   1  ATGTCAGGAC CCTCACGTAC TGAGAGCTCT CAAGTTTCTG TACTATCCTA
  51  TGTGCCTCGG GATAAAGAAA TTGCTCCTAA AAAACAGTTT ACCATAGCAA
 101  AAATATCCAC TCTTGCAATC CTAGCTTCTT TAGCTTTAGG AGCTTTGGTG
 151  GCTGGAATCT CTTTAACGAT AGTATTAGGG AACCCTGTAT TTTTGGCTCT
 201  TCTCATTACC ACGGCCCTCT TCTCAGTTGT AACCTTCTTA GTCTACCACC
 251  AAATGACCTC AAAGGTATCT TCTAACTGGC AGAAAGTTCT AGAGCAAAAC
 301  TTCAAGCCTT TGGGAAAAGC GTGGCAAGAA AAAAACGTAG ACTGCTACTC
 351  AAACGAGATG CAATTTTACA ATAATCACCT GAACCCTAAG TTCAAGGTAG
 401  CGATACAAAC AGATGCGTCT CAACCATTTC AGCCTACTTT CTTAACTGGA
 451  CTTAGAGTGA TCGAAAAAAA TCAATCCACA GGGATCATCT TTAATCCCGT
 501  AGGCCCAACG AATCTGATCG ACAACACTGC AACGAACCTC TCTACTATCC
 551  TTTACTCCAC CCTAAAAGAT AAAAGCGTGT GGGATACATG CAAGCAACGC
 601  GAAGGGGGTC CCGCAAAAGG AGAAGACCCC TTTTCCCCTA CCGAAGTGAG
 651  AGTAGTAAAA CTTCCAAACG AAGCTCTAGA TCAAACGTTT AATCTAAATT
 701  TAAGCTCTGC AGAAAAGAAA AGTATTCTTC CGACCTTTTT AGGCCACGTA
 751  TGCGGCCCCTA AATCTGAAGA GTTACCAAAT CAGCAAGAAT ATTATCGCCA
 801  AGCTTTACTA GCGTACGAGA ACTGCCTTAA AGCAGCTATA GAAAGTCATG
 851  CAGCAATCGT TGCTCTTCCT CTCTTTACTT CGGTCTATGA AGTGCCTCCA
 901  GAAGAGATTC TTCCTAAAGA AGGCACTTTC TATTGGGACA ACCAAACTCA
 951  AGCGTTTTGC AAACGCGCTT TATTGGACGC TATTCAAAAT ACGGCCCTAC
1001  GCTATCCTCA AAGATCTTTA CTTGTTATAC TCCAAGATCC TTTTAATACT
1051  ATAGAATCAC AAAGTCGTTC TGAGGAGTAA
```

The PSORT algorithm predicts inner membrane (0.4291).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 135A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 135B) and for FACS analysis.

These experiments show that cp6813 is a surface-exposed and immunoaceessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 136

The following *C.pneumoniae* protein (PID 4376844) was expressed <SEQ ID 271; cp6844>:

```
  1 MWRVVLRFLI IFILGRAVFP LRASESFSWE TSTCLTVLGI PFIDIILTTN
 51 EDFVAQCGLQ IGTISSTNNA KIKEIFLIYK EKFPEASISF KRKEPLNLSQ
101 SHLSDLGILC MRNGETYAEG MANKENGPAL KQPKDLRLVL RCPNQPDTLL
151 YSEKEAEKGI ETNTCLCNQG YTLLDGQLIL YGDSIEKFLK ETKRKNNHTL
201 VDLCDSQVVT TFLGRFWSLL NYVQVLFLSE DSAKILAGIP DLAQATQLLS
251 HTVPLLFIYT NDSIHIIEQG KESSFTYNQD LTEPILGFLF GYINRGSMEY
301 CFNCAQSSLG ET*
```

The cp6844 nucleotide sequence <SEQ ID 272> is:

```
  1 ATGTGGCGCG TTGTCCTCAG ATTCCTTATA ATTTTTATCT TGGGAAGAGC
 51 CGTCTTCCCT CTAAGAGCTT CAGAAAGCTT CTCCTGGGAA ACATCGACCT
101 GTTTAACAGT GCTAGGGATT CCTTTCATAG ATATTATCCT CACAACGAAT
151 GAGGACTTTG TTGCCCAGTG CGGCCTGCAA ATAGGAACCA TTTCTTCGAC
201 TAATAACGCA AAAATAAAAG AAATTTTTTT GATATATAAG GAAAAATTTC
251 CAGAAGCCTC TATCAGTTTC AAACGAAAAG AACCTCTAAA CCTTTCCCAA
301 TCCCATCTCT CCGATTTAGG TATTTTATGT ATGCGTAACG GAGAAACTTA
351 CGCTGAGGGA ATGGCAAATA AAGAAAACGG ACCCGCTCTA AAACAACCCA
401 AGGATCTAAG ATTAGTTTTA CGTTGTCCTA ACCAACCAGA TACCCTGCTC
451 TACTCGGAAA AAGAAGCAGA AAAGGGCATA GAAACAAATA CTTGCCTATG
501 CAATCAGGGA TACACACTCC TGGATGGGCA ATTGATTCTC TACGGGGATA
551 GTATAGAAAA GTTTCTGAAA GAGACCAAAA GAAAGAATAA CCACACGCTT
601 GTTGATCTTT GTGACTCACA AGTCGTGACC ACGTTCCTCG GTCGCTTTTG
651 GTCTCTTCTA AACTACGTTC AAGTTCTTTT CCTATCTGAA GACTCCGCTA
701 AAATTCTTGC GGGCATCCCA GACCTAGCTC AAGCTACGCA ATTGCTTTCC
751 CACACCGTAC CTTTGCTTTT TATTTATACC AACGATTCTA TTCACATCAT
801 AGAACAAGGC AAAGAAAGTA GTTTTACCTA TAACCAAGAT TTAACAGAGC
851 CCATTTTAGG ATTTCTCTTT GGTTACATAA ATCGCGGCTC TATGGAATAC
901 TGCTTTAATT GTGCACAGTC TTCATTAGGA GAAACCTAA
```

The PSORT algorithm predicts inner membrane (0.1786).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 136A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 136B) and for FACS analysis.

These experiments show that cp6844 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 137

The following *C.pneumoniae* protein (PID 4377201) was expressed <SEQ ID 273; cp7201>:

```
  1 VLVGICPSLY PEHPRSFYYR VSGDIGSRFD DRGFVNSGVE TLPYSSGSFG
 51 IFWISFTDPT FNFAIVNTFM RTAGINEVSR PMTQDTETSL IEMRDLSEQQ
101 EANNTDSLEQ EESLMGIVGH TVGGVSMTVT SSPNIFYRIQ TLLGLPETLA
151 EAEENPTFPN STIDSLAEIM MNLVRISDAV SIFWIFPIVD TTYNGVLLAV
```

```
201  CIGFFGINGI CSTFLMLTNP RSRRDRWRNL RIMVLCYRSL GSGMNLFDLS
251  NNVRMAARRH VTSCTVALYA MVTLFGWTVA IQDALQYGFP SVRDAFYRYC
301  LRHRYCLTQR NEDSLQTTGT RFQVTRTHLE DQQMVASILN LSVFGLFFGF
351  VGLMTTFGGL EISPSCRWDA ANNRTVGIF*
```

The cp7201 nucleotide sequence <SEQ ID 274> is:

```
   1  GTGCTCGTTG GTATCTGTCC TTCTCTATAT CCAGAACATC CTCGCTCCTT
  51  TTATTATCGT GTTTCTGGAG ATATAGGCTC CCGATTCGAC GATAGAGGAT
 101  TTGTAAACTC TGGAGTCGAA ACCCTGCCAT ACTCTTCAGG CAGCTTTGGG
 151  ATTTTTTGGA TCTCGTTTAC GGATCCCACA TTTAATTTTG CTATCGTAAA
 201  TACCTTTATG CGAACTGCAG GGATCAATGA AGTCTCTAGA CCCATGACAC
 251  AAGATACAGA AACTTCATTG ATAGAAATGA GAGACCTAAG TGAACAACAA
 301  GAAGCGAATA ACACAGATTC TTTAGAGCAA GAAGAGAGCT TAATGGGTAT
 351  TGTAGGACAT ACTGTGGGAG GAGTTTCCAT GACCGTGACC TCCAGTCCAA
 401  ATATCTTTTA TCGTATACAA ACACTTCTGG GACTGCCAGA GACTCTTGCA
 451  GAAGCTGAAG AAAATCCTAC CTTCCCAAAT TCTACTATAG ATAGCCTTGC
 501  AGAAATAATG ATGAACCTCG TAAGGATCTC TGATGCTGTC TCTATTTTCT
 551  GGATTTTTCC TATCGTAGAT ACTACATATA ATGGAGTTTT ATTAGCCGTC
 601  TGTATCGGCT TCTTCGGAAT CAATGGGATT TGTTCCACGT TCCTTATGCT
 651  TACGAATCCA CGCTCTCGTC GAGATAGATG GAGGAATTTA CGCATCATGG
 701  TTCTTTGCTA TCGTTCTTTG GGAAGCGGAA TGAATCTCTT TGATCTTAGC
 751  AATAATGTGC GCATGGCAGC ACGTAGGCAT GTGACATCAT GTACAGTAGC
 801  TCTCTATGCT ATGGTCACTC TATTTGGATG GACAGTAGCA ATACAAGATG
 851  CTTTGCAATA TGGTTTCCCT AGCGTTCGGG ATGCCTTCTA TAGATATTGC
 901  TTACGCCACA GATATTGCTT AACTCAAAGA AACGAAGACT CTCTGCAAAC
 951  TACAGGAACG CGCTTTCAGG TTACCCGTAC ACATCTAGAA GATCAACAGA
1001  TGGTGGCTTC TATTTTGAAT TTGAGTGTTT TTGGGCTCTT TTTTGGATTC
1051  GTAGGGCTAA TGACCACGTT TGGAGGATTA GAAATCTCAC CATCTTGTCG
1101  GTGGGATGCA GCAAATAACC GAACGGTAGG TATTTTTTAG
```

The PSORT algorithm predicts inner membrane (0.3102).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 137A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 137B) and for FACS analysis.

These experiments show that cp7201 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 138

The following *C.pneumoniae* protein (PID 4377251) was expressed <SEQ ID 275; cp7251>:

```
  1  MAPIHGSNAF VEDILHSHPS PQATYFSSTR AQKLHEFKDR HPVLTRIASV
 51  IIKIFKVLIG LIILPLGIYW LCQTLCTNSI LPSKNLLKIF KKQPNTKTLK
101  TNYLHALQDY SSKNRVASMR RVPILQDNVL IDTLEICLSQ APTNRWMLIS
151  LGSDCSLEEI ACKEIFDSWQ RFAKLIGANI LVYNYPGVMS STGSSSLKDL
201  ASAHNICTRY LKDKEQGPGA KEIITYGYSL GGLIQAEALR DQKIVANDDT
251  TWIAVKDRCP LFISPEGFHS CRRIGKLVAR LFGWGTKAVE RSQDLPCLEI
301  FLYPTDSLRR STVRQNKLLA PELTLAHAIK NSPYVQNKEF IEVRLSSDID
351  PIDSKTRVAL ATPILKKLS*
```

The cp7251 nucleotide sequence <SEQ ID 276> is:

```
  1  ATGGCTCCAA TTCACGGAAG TAATGCGTTT GTTGAGGATA TTTTACATTC
 51  CCACCCTTCT CCACAAGCGA CTTATTTTTC TTCAACACGC GCCCAAAAAC
101  TTCATGAGTT TAAAGACAGG CATCCCGTGC TTACACGGAT TGCTTCTGTA
151  ATTATTAAAA TTTTTAAAGT TCTGATAGGG CTGATCATCC TTCCCTTAGG
201  AATCTACTGG CTATGTCAAA CGCTTTGTAC AAACTCGATT CTCCCTTCCA
251  AGAATTTATT AAAAATTTTC AAGAAGCAAC CCAACACTAA AACCTTAAAA
301  ACTAATTATT TGCATGCTTT GCAAGATTAT TCCTCGAAAA ACCGCGTTGC
351  TTCCATGAGA CGAGTTCCTA TCCTCCAGGA TAATGTTCTC ATCGACACTT
401  TGGAAATATG CCTTTCACAA GCACCTACGA ATCGTTGGAT GCTCATTTCT
451  TTAGGAAGTG ACTGTAGCTT GGAAGAAATC GCTTGTAAGG AGATCTTTGA
```

```
 501  TTCTTGGCAA AGATTTGCCA AGTTGATAGG GGCCAATATA CTCGTTTATA
 551  ACTACCCCGG AGTCATGTCC AGCACAGGGA GCAGCAGCCT AAAGGACCTA
 601  GCATCAGCTC ATAATATTTG TACAAGATAC CTTAAAGATA AAGAACAGGG
 651  CCCTGGAGCA AAAGAAATCA TTACCTATGG GTACTCCCTA GGAGGTTTGA
 701  TACAAGCAGA AGCATTGCGA GACCAGAAGA TTGTTGCAAA CGATGATACT
 751  ACTTGGATAG CAGTCAAAGA TAGGTGTCCT CTCTTTATAT CTCCAGAAGG
 801  TTTCCACAGT TGCAGACGCA TAGGAAAGCT AGTAGCTCGT CTTTTTGGCT
 851  GGGGGACCAA AGCCGTAGAG AGAAGCCAAG ACCTTCCCTG CCTAGAAATT
 901  TTTCTCTATC CTACGGATTC CTTACGAAGA TCAACAGTCA GACAGAACAA
 951  GCTCTTAGCA CCTGAACTTA CTCTCGCTCA TGCGATAAAA AATAGTCCCT
1001  ATGTTCAAAA TAAAGAATTT ATAGAAGTAC GATTATCGTC TGATATCGAT
1051  CCCATCGACA GCAAAACAAG AGTGGCTCTT GCCACACCAA TTTTGAAAAA
1101  GCTCTCTTAG
```

The PSORT algorithm predicts inner membrane (0.4545).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 138A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 138B) and for FACS analysis.

These experiments show that cp7251 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 139

The following *C.pneumoniae* protein (PID 4377288) was expressed <SEQ ID 277; cp7288>:

```
  1  MHMSNPISLF SPAELIAKYN LIPKTSPIYP RRTELIILEE NACQTRLTNV
 51  AQVLHPSSLF SMSKKILNPC GCSGGPLCWV ILNILAFIIT SVLFIILLPV
101  NLIVAGLRLF MPLPPKKIVE DLSEPTTEET NEVIQPFIFA LQALLFEDNK
151  LRSFKIVEQS VGKAPLPNPF LNRLVAISPQ ESQEAMRKIP DLCSQLKKVL
201  KSLGVLTPEW KHMLKYFEGL KNEHDSNPDK KTFPILIKLL IEALTGKSSL
251  PKTPSTKEKM QAALFIASSC KTCKPTWGEV ITRSLNRLYS IANEGDNQLL
301  IWVQEFKERE LMSIQDGDDA EEYRFAAQQH GERYTEAIEQ VLRNESAAKL
351  QWHVINTMKF FHGKNLGLVT EHLQDTLGAL TLRQTTVDTH QGREDADLSA
401  ALFLNKYLNS GNQLVNSVFK SMQKADPETK ALIREFALDI LYASLRLPQT
451  SAHTEVFSTL LMDPETYEPN KACIAYLLYV LKIIEL*
```

The cp7288 nucleotide sequence <SEQ ID 278> is:

```
   1  ATGCATATGT CTAACCCCAT CTCTTTGTTT TCCCCTGCAG AGTTAATAGC
  51  AAAGTACAAT TTAATTCCAA AAACTTCGCC GATTTATCCT CGGAGGACGG
 101  AACTTATTAT CTTGGAAGAA AATGCGTGTC AAACACGCCT AACCAACGTG
 151  GCTCAGGTCC TACATCCTTC TAGCCTATTC AGTATGTCAA AAAAAATACT
 201  GAATCCCTGC GGGTGCTCTG GTGGTCCCTT ATGTTGGGTG ATTCTCAACA
 251  TCCTAGCATT TATTATTACT TCAGTACTGT TTATCATTCT TTTACCGGTG
 301  AATCTCATCG TAGCAGGTCT TCGTCTCTTC ATGCCTCTTC CCCCTAAAAA
 351  AATCGTAGAG GATTTAAGTG AACCTACTAC TGAAGAAACG AATGAGGTCA
 401  TTCAACCCTT CATTTTCGCT TTGCAAGCGT TGCTTTTTGA GGATAACAAA
 451  CTTCGCTCTT TTAAAATTGT TGAACAAAGT GTAGGCAAAG CACCCTTACC
 501  TAATCCCTTT TTAAATAGAC TAGTAGCAAT TTCGCCGCAA GAAAGCCAAG
 551  AAGCCATGCG GAAGATTCCG GATCTATGCT CACAACTGAA AAAAGTATTA
 601  AAGTCTCTAG GCGTGCTAAC TCCAGAATGG AAGCACATGC TGAAGTACTT
 651  TGAGGGACTG AAAAACGAAC ATGATAGTAA TCCTGATAAA AAGACGTTCC
 701  CAATATTGAT CAAGCTCCTC ATAGAAGCTC TTACTGGAAA GTCCTCTTTA
 751  CCCAAAACTC CTAGTACAAA GGAAAAAATG CAAGCGGCCT TATTTATTGC
 801  AAGTTCTTGC AAGACTTGTA AGCCGACTTG GGGAGAAGTC ATAACCAGAT
 851  CTCTTAACAG ACTCTATAGT ATAGCTAATG AAGGAGACAA TCAGCTTCTG
 901  ATTTGGGTTC AAGAGTTTAA AGAACGAGAG CTGATGTCCA TCCAAGATGG
 951  TGATGATGCT GAAGAGTATC GGTTTGCGGC TCAGCAACAC GGTGAGCGTT
1001  ACACAGAGGC AATAGAACAA GTTCTACGAA ACGAGTCAGC AGCCAAACTA
1051  CAATGGCATG TGATCAACAC TATGAAATTC TTCCATGGGA AAAATCTCGG
1101  TCTAGTTACA GAACACCTAC AAGATACTCT CGGCGCCCTA ACTTTACGTC
1151  AAACTACAGT GGACACACAT CAAGGCAGAG AAGACGCTGA TTTGTCAGCT
1201  GCTCTTTTCC TAAATAAGTA TTTAAATTCT GGAAATCAAC TTGTTAATAG
```

```
1251  CGTCTTTAAA TCCATGCAAA AAGCAGATCC AGAAACCAAA GCTTTAATCC
1301  GTGAGTTTGC TCTAGATATA TTATATGCAT CCTTACGGCT TCCTCAAACT
1351  TCCGCTCATA CCGAGGTCTT TTCTACACTC TTAATGGACC CAGAGACCTA
1401  TGAACCTAAT AAAGCTTGTA TCGCCTACTT GCTCTATGTA TTAAAGATCA
1451  TCGAACTATA A
```

The PSORT algorithm predicts inner membrane (0.5989).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 139A). The recombinant protein was used to immunise miee, whose sera were uscd in a Western blot (Figure 139B) and for FACS analysis.

These experiments show that cp7288 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 140

The following *C.pneumoniae* protein (PID 4377359) was expressed <SEQ ID 279; cp7359>:

```
  1  MPGSVSSPPL SPVIVRERVP SSSGSDLIQP HAVLKISILI FALVTILGIV
 51  LVVLSSALGA LPSLVLTVSG CIAIAVGLIG LGILVTRLIL STIRKVDAMG
101  YDAAVKEEQY LSRIRELESE NREIRDRNRA VEDQCAHLSE ENKDLRDPEY
151  LHGMTERLIA SLEIENQALV AENILLKDWN ASLSRDFRAY KQKFPLGALE
201  PWKEDIACIM EQNLFLKPEC IAMVKSLPLE TQRLFLYPKG FQSLVNRFAP
251  RSRFFQTPKY EYNSRNENED GKVAAVCARL KKEFFSAVLG ACSYEELGGI
301  CERAVALKET LPLPEAVYDT LVQEFPNLLT AESLWKEWCF YSYPYLRPYL
351  SVDYCKRLFV QLFEELCLKL FTTGSPEDQA LVRLFSYYRN HIPAVLASFG
401  LPPPETGGSV FVLLPKQENL LWSQIEVLAT RYLKDTFVRN SEWTGSFEMM
451  FSYNEMCKEI SEGRIRFAED YETRHSEEFP PSPLSEEGEG EEFLPPCSEE
501  EVSVLERPDL DVDSMWVWHP PVPKGPL*
```

The cp7359 nucleotide sequence <SEQ ID 280> is:

```
   1  ATGCCAGGTT CTGTGTCATC ACCTCCTTTG TCTCCTGTAA TTGTCCGTGA
  51  AAGGGTCCCA TCCTCTTCAG GATCCGACCT CATACAGCCT CATGCTGTTT
 101  TAAAGATCTC CATCCTAATT TTTGCGCTTG TGACAATTTT AGGAATTGTT
 151  CTTGTAGTGT TGTCTAGTGC TTTAGGAGCT CTTCCTAGTT TAGTTTTGAC
 201  GGTTTCTGGT TGTATTGCAA TAGCTGTAGG CCTGATTGGT TTAGGGATTC
 251  TTGTGACACG GCTGATTCTC TCTACGATCA GAAAAGTAGA TGCCATGGGT
 301  TATGATGCTG CGGTCAAAGA AGAGCAGTAT TTGTCACGTA TCAGAGAATT
 351  AGAGTCTGAA AATAGAGAGA TTAGAGATAG AAATCGTGCT GTCGAAGATC
 401  AGTGTGCCCA TTTATCCGAA GAGAACAAGG ACCTTAGGGA TCCCGAATAT
 451  CTACATGGAA TGACTGAAAG GCTCATTGCG AGCTTAGAAA TAGAGAATCA
 501  AGCTCTCGTA GCTGAGAACA TTCTTCTCAA AGACTGGAAT GCAAGCCTAT
 551  CTAGAGATTT CCGCGCATAT AAGCAAAAAT TTCCTCTTGG GGCATTAGAA
 601  CCCTGGAAAG AAGATATTGC ATGTATCATG GAACAAAATC TCTTTTTAAA
 651  ACCGGAATGT ATCGCGATGG TTAAGTCTCT TCCATTAGAG ACGCAACGGC
 701  TGTTTTTATA TCCAAAAGGA TTTCAGTCTT TAGTTAATCG ATTTGCTCCG
 751  CGGTCTCGCT TTTTCCAGAC TCCAAAGTAT GAATATAACA GTAGGAATGA
 801  AAATGAGGAC GGAAAGGTAG CCGCAGTGTG CGCCCGTTTG AAAAAAGAAT
 851  TCTTCAGTGC TGTTTTAGGA GCCTGTAGTT ACGAAGAACT AGGGGGCATT
 901  TGTGAAAGAG CAGTAGCACT TAAAGAGACG TTGCCATTGC CTGAAGCTGT
 951  CTATGATACC CTAGTTCAGG AGTTCCCAAA TCTTCTTACT GCTGAGAGTT
1001  TATGGAAAGA ATGGTGCTTC TATTCCTATC CCTACCTTCG TCCCTATCTT
1051  TCTGTGGATT ACTGTAAGAG GTTATTTGTA CAACTTTTTG AGGAACTCTG
1101  CCTAAAGCTT TTTACAACGG GATCTCCAGA AGACCAAGCT TTGGTTCGCC
1151  TTTTCTCTTA CTATAGGAAT CATATTCCCG CAGTCTTGGC CTCATTTGGT
1201  TTGCCCCCGC CTGAGACAGG GGGGTCTGTA TTTGTATTGC TACCAAAACA
1251  AGAAAACCTT CTTTGGAGTC AAATTGAGGT GCTGGCTACA AGGTATCTCA
1301  AAGATACCTT CGTGAGAAAC TCAGAATGGA CGGGCTCTTT CGAGATGATG
1351  TTTTCTTATA ACGAGATGTG TAAGGAGATC TCCGAAGGAA GGATTCGTTT
1401  TGCTGAAGAC TATGAAACGA GGCATTCCGA AGAATTCCCT CCTTCCCCTC
1451  TCTCTGAAGA AGGAGAGGGC GAAGAATTCC TTCCTCCTTG CTCTGAAGAA
1501  GAGGTTTCGG TTCTTGAGCG CCCAGATCTA GATGTAGACT CTATGTGGGT
1551  CTGGCATCCG CCGGTCCCTA AGGGACCTCT TTAA
```

The PSORT algorithm predicts inner membrane (0.7453).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 140A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 140B) and for FACS analysis.

These experiments show that cp7359 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 141

The following *C.pneumoniae* protein (PID 4377374) was expressed <SEQ ID 281; ep7374>:

```
  1 MDKQSSGNSG CIWHPFTQSA LDSTPIKIVR GEGAYLYAES GTRYLDAISS
 51 WWCNLHGHGH PYITKKLCEQ AQKLEHVIFA NFTHEPALEL VSKLAPLLPE
101 GLERFFFSDN GSTSIEIAMK IAVQYYYNQN KAKSHFVGLS NAYHGDTFGA
151 MSIAGTSPTT VPFHDLFLPS STIAAPYYGK EELAIAQAKT VFSESNIAAF
201 IYEPLLQGAG GMLMYNPEGL KEILKLAKHY GVLCIADEIL TGFGRTGPLF
251 ASEFTDIPPD IICLSKGLTG GYLPLALTVT TKEIHDAFVS QDRMKALLHG
301 HTFTGNPLGC SAALASLDLT LSPECLQQRQ MIERCHQEFQ EAHGSLWQRC
351 EVLGTVLALD YPAEATGYFS QYRDHLNRFF LERGVLLRPL GNTLYVLPPY
401 CIQEEDLRII YSHLQDALCL QPQ*
```

The cp7374 nucleotide sequence <SEQ ID 282> is:

```
   1 ATGGACAAGC AATCATCAGG GAATTCAGGG TGTATCTGGC ACCCCTTCAC
  51 TCAATCTGCA TTAGATTCTA CACCCATAAA GATTGTAAGG GGAGAAGGTG
 101 CTTACCTCTA TGCGGAATCA GGAACAAGAT ATCTTGATGC GATATCTTCA
 151 TGGTGGTGCA ACCTCCACGG TCATGGGCAT CCCTACATTA CAAAAAAATT
 201 ATGTGAGCAA GCACAGAAGT TAGAACATGT GATCTTCGCA AATTTCACCC
 251 ATGAACCGGC TCTAGAGCTC GTATCGAAAC TCGCTCCCCT CCTTCCTGAA
 301 GGTCTAGAAC GTTTCTTTTT CTCTGACAAC GGATCAACGT CTATCGAAAT
 351 AGCAATGAAA ATTGCTGTGC AATATTACTA CAATCAAAAC AAGGCTAAGA
 401 GCCATTTTGT TGGACTCAGC AATGCCTATC ACGGAGATAC ATTTGGAGCT
 451 ATGTCGATAG CTGGCACGAG CCCTACTACA GTTCCCTTTC ATGATCTTTT
 501 TCTTCCTTCC AGTACAATTG CTGCTCCCTA TTATGGCAAG GAAGAGCTTG
 551 CCATTGCCCA AGCAAAAACA GTCTTTTCTG AAAGCAATAT CGCAGCGTTT
 601 ATCTATGAGC CGCTATTGCA AGGTGCTGGA GGGATGTTAA TGTATAATCC
 651 CGAAGGCCTA AAGGAGATTC TCAAGCTTGC CAAGCATTAC GGGGTTCTCT
 701 GTATTGCTGA TGAAATTCTT ACTGGCTTTG GCCGTACGGG TCCACTGTTT
 751 GCTTCTGAAT TTACAGACAT TCCTCCTGAC ATTATCTGTC TTTCTAAAGG
 801 TCTTACAGGA GGCTATCTCC CTCTAGCCTT GACAGTAACC ACTAAAGAAA
 851 TTCATGATGC CTTTGTCTCC CAAGATCGGA TGAAGGCACT GCTTCATGGC
 901 CATACCTTCA CAGGAAATCC TTTAGGCTGT AGTGCTGCCC TCGCTTCTTT
 951 GGATCTCACC CTATCTCCAG AATGCCTACA ACAAAGGCAA ATGATAGAAC
1001 GGTGTCATCA AGAGTTTCAA GAAGCTCATG GTTCCCTATG GCAACGGTGT
1051 GAGGTTCTGG GCACGGTACT CGCTCTAGAT TACCCTGCAG AAGCTACAGG
1101 ATATTTTTCA CAATATAGAG ACCATCTCAA TCGCTTTTTC TTAGAACGTG
1151 GAGTCCTTCT TCGTCCTTTA GGGAACACAC TGTATGTGCT GCCCCCCTAC
1201 TGTATCCAAG AAGAAGATCT CCGGATTATT TATTCTCACC TACAGGATGC
1251 CCTATGTCTA CAACCACAGT AA
```

The PSORT algorithm predicts cytoplasm (0.2930).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 141A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 141B) and for FACS analysis.

These experiments show that cp7374 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 142

The following *C.pneumoniae* protein (PID 4377377) was expressed <SEQ ID 283; cp7377>:

```
  1 MREETVSWSL EDIREIYHTP VFELIHKANA ILRSNFLHSE LQTCYLISIK
 51 TGGCVEDCAY CAQSSRYHTH VTPEPMMKIV DVVERAKRAV ELGATRVCLG
101 AAWRNAKDDR YFDRVLAMVK SITDLGAEVC CALGMLSEEQ AKKLYDAGLY
151 AYNHNLDSSP EFYETIITTR SYEDRLNTLD VVNKSGISTC CGGIVGMGES
201 EEDRIKLLHV LATRDHIPES VPVNLLWPID GTPLQDQPPI SFWEVLRTIA
251 TARVVFPRSM VRLAAGRAFL TVEQQTLCFL AGANSIFYGD KLLTVENNDI
301 DEDAEMIKLL GLIPRPSFGI ERGNPCYANN S*
```

The ep7377 nucleotide sequence <SEQ ID 284> is:

```
  1 ATGCGTGAAG AAACTGTATC CTGGTCATTA GAAGACATCC GCGAAATTTA
 51 TCACACTCCC GTATTTGAGC TGATTCACAA AGCCAATGCC ATATTGCGTA
101 GTAATTTCCT CCATTCAGAA CTGCAGACTT GCTATCTGAT TTCGATTAAA
151 ACTGGTGGAT GCGTTGAAGA TTGCGCCTAC TGTGCCCAAT CTTCCCGCTA
201 TCATACCCAC GTCACACCAG AACCTATGAT GAAAATTGTA GACGTTGTGG
251 AAAGGGCAAA ACGTGCTGTA GAGCTAGGCG CCACTCGTGT GTGTCTTGGG
301 GCTGCCTGGC GCAATGCTAA GGACGATCGA TACTTTGATA GAGTCCTCGC
351 TATGGTGAAA AGTATCACAG ATCTCGGAGC CGAGGTTTGT TGTGCTTTAG
401 GCATGCTCTC CGAAGAGCAA GCTAAAAAAC TGTATGATGC AGGACTTTAT
451 GCCTACAATC ATAATTTAGA CTCTTCTCCG GAATTCTATG AAACTATAAT
501 CACAACACGT TCTTATGAAG ATCGCCTCAA CACTCTTGAT GTAGTAAATA
551 AATCTGGCAT TAGTACATGC TGCGGTGGTA TTGTAGGTAT GGGAGAATCT
601 GAAGAAGACC GTATAAAGCT TCTTCATGTT CTTGCAACAA GAGATCATAT
651 CCCAGAATCC GTACCTGTAA ATTTACTTTG GCCGATTGAC GGCACGCCTT
701 TGCAAGACCA GCCTCCGATT TCTTTCTGGG AAGTCTTGCG AACCATAGCA
751 ACGGCACGGG TTGTTTTCCC CAGATCCATG GTACGACTTG CTGCAGGACG
801 CGCTTTCCTC ACAGTAGAAC AACAAACCTT ATGTTTTCTA GCCGGTGCCA
851 ACTCCATATT CTATGGAGAT AAACTGTTGA CTGTAGAAAA CAATGATATA
901 GATGAAGATG CTGAAATGAT CAAACTTTTA GGCTTAATCC CTCGCCCTTC
951 ATTTGGAATA GAAAGAGGTA ACCCATGTTA TGCCAACAAT TCCTAA
```

The PSORT algorithm predicts cytoplasm (0.2926).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 142A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 142B) and for FACS analysis.

These experiments show that cp7377 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 143

The following *C.pneumoniae* protein (PID 4377407) was expressed <SEQ ID 285; cp7407>:

```
  1 MVCPNNSWFR MCGNFNCEWV EVTTTEETTR QSASDISEEA GSSGGAAPIT
 51 TQPTKITKVE KRVQFNTAQG DESTIHMIQE AGELVDSILS HRRTQGCTEY
101 CYDSYATGCG QRCGSFGRLI CGTYKACCLD REDNQVAGLV HECEQTHGPI
151 AVALAAKTMG LNLMELVEKN TILSEEQKNE FRQHCSEAKT QLYGTMQSLS
201 QNFFLEGVNS IRERGLDDSL VQAVLSFIAT RSWEKTIESE EASGTSSASN
251 STRIPACYIL NTSPLTTSRL SCGSRDARRP SSVGAEPQYV AKKYNDNGMA
301 RQLGKIQVTN LKTGDFSALG PFGLLIVKML NSFLLSASQS TSSILKHTGG
351 EICYTCPNFR DIVVLLMLAI GYCPANTDET SVVDIHMIDD PIMTIFYRLQ
401 YSYRTGKTSA SFLKKKPSLV RQESLDCPTP AESVPLMSSL EEEDENEDDD
451 EDGNLAYQQR ILECSGHLQT LFLGIKINKE *
```

The cp7407 nucleotide sequence <SEQ ID 286> is:

```
  1 ATGGTTTGCC CAAATAATTC TTGGTTCAGA ATGTGTGGAA ATTTCAACTG
 51 CGAATGGGTT GAAGTAACAA CAACAGAAGA AACAACGCGG CAATCGGCTT
101 CAGATATAAG CGAAGAAGCT GGTTCGAGTG GAGGAGCTGC TCCTATAACT
151 ACGCAACCTA CTAAAATTAC AAAAGTAGAG AAACGTGTCC AATTTAATAC
```

```
 201  TGCTCAAGGT GATGAAAGTA CAATACACAT GATCCAAGAA GCAGGAGAAT
 251  TGGTAGACTC CATTCTATCA CATAGACGAA CGCAAGGATG TACAGAGTAT
 301  TGTTATGACA GTTACGCAAC TGGATGTGGT CAGCGTTGCG GATCTTTTGG
 351  AAGACTCATT TGTGGAACGT ATAAAGCGTG TTGCTTAGAC AGAGAGGATA
 401  ATCAGGTTGC TGGACTTGTC CATGAATGCG AACAGACCCA TGGTCCTATT
 451  GCCGTTGCTT TAGCTGCTAA AACTATGGGC CTCAACTTAA TGGAACTTGT
 501  AGAAAAAAAC ACTATTTTGT CTGAAGAACA GAAAAATGAA TTTAGACAGC
 551  ATTGCTCGGA AGCTAAAACC CAACTCTATG GAACGATGCA GAGCCTTTCT
 601  CAAAACTTTT TCCTTGAAGG AGTCAACAGC ATTAGAGAAC GCGGTCTAGA
 651  CGATTCACTA GTCCAAGCCG TGCTAAGCTT TATTGCTACA AGGTCTTGGG
 701  AAAAAACTAT AGAATCAGAG GAAGCCTCAG GAACATCTTC TGCTTCTAAT
 751  TCTACACGCA TTCCTGCGTG CTATATCTTA AATACGAGCC CCTTAACGAC
 801  GTCACGCCTA TCCTGTGGAT CAAGAGATGC GCGACGCCCA TCTTCAGTCG
 851  GTGCAGAGCC CCAGTACGTA GCAAAAAAAT ACAATGACAA TGGCATGGCC
 901  AGACAATTAG GAAAAATCCA AGTCACCAAT CTAAAAACAG GAGATTTTTC
 951  AGCTTTAGGT CCTTTTGGTC TCCTGATTGT GAAAATGCTG AATAGCTTTC
1001  TCTTATCTGC ATCACAAAGC ACATCTTCTA TTCTAAAGCA CACAGGTGGA
1051  GAAATATGTT ATACGTGCCC AAATTTTCGT GATATCGTCG TTTTATTGAT
1101  GTTAGCGATT GGCTATTGCC CTGCAAATAC CGATGAGACA TCTGTCGTAG
1151  ATATACACAT GATAGATGAT CCGATTATGA CCATCTTCTA TCGACTACAA
1201  TACAGCTATA GAACAGGGAA AACTTCAGCA TCGTTTTTAA AAAAGAAACC
1251  CTCATTAGTA AGACAGGAAA GTCTTGATTG TCCTACCCCT GCAGAATCTG
1301  TCCCTCTCAT GTCAAGTCTC GAAGAAGAAG ATGAAAATGA AGATGATGAT
1351  GAGGATGGGA ATTTGGCGTA TCAACAGCGT ATCCTTGAAT GCTCGGGTCA
1401  TTTACAAACT CTATTTTTAG GGATAAAAAT AAACAAAGAA TAA
```

The PSORT algorithm predicts inner membrane (0.1319).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 143A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 143B) and for FACS analysis.

These experiments show that cp7407 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 144

The following *C.pneumoniae* protein (PID 4376432) was expressed <SEQ ID 287; cp6432>:

```
  1  MTRSTIESSD SLCSRSFSQK LSVQTLKNLC ESRLMKITSL VIAFLTLIVG
 51  GALIALAGGG VLSFPLGLIL GSVLVLFSSI YLVSCCKFFT LKEMTMTCSV
101  KSKINIWFEK QRNKDIEKAL ENPDLFGENK RNVGNRSARN QLEMILHETD
151  GIILKRYMKG AKMYFYL*
```

The cp6432 nucleotide sequence <SEQ ID 288> is:

```
  1  ATGACTAGAA GTACTATTGA AAGCAGTGAT TCGCTATGCT CAAGGTCTTT
 51  TTCTCAAAAA TTAAGTGTCC AGACATTAAA AAATCTCTGT GAAAGTAGAT
101  TAATGAAGAT CACTTCTCTT GTGATTGCTT TCCTAACTCT AATTGTGGGG
151  GGTGCTCTTA TAGCTTTAGC AGGAGGGGGG GTTCTTTCTT TCCCTCTTGG
201  GCTAATCTTA GGAAGCGTAC TCGTTTTGTT TTCTTCTATC TATTTAGTCT
251  CTTGTTGTAA ATTTTTTACT TTAAAAGAGA TGACAATGAC CTGTAGTGTC
301  AAATCTAAAA TCAATATATG GTTTGAAAAG CAACGAAACA AAGACATCGA
351  AAAGGCATTA GAGAATCCAG ATCTCTTTGG AGAAAATAAG AGAAATGTTG
401  GAAATCGTTC GGCAAGAAAT CAACTAGAAA TGATCTTACA CGAGACTGAC
451  GGAATTATTT TGAAAAGATA TATGAAAGGA GCTAAAATGT ACTTTTATTT
501  ATGA
```

The PSORT algorithm predicts inner membrane (0.5394).

The protein was expressed in *E.coli* and purified as a his-tagged product (Figure 144A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 144B) and for FACS analysis.

These experiments show that cp6432 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 145

The following *C.pneumoniae* protein (PID 4376433) was expressed <SEQ ID 289; cp6433>:

```
  1  MNWVPKTIDH VDPESEIDIR KVVSCYKLIK ECQPEFRSLI SELLGVIRCG
 51  LRLLKRSKYQ EQARTVSDED APLFCLTRSY YQDGYLTPLR AGPRDLINHY
101  IHLRRRENPK HFFSPKHPCY YARLAFNESV CVYRELFDIE RLTKMYVEGD
151  YSKEQEKNLQ AILSFVKTLD EGKDFLIEHK DTDLIGRGFT DVFCT*
```

The cp6433 nucleotide sequence <SEQ ID 290> is:

```
  1  ATGAATTGGG TTCCAAAAAC AATAGACCAT GTAGATCCAG AATCAGAGAT
 51  AGATATACGT AAAGTCGTCT CCTGCTATAA GTTGATAAAA GAATGTCAAC
101  CTGAATTTCG ATCTCTTATA AGTGAATTAC TAGGAGTGAT TCGGTGTGGC
151  TTAAGACTAT TAAAACGTTC TAAGTATCAA GAACAGGCTA GAACTGTATC
201  TGATGAAGAT GCACCTCTTT TCTGCCTGAC TCGTTCTTAT TATCAAGATG
251  GTTATCTCAC GCCATTAAGA GCAGGACCTC GTGATCTTAT AAATCACTAT
301  ATACACTTGC GTCGCCGAGA GAATCCTAAG CATTTTTTCA GTCCTAAGCA
351  TCCATGTTAT TATGCTCGAT TGGCTTTTAA TGAGTCAGTG TGTGTCTATA
401  GAGAACTCTT TGATATAGAG CGACTTACAA AAATGTATGT CGAGGGTGAT
451  TATTCTAAAG AACAAGAGAA AAACCTACAG GCTATTCTTA GTTTTGTGAA
501  AACTCTAGAT GAAGGAAAGG ACTTTCTTAT TGAACATAAA GATACCGATC
551  TCATTGGGAG AGGTTTTACT GATGTGTTCT GCACTTAA
```

The PSORT algorithm predicts cytoplasm (0.4068).

The protein was expressed in *E.coli* and purified as a his-tagged product (Figure 145A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 145B) and for FACS analysis.

These experiments show that cp6433 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 146

The following *C.pneumoniae* protein (PID 4376643) was expressed <SEQ ID 291; cp6643>:

```
  1  MGYLPVSATD VLFESPAAPL INSANTQNQK LIELKGKQQA ESSPRTITSV
 51  ILEVLLVIGC CLIVLSLLAI RPALQFTLET GHPAAIAVLA VSGTILLVAV
101  IILFCFLAAV PFAAKKTYKY VKTVDDYASW HSHQQTPTLG TIFSGIVYAE
151  SQAQL*
```

The cp6643 nucleotide sequence <SEQ ID 292> is:

```
  1  ATGGGATATC TTCCAGTATC TGCTACGGAC GTTCTTTTTG AAAGTCCAGC
 51  CGCTCCCTTA ATCAATAGCG CAAACACACA AAATCAGAAA CTCATAGAAC
101  TCAAGGGGAA GCAGCAAGCT GAGTCTTCTC CACGGACAAT CACTTCTGTC
151  ATATTGGAAG TTCTCCTAGT GATCGGATGC TGCCTCATAG TTCTTAGTTT
201  ATTGGCAATC CGCCCTGCTC TGCAATTCAC TCTAGAAACT GGACATCCAG
251  CTGCCATTGC AGTCCTTGCT GTCTCAGGAA CAATTCTATT GGTGGCTGTT
301  ATCATCTTGT TTTGCTTTCT AGCAGCTGTG CCATTCGCTG CTAAGAAAAC
351  TTATAAATAT GTTAAGACGG TTGATGACTA TGCTTCTTGG CATTCTCATC
401  AGCAAACACC GACCCTAGGC ACTATCTTTT CAGGTATCGT CTATGCAGAA
451  TCCCAGGCGC AATTATAG
```

The PSORT algorithm predicts inner membrane (0.6859).

The protein was expressed in *E.coli* and purified as a his-tagged produet (Figure 146A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 146B) and for FACS analysis.

These experiments show that cp6643 is a surfaee-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 147

The following *C.pneumoniae* protein (PID 4376722) was expressed <SEQ ID 293; cp6722>:

```
  1 VSSTLNGVFP SSLPEESADL FITNKEIVAL GEKGNVFLTH SIPMHIAAIT
 51 ILVIVALAGI AIICLGCYSQ SILLIAVGIV LTILTLLCLQ ALVGFIKFIR
101 QLPQQLHTTV QFIREKIRPE SSLQLVTNAQ RKTTQDTLKL YEELCDLSQK
151 EFKLQSTLYQ KRFELSHKNE KTNQN*
```

The cp6722 nucleotide sequence <SEQ ID 294> is:

```
  1 GTGTCTAGTA CTTTAAACGG GGTATTTCCC TCATCCCTTC CGGAAGAGTC
 51 TGCTGATTTA TTCATTACGA ATAAGGAGAT CGTAGCTTTG GGGGAGAAGG
101 GCAATGTTTT TCTCACCCAC TCCATTCCTA TGCATATTGC TGCGATTACG
151 ATCTTAGTGA TTGTAGCTCT TGCTGGAATC GCTATTATCT GTTTGGGTTG
201 CTATAGCCAA AGCATTCTGT TGATTGCCGT TGGCATTGTT CTTACTATTT
251 TGACTCTTCT CTGCCTACAA GCCTTGGTAG GATTTATTAA ATTCATCCGG
301 CAGCTCCCTC AGCAGCTCCA TACGACAGTA CAATTTATCA GGGAGAAGAT
351 TCGACCTGAA TCCTCTCTAC AGCTTGTAAC CAATGCACAG AGAAAAACCA
401 CTCAAGATAC GCTAAAGTTA TACGAAGAAC TCTGCGACCT CTCACAAAAA
451 GAGTTCAAAC TGCAATCAAC TCTTTATCAA AAACGTTTTG AGCTTTCTCA
501 CAAGAATGAA AAGACAAATC AAAACTAG
```

The PSORT algorithm predicts inner membrane (0.6668).

The protein was expressed in *E.coli* and purified as a his-tagged product (Figure 147A). The reeombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 147B) and for FACS analysis.

These experiments show that cp6722 is a surface-exposed and immunoaecessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 148

The following *C.pneumoniae* protein (PID 4377253) was expressed <SEQ ID 295; cp7253>:

```
  1 MSELAPCSTG LQMVPHTQVH HALDTRRVIL TIAACLSLIA GIVLVGLGAA
 51 AILPSLFGVI GGMILILFSS IALIYLYKKT REVDQIALEP LPEMISKDQS
101 IIDFVKTRDY ASLEKKATFA YTHTHYYDGS MVFYREIPRF MLGSYLALRK
151 DMDRQALF*
```

The cp7253 nucleotide sequence <SEQ ID 296> is:

```
  1 ATGAGCGAGC TCGCCCCCTG CTCGACAGGA TTGCAGATGG TCCCCCATAC
 51 GCAGGTCCAT CATGCCCTTG ATACGCGGAG AGTCATTCTA ACGATAGCCG
101 CCTGTCTGTC TTTAATTGCA GGAATCGTGT TGGTTGGCTT AGGTGCTGCA
151 GCAATCCTGC CCTCGCTTTT TGGAGTCATT GGAGGAATGA TTCTTATTCT
201 GTTTTCTTCG ATCGCCCTCA TTTATTTATA CAAGAAGACA AGGGAGGTGG
251 ATCAGATTGC TCTGGAGCCT CTTCCTGAGA TGATTTCTAA AGATCAAAGC
301 ATTATAGATT TTGTAAAGAC ACGAGACTAT GCATCTTTAG AAAAGAAAGC
351 GACCTTTGCT TATACTCATA CTCATTATTA CGATGGAAGC ATGGTCTTCT
401 ATAGGGAGAT CCCTAGATTT ATGTTAGGCT CTTATCTCGC GCTTCGCAAA
451 GACATGGACC GCCAAGCTCT TTTTTGA
```

The PSORT algorithm predicts inner membrane (0.5394).

The protein was expressed in *E.coli* and purified as a his-tagged product (Figure 148A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 148B) and for FACS analysis.

These experiments show that cp7253 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 149

The following *C.pneumoniae* protein (PID 4376264) was expressed <SEQ ID 297; cp6264>:

```
  1  VISGLLFLLV RREVPTVRSE EIPRGVSVTP SEEPALEKAQ KEPETKKILD
 51  RLPKELDQLD TYIQEVFACL ERLKDPKYED RGLLTEAKEK LRVFDVVEKD
101  MMSEFLDIQR VLNEEAYYVE HCQDPLENIA YEIFSSQELR DYYCAGVCGY
151  LPSGDARADR LKRSVKEVMD RFMRVTWKSW EASVMLDHSY GVARELFKKA
201  VGVLEESVYK ILFKSYRDAF YECEKAKIQR DGRFKWL*
```

The cp6264 nucleotide sequence <SEQ ID 298> is:

```
  1  GTGATTTCGG GACTTCTATT CCTTCTAGTA AGACGAGAGG TTCCGACAGT
 51  ACGTTCAGAG GAAATTCCCA GAGGGGTTTC TGTGACCCCT TCTGAAGAGC
101  CTGCTCTAGA GAAGGCTCAA AAAGAACCGG AGACAAAGAA AATTTTAGAT
151  CGGTTGCCGA AGGAATTGGA TCAGTTAGAT ACGTATATTC AGGAAGTGTT
201  TGCATGTTTA GAGAGGCTGA AGGATCCTAA GTACGAAGAT CGAGGTCTTT
251  TAACAGAGGC GAAGGAGAAA CTTCGAGTTT TTGACGTTGT TGAGAAAGAT
301  ATGATGTCAG AGTTTTTAGA CATACAACGA GTGTTGAATG AGGAAGCATA
351  TTATGTAGAA CATTGTCAAG ATCCCCTAGA GAATATAGCC TACGAGATTT
401  TCTCTTCCCA AGAGCTTCGT GATTACTACT GTGCAGGGGT GTGTGGGTAT
451  TTGCCTTCTG GGGATGCTCG AGCGGATCGA TTAAAGAGAT CAGTTAAGGA
501  GGTAATGGAT CGCTTTATGA GGGTGACCTG GAAATCTTGG GAGGCATCAG
551  TCATGTTGGA TCATAGCTAT GGGGTAGCGC GAGAGTTATT CAAGAAGGCA
601  GTAGGAGTAC TAGAGGAGAG TGTCTATAAA ATTCTGTTTA AGAGCTATAG
651  AGATGCGTTT TATGAATGTG AGAAGGCAAA GATCCAGAGG GATGGGCGTT
701  TCAAATGGTT ATAG
```

The PSORT algorithm predicts cytoplasm (0.2817).

The protein was expressed in *E.coli* and purified as a his-tagged product (Figure 149A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 149B) and for FACS analysis.

These experiments show that cp6264 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 150

The following *C.pneumoniae* protein (PID 4376266) was expressed <SEQ ID 299; cp6266>:

```
  1  MLLLISGALF LTLGIPGLSA AISFGLGIGL SALGGVLMIS GLLCLLVKRE
 51  IPTVRPEEIP EGVSLAPSEE PALQAAQKTL AQLPKELDQL DTDIQEVFAC
101  LRKLKDSKYE SRSFLNDAKK ELRVFDFVVE DTLSEIFELR QIVAQEGWDL
151  NFLINGGRSL MMTAESESLD LFHVSKRLGY LPSGDVRGEG LKKSAKEIVA
201  RLMSLHCEIH KVAVAFDRNS YAMAEKAFAK ALGALEESVY RSLTQSYRDK
251  FLESERAKIP WNGHITWLRD DAKSGCAEKK LGMPRNVGRN LGKQSFG*
```

The cp6266 nucleotide sequence <SEQ ID 300> is:

```
  1  ATGCTCTTAC TGATTTCAGG AGCTCTCTTT CTGACGTTAG GGATTCCAGG
 51  ATTGAGTGCA GCAATTTCTT TTGGATTAGG CATCGGTCTC TCCGCATTAG
101  GAGGAGTGCT GATGATTTCG GGACTACTAT GTCTTTTAGT AAAACGAGAG
151  ATTCCGACAG TACGACCAGA AGAAATTCCT GAAGGGGTTT CGCTGGCTCC
```

```
201  TTCTGAGGAG CCAGCTCTAC AGGCAGCTCA GAAGACTTTA GCTCAGCTGC
251  CTAAGGAATT GGATCAGTTA GATACAGATA TTCAGGAAGT GTTCGCATGT
301  TTAAGAAAGC TGAAAGATTC TAAGTATGAA AGTCGAAGTT TTTTAAACGA
351  TGCTAAGAAG GAGCTTCGAG TTTTTGACTT TGTGGTTGAG GATACCCTCT
401  CGGAGATTTT CGAGTTGCGG CAGATTGTGG CTCAAGAGGG ATGGGATTTA
451  AACTTTTTGA TCAATGGGGG ACGAAGCCTC ATGATGACTG CAGAATCTGA
501  ATCGCTTGAT TTGTTTCATG TATCGAAGCG GCTAGGGTAT TTACCTTCTG
551  GGGATGTTCG AGGGGAGGGG TTAAAGAAAT CTGCGAAGGA GATAGTCGCT
601  CGTTTGATGA GCTTGCATTG CGAGATTCAC AAGGTGGCGG TAGCGTTTGA
651  TAGGAATTCC TATGCGATGG CAGAAAAGGC GTTTGCGAAA GCGTTGGGAG
701  CTTTAGAAGA GAGTGTGTAT CGGAGTCTGA CGCAGAGTTA TAGAGATAAA
751  TTTTTGGAGA GCGAGAGGGC GAAGATCCCA TGGAATGGGC ATATAACCTG
801  GTTAAGAGAT GATGCGAAGA GTGGGTGTGC TGAAAAGAAG CTCGGGATGC
851  CGAGGAACGT TGGAAGAAAT TTAGGAAAGC AGTCTTTTGG GTAG
```

The PSORT algorithm predicts inner membrane (0.3590).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 150A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 150) and for FACS analysis.

These experiments show that cp6266 is a surface-exposed and immunoaccessible protein and that they it is a useful immunogen. These properties are not evident from the sequence alone.

Example 151

The following *C.pneumoniae* protein (PID 4376895) was expressed <SEQ ID 301; cp6895>:

```
  1  MKIKKSFQYS LCQAKRFQNM LPNHFDPCLQ PVNLQLKQDR LAYGELIILL
 51  SKYQQKTFSS LLKEETCSLN RAKQHLLYKI LRDFNTMQHL RSLGLNGWGE
101  IPMSPCL*
```

The cp6895 nucleotide sequence <SEQ ID 302> is:

```
  1  ATGAAGATTA AAAAATCTTT TCAATACAGT TTATGCCAAG CAAAGAGATT
 51  TCAGAACATG CTGCCAAACC ACTTTGATCC ATGTTTGCAG CCAGTGAATT
101  TACAACTCAA ACAAGACAGA TTGGCATACG GGGAGCTCAT CATATTGCTA
151  TCTAAATATC AACAAAAGAC CTTTTCCTCT TTGTTGAAGG AAGAAACATG
201  TTCTCTTAAT CGTGCGAAGC AGCACTTATT GTATAAGATT TTGAGAGATT
251  TTAATACTAT GCAGCATCTA AGGTCCCTCG GATTAAATGG TTGGGGAGAG
301  ATCCCTATGA GTCCTTGCCT CTAA
```

The PSORT algorithm predicts cytoplasm (0.3264).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 151A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 151B) and for FACS analysis.

These experiments show that cp6895 is a surface-exposed and immunoaccessible protein and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 152 and
Example 153

The following *C.pneumoniae* protein (PID 4376282) was expressed <SEQ ID 303; cp6282>:

```
  1  MSLLNLPSSQ DSASEDSTSQ SQIFDPIRNR ELVSTPEEKV RQRLLSFLMH
 51  KLNYPKKLII IEKELKTLFP LLMRKGTLIP KRRPDILIIT PPTYTDAQGN
101  THNLGDPKPL LLIECKALAV NQNALKQLLS YNYSIGATCI AMAGKHSQVS
151  ALFNPKTQTL DFYPGLPEYS QLLNYFISLN L*
```

The cp6282 nucleotide sequence <SEQ ID 304> is:

```
  1 ATGTCCTTAT TGAACCTTCC CTCAAGCCAG GATTCTGCAT CTGAGGACTC
 51 CACATCGCAA TCTCAAATCT TCGATCCCAT TAGAAATCGG GAGTTAGTTT
101 CTACTCCCGA AGAAAAAGTC CGCCAAAGGT TGCTCTCCTT CCTAATGCAT
151 AAGCTGAACT ACCCTAAGAA ACTCATCATC ATAGAAAAAG AACTCAAAAC
201 TCTTTTTCCT CTGCTTATGC GTAAAGGAAC CCTAATCCCA AAACGCCGCC
251 CAGATATTCT CATCATCACT CCCCCCACAT ACACAGACGC ACAGGGAAAC
301 ACTCACAACC TAGGCGACCC AAAACCCCTG CTACTTATCG AATGTAAGGC
351 CTTAGCCGTA AACCAAAATG CACTCAAACA ACTCCTTAGC TATAACTACT
401 CTATCGGAGC CACCTGCATT GCTATGGCAG GGAAACACTC TCAAGTGTCA
451 GCTCTCTTCA ATCCAAAAAC ACAAACTCTT GATTTTTATC CTGGCCTCCC
501 AGAGTATTCC CAACTCCTAA ACTACTTTAT TTCTTTAAAC TTATAG
```

The PSORT algorithm predicts cytoplasm (0.362).

The following *C.pneumoniae* protein (PID 4377373) was also expressed <SEQ ID 305; cp7373>:

```
  1 MSTTTVKHFI HTASRWEPVL KEIVASNYWH AQWINTLSFL ENSGAKKISA
 51 SEHPTEVKEE VLKHAAEEFR HGHYLKTQIS RISETSLPDY TSKNLLGGLL
101 TKYYLHLLDL RTCRVLENEY SLSGQTLKTA AYILVTYAIE LRASELYPLY
151 HDILKEAQSK ITVKSIILEE QGHLQEMERE LKDLPHGEEL LGYACQFEGE
201 LCLQFVERLE QMIFDPSSTF TKF*
```

The cp7373 nucleotide sequence <SEQ ID 306> is:

```
  1 ATGTCTACAA CCACAGTAAA ACACTTTATC CACACAGCCT CTCGTTGGGA
 51 GCCCGTTCTC AAAGAGATCG TAGCTTCCAA CTATTGGCAT GCACAATGGA
101 TAAATACCCT GTCCTTTTTA GAAAATAGTG GAGCAAAAAA AATCTCCGCA
151 AGTGAACATC CTACGGAGGT AAAGGAAGAA GTTTTAAAAC ATGCTGCTGA
201 AGAATTTCGT CATGGTCACT ATCTAAAAAC TCAGATTTCT AGAATCTCAG
251 AGACTTCTCT CCCTGACTAT ACATCTAAAA ATCTTCTGGG AGGCTTACTT
301 ACAAAATATT ACCTCCATCT TCTAGATTTA AGGACGTGCC GAGTACTGGA
351 AAATGAATAC TCCCTATCGG GACAAACGTT AAAAACTGCA GCGTATATTT
401 TAGTTACCTA CGCAATCGAA CTTCGTGCTT CTGAACTTTA TCCTCTGTAT
451 CACGATATTC TGAAAGAAGC TCAAAGTAAA ATAACGGTAA AATCCATTAT
501 CTTAGAAGAG CAAGGCCATC TGCAAGAGAT GGAACGTGAA CTTAAAGATC
551 TCCCCCACGG GGAGGAACTC TTAGGCTATG CTTGCCAATT CGAAGGGGAG
601 CTTTGCTTGC AGTTTGTAGA GAGATTAGAA CAAATGATCT TCGATCCTTC
651 CTCGACTTTT ACAAAGTTCT AG
```

The PSORT algorithm predicts cytoplasm (0.1069).

The proteins were expressed in *E.coli* and purified as his-tag products (Figure 152A; 6282 = lanes 8 & 9; 7373 = lanes 2-4). The recombinant proteins were used to immunise mice, whose sera were used in Western blots (Figures 152B & 153) and for FACS analysis.

These experiments show that cp6282 & cp7373 are surface-exposed and immunoaccessible proteins and that they are useful immunogens. These properties are not evident from the sequence alone.

Example 154 ,
Example 155 ,
Example 156 ,
Example 157 and
Example 158

The following *C.pneumoniae* protein (PID 4376412) was expressed <SEQ ID 307; cp6412>:

```
  1 MSSSEVVFQT VHGLGFGGLS SKSVVPFKKS LSDAPRVVCS ILVLTLGLGA
 51 LVCGIAITCW CVPGVILMGG ICAIVLGAIS LALSLFWLWG LFSNCCGSKR
101 VLPGEGLLRD KLLDGGFSRA APSGMGLPGD GSPRASTPSC LEELQAEIQA
151 VTQAIDQMSD D*
```

The cp6412 nucleotide sequence <SEQ ID 308> is:

```
  1  ATGAGCAGTT CGGAAGTTGT TTTCCAGACA GTTCATGGCC TTGGCTTTGG
 51  TGGATTGTCT TCAAAAAGTG TTGTCCCTTT TAAGAAAAGT CTTTCGGATG
101  CGCCCCGTGT TGTGTGCTCG ATTTTAGTTT TGACTCTGGG GTTGGGAGCG
151  CTTGTTTGTG GTATTGCCAT TACTTGTTGG TGTGTCCCGG GAGTTATTTT
201  AATGGGGGGA ATTTGCGCTA TAGTTTTAGG TGCAATTTCT TTAGCTTTAA
251  GTCTATTTTG GTTGTGGGGT TTATTTTCTA ATTGTTGTGG TTCTAAGAGA
301  GTTTTACCGG GTGAGGGATT GCTACGGGAT AAGCTTTTAG ATGGTGGATT
351  TTCAAGAGCG GCACCTTCAG GAATGGGACT TCCGGGTGAT GGATCTCCAA
401  GAGCGTCAAC GCCATCTTGC CTAGAGGAAC TTCAAGCAGA GATACAGGCA
451  GTTACTCAAG CTATCGATCA GATGTCAGAT GATTGA
```

The PSORT algorithm predicts inner membrane (0.4864).

The following *C.pneumoniae* protein (PID 4376431) was also expressed <SEQ ID 309; cp6431>:

```
  1  LRAGGSLVTT YPKEGQRLRS PEQLRVLDDL VQSYPNHLHA IELDCGAIPQ
 51  DLIGATYIIT FADFSTYILS LRSYQANSPS DDTWGIWFGS IDDPVQAVIS
101  FLKDHGFALP STLAQDPLLC TNK*
```

The cp6431 nucleotide sequence <SEQ ID 310> is:

```
  1  TTGCGAGCAG GAGGTAGTCT TGTTACAACA TACCCTAAGG AAGGTCAGAG
 51  ATTGCGCTCC CCAGAACAGT TAAGAGTTCT GGATGATTTA GTGCAAAGCT
101  ATCCAAATCA CCTACATGCG ATTGAACTTG ATTGTGGTGC AATCCCTCAA
151  GATTTGATCG GAGCCACCTA TATCATCACG TTCGCCGATT TTTCCACCTA
201  TATTCTCTCT TTAAGAAGCT ACCAAGCCAA TTCTCCCTCC GATGATACAT
251  GGGGGATTTG GTTTGGATCT ATTGACGATC CTGTTCAAGC AGTCATATCA
301  TTTTTAAAAG ATCATGGATT TGCTCTTCCC TCGACCTTAG CTCAAGATCC
351  TTTGCTTTGT ACTAACAAGT AA
```

The PSORT algorithm predicts cytoplasm (0.2115).

The following *C.pneumoniae* protein (PID 4376443) was also expressed <SEQ ID 311; cp6443>:

```
  1  MIMTTISNSP SPALNPELSL IPPPTLVSSG TQTSLAYTIP AQGRRSTLRI
 51  ILDIFIIILG LATIISTFIV IFFLNGLNLL STPSIISSSC LIIVGLLFLI
101  MGLYFMISSL DQGLVGLLQK ELSQAEEREE EYIQEIEALR GAPRAESPTE
151  SPSTWL*
```

The cp6443 nucleotide sequence <SEQ ID 312> is:

```
  1  ATGATTATGA CTACTATATC TAACTCACCC TCCCCTGCAT TGAATCCCGA
 51  ACTTTCCCTT ATTCCTCCAC CAACACTTGT ATCTTCAGGT ACGCAAACAT
101  CTCTAGCTTA TACGATCCCC GCACAAGGAC GAAGATCCAC CCTACGTATT
151  ATATTAGATA TATTCATTAT CATTCTTGGT TTAGCTACGA TCATTTCTAC
201  CTTTATTGTT ATTTTCTTTT TAAATGGGCT GAACTTGCTC TCGACCCCAT
251  CTATTATCTC TTCGTCATGT TTAATCATTG TTGGATTGCT TTTTTTGATT
301  ATGGGGTTAT ATTTCATGAT CTCGAGTTTG GATCAGGGGC TTGTAGGCCT
351  TCTGCAAAAG GAACTCTCTC AAGCCGAAGA AAGAGAAGAA GAGTATATCC
401  AGGAAATCGA AGCTTTAAGA GGAGCTCCTA GAGCAGAATC TCCCACAGAG
451  TCTCCTAGTA CCTGGTTATG A
```

The PSORT algorithm predicts inner membrane (0.5585).

The following *C.pneumoniae* protein (PID 4376496) was also expressed <SEQ ID 313; cp6496>:

```
  1  MLIGRYSSDD QFTEATKNTP TIIKLGFVRD NLEGLTNPIS EIVSETSSSI
 51  KDSVLRSLPI LGSILGCARL YSTLSTNDPL DETQEKIWHT IFGALETLGL
101  GILILLFKII FVILHCIFHL VIGFCK*
```

The cp6496 nucleotide sequence <SEQ ID 314> is:

```
  1  ATGCTAATAG GCAGATACAG TAGTGATGAC CAATTCACTG AAGCAACAAA
 51  AAACACCCCA ACCATAATTA AGCTAGGTTT TGTTAGAGAT AATCTCGAGG
101  GATTAACGAA CCCTATCTCT GAAATCGTCT CGGAAACCTC CTCTTCTATT
151  AAAGATTCCG TTCTTCGCTC TCTTCCTATT TTAGGGTCCA TTTTAGGATG
201  CGCCCGACTT TACAGCACAC TCTCTACAAA TGATCCTCTT GACGAAACTC
251  AAGAAAAGAT TTGGCACACT ATATTTGGAG CCTTAGAAAC CTTAGGCTTA
301  GGGATTCTCA TCCTCTTATT TAAAATTATT TTTGTTATAT TACACTGCAT
351  ATTTCATCTA GTTATTGGGT TCTGCAAATA A
```

The PSORT algorithm predicts inner membrane (0.5989).

The following *C.pneumoniae* protein (PID 4376654) was also expressed <SEQ ID 315; cp6654>:

```
  1 MKTKMNSRKK AGQWAIFNSP TPGVSSTLVL AWTPWGYYDK DVQDILERKD
 51 PMSSSLSEKD SKEFLKNLFV DLLENGFTSV HIHAEEAFTP LDHTGKPHFK
101 RDNVYLPGKL LGALNEAAVQ ANVSADTQFT LFLTQDECNP FHDKKRG*
```

The cp6654 nucleotide sequence <SEQ ID 316> is:

```
  1 ATGAAAACTA AAATGAACTC TAGAAAAAAA GCAGGTCAAT GGGCAATTTT
 51 CAATTCTCCA ACTCCTGGTG TCAGTTCAAC TTTAGTTTTA GCATGGACTC
101 CTTGGGGTTA TTACGACAAG GATGTACAAG ATATCTTAGA AAGAAAAGAT
151 CCGATGAGCT CTTCGCTTTC TGAAAAAGAC TCAAAGGAGT TCTTGAAAAA
201 TCTGTTTGTA GATCTCTTAG AAAATGGCTT CACATCAGTA CATATTCACG
251 CAGAAGAAGC TTTCACTCCT CTTGATCATA CCGGGAAACC TCACTTTAAA
301 AGAGACAATG TGTACTTACC CGGAAAGTTG TTAGGCGCCT TGAATGAGGC
351 TGCGGTACAA GCCAATGTAA GTGCGGATAC TCAATTTACA TTGTTCCTTA
401 CTCAAGATGA GTGCAATCCT TTTCATGATA AGAAAAGAGG TTAA
```

The PSORT algorithm predicts cytoplasm (0.0730).

The proteins were expressed in *E.coli* and purified as his-tag products (Figure 154A; 6412 = lanes 2-3; 6431 = lanes 11-12; 6443 = lanes 5-6; 6496 = lanes 8-9; 6654 = lane 10; markers in lanes 1, 4, 7). The recombinant proteins were used to immunise mice, whose sera were used in Western blots (Figures 154B, 155, 156, 157 & 158) and for FACS analysis.

These experiments show that cp6412, cp6431, cp6443, cp6496 & cp6654 are surface-exposed and immunoaccessible proteins and that they are useful immunogens. These properties are not evident from their sequences alone.

Example 159 and
Example 160

The following *C.pneumoniae* protein (PID 4376477) was expressed <SEQ ID 317; cp6477>:

```
  1 LLKFFLVCEE LCILTVATHR ALLETPLALS FFKELKTKYV YRAKDILQLH
 51 NYKGFTILNT SPLCS*
```

The cp6477 nucleotide sequence <SEQ ID 318> is:

```
  1 TTGCTAAAGT TCTTTCTAGT ATGTGAAGAG TTATGTATAC TTACTGTTGC
 51 TACACATAGA GCTCTCTTAG AAACTCCTTT AGCTCTATCA TTTTTTAAAG
101 AACTTAAGAC AAAATATGTC TACAGGGCGA AAGACATACT ACAACTACAT
151 AACTATAAAG GATTTACTAT CCTTAATACA TCACCGTTAT GTTCTTAA
```

The PSORT algorithm predicts inner membrane (0.128).

The following *C.pneumoniae* protein (PID 4376435) was also expressed <SEQ ID 319; cp6435>:

```
  1 LWSHFPRGFF MLPFCPTILL AKPFLNSENY GLERLAATVD SYFDLGQSQI
 51 VFLSKQDQGI TVEELSAKDR KFKPGSMNCT LYTEDPILPA HNSFSNCSDI
101 QMRTPISPIH *
```

The cp6435 nucleotide sequence <SEQ ID 320> is:

```
  1 TTGTGGTCGC ATTTCCCAAG AGGATTTTTT ATGCTCCCTT TTTGCCCTAC
 51 CATCCTTCTT GCTAAACCTT TTTTAAATAG CGAGAATTAC GGCTTAGAAC
101 GTTTAGCTGC AACCGTAGAT TCTTATTTTG ATCTGGGACA GTCTCAAATA
151 GTCTTCCTAA GCAAACAGGA TCAAGGAATC ACTGTGGAAG AATTGAGTGC
201 TAAAGATAGG AAATTCAAGC CAGGCTCTAT GAACTGTACA CTGTACACTG
251 AAGATCCTAT CTTACCTGCT CATAATTCCT TTAGTAATTG CTCTGATATT
301 CAAATGCGTA CTCCGATTAG CCCTATACAT TAA
```

The PSORT algorithm predicts periplasmic space (0.4044).

The proteins were expressed in *E.coli* and purified as his-tag products (Figure 159A; 6435 = lanes 2-4; 6477 = lanes 5-7). The recombinant proteins were used to immunise mice, whose sera were used in Western blots (Figures 159B & 160) and for FACS analysis.

These experiments show that cp6477 & cp6435 are surface-exposed and immunoaccessible proteins and that they are useful immunogens. These properties are not evident from the sequences alone.

Example 161 and
Example 162 and
Example 163

The following *C.pneumoniae* protein (PID 4376441) was expressed <SEQ ID 321; cp6441>:

```
  1 VEAGANVLVI DTAHAHSKGV FQTVLEIKSQ FPQISLVVGN LVTAEAAVSL
 51 AEIGVDAVKV GIGPGSICTT RIVSGVGYPQ ITAITNVAKA LKNSAVTVIA
101 DGRIRYSGDV VKALAAGADC VMLGSLLAGT DEAPGDIVSI DEKLFKRYRG
151 MGSLGAMKQG SADRYFQTQG QKKLVPGGVE GLVAYKGSVH DVLYQILGGI
201 RSGMGYVGAE TLKDLKTKAS FVRITESGRA ESHIHNIYKV QPTLNY
```

The cp6441 nucleotide sequence <SEQ ID 322> is:

```
  1 GTGGAAGCTG GAGCAAATGT TCTAGTCATT GACACAGCTC ATGCACACTC
 51 TAAAGGAGTA TTCCAAACAG TTTTAGAAAT AAAATCCCAG TTCCCACAAA
101 TTTCTTTAGT TGTAGGGAAT CTTGTTACAG CTGAAGCCGC AGTTTCCTTA
151 GCTGAGATTG GAGTTGACGC TGTAAAGGTA GGTATTGGCC CAGGATCTAT
201 CTGTACAACT AGAATCGTTT CAGGGGTCGG TTATCCACAA ATTACTGCCA
251 TTACAAACGT AGCAAAAGCT CTTAAAAACT CTGCCGTGAC TGTAATTGCT
301 GATGGGAGAA TCCGCTATTC TGGAGATGTG GTAAAAGCAT TAGCAGCAGG
351 AGCAGACTGT GTCATGCTAG GAAGTTTGCT TGCAGGGACT GATGAAGCTC
401 CTGGGGATAT CGTTTCTATC GATGAGAAGC TTTTTAAAAG GTACCGCGGC
451 ATGGGATCTT TAGGCGCTAT GAAACAAGGA AGTGCTGACC GGTATTTTCA
501 AACACAGGGA CAGAAAAAGC TGGTTCCTGG GGGAGTTGAA GGACTAGTCG
551 CTTATAAAGG CTCTGTCCAC GATGTCCTCT ATCAAATTTT AGGAGGAATA
601 CGCTCAGGTA TGGGGTATGT TGGAGCTGAA ACTCTCAAAG ATTTAAAAAC
651 TAAGGCTTCC TTTGTTCGAA TTACTGAATC TGGAAGAGCT GAAAGTCATA
701 TTCATAATAT TTACAAAGTT CAACCAACCT TAAATTATTA A
```

The PSORT algorithm predicts bacterial inner membrane (0.132).

The following *C.pneumoniae* protein (PID 4376748) was also expressed <SEQ ID 323; cp6748>:

```
  1 LFSEGTALNL FRIFAPLRNR VTTEYSRARQ PDLHRIAIVY IGVLDSESSK
 51 ILERLISYMS CIYSESQMYL RFFMGKNVNQ SAVLSKLHVE NLHIRCGFFS
101 EDAVPESEPF DLSIYVHTDR SCPLPTKKRS SSWELQTVEL PESIYPQSEF
151 LLMRPRMLS*
```

The cp6748 nucleotide sequence <SEQ ID 324> is:

```
  1 TTGTTCTCTG AGGGGACAGC TCTAAATTTA TTTCGTATAT TTGCTCCACT
 51 ACGCAACCGT GTGACTACAG AATACAGTCG TGCTAGGCAA CCCGACCTAC
101 ATAGAATTGC CATCGTCTAT ATAGGAGTTC TCGATTCAGA AAGTTCCAAG
151 ATCCTAGAGC GGCTAATCTC TTATATGAGT TGTATCTATT CTGAATCGCA
201 AATGTATTTA AGATTCTTTA TGGGCAAGAA TGTAAATCAA AGTGCTGTAC
251 TCTCAAAATT ACATGTAGAA AATCTGCACA TCCGTTGTGG GTTTTTCAGC
301 GAGGATGCTG TTCCAGAGAG TGAGCCCTTC GATCTCTCCA TCTACGTGCA
351 CACAGATCGT AGCTGTCCTC TCCCTACGAA AAAACGGAGC AGCTCCTGGG
401 AACTCCAAAC TGTAGAACTC CCAGAGTCAA TATATCCACA GTCGGAATTC
451 CTATTGATGA GACCTCGAAT GCTTTCGTAG
```

The PSORT algorithm predicts cytoplasm (0.170).

The following *C.pneumoniae* protein (PID 4376881) was also expressed <SEQ ID 325; cp6881>:

```
  1 MRPHRKHVSS KSLALKQSAS THVEITTKAF RLSMPLKQLI LEKSDHLPPM
 51 ETIRVVLTSH KDKLGTEVHV VASHGKEILQ TKVHNANPYT AVINAFKKIR
101 TMANKHSNKR KDRTKHDLGL AAKEERIAIQ EEQEDRLSNE WLPVEGLDAW
151 DSLKTLGYVP ASAKKKISKK KMSIRMLSQD EAIRQLESAA ENFLIFLNEQ
201 EHKIQCIYKK HDGNYVLIEP SLKPGFCI*
```

The cp6881 nucleotide sequence <SEQ ID 326> is:

```
  1 ATGAGACCTC ATCGTAAACA CGTATCATCT AAAAGCTTAG CTTTAAAGCA
 51 ATCTGCATCA ACTCATGTAG AGATCACAAC AAAAGCCTTT CGTCTCTCTA
101 TGCCTCTAAA ACAGCTGATC CTAGAGAAAA GCGACCACCT CCCCCCTATG
151 GAAACAATCC GTGTGGTGCT AACCTCTCAT AAAGATAAGC TAGGCACCGA
201 GGTGCATGTT GTAGCTTCTC ATGGCAAAGA AATCCTTCAA ACTAAGGTTC
251 ATAACGCAAA CCCATACACT GCAGTGATCA ATGCTTTTAA GAAAATCCGC
301 ACCATGGCAA ATAAGCACTC CAATAAACGT AAAGACAGGA CAAAACATGA
351 TCTAGGTCTT GCAGCAAAAG AAGAACGTAT CGCAATACAG GAAGAACAAG
401 AAGATCGCCT TAGCAACGAG TGGCTTCCTG TCGAAGGCCT CGATGCCTGG
451 GATTCTCTAA AAACTCTTGG GTATGTTCCC GCATCAGCGA AAAAGAAGAT
501 CTCCAAGAAA AAGATGAGCA TTCGTATGCT ATCTCAAGAC GAGGCTATCC
551 GCCAGCTAGA GTCTGCCGCA GAAAACTTCC TGATCTTCTT GAACGAGCAA
601 GAGCATAAAA TCCAATGCAT TTATAAAAAA CATGACGGCA ACTATGTCCT
651 TATTGAACCT TCCCTCAAGC CAGGATTCTG CATCTGA
```

The PSORT algorithm predicts cytoplasm (0.249).

The proteins were expressed in *E.coli* and purified as his-tag products (Figure 161A; 6441= lanes 7-9; 6748 = lanes 2-3; 6881 = lanes 4-6). The recombinant protein was used to immunise mice, whose sera were used in Western blots (Figures 161B, 162 & 163) and for FACS analysis.

These experiments show that cp6441, cp6748 & cp6881 are surface-exposed and immunoaccessible proteins and that they are useful immunogens. These properties are not evident from the sequence alone.

Example 164 and
Example 165
Example 166

The following *C.pneumoniae* protein (PID 4376444) was expressed <SEQ ID 327; cp6444>:

```
  1 MEQPNCVIQD TTTVLYALNS FDPRLSDDTH RLGKQSPLEA ENALGEFIEG
 51 LDTNSFPLEE VAIPILPGYH PKFYLSFIDR DDQGVHYEVL DGVFLKTVAA
101 CIIENSFLTD SMSPELLSEV KEALKR*
```

The cp6444 nucleotide sequence <SEQ ID 328> is:

```
  1 ATGGAGCAAC CCAATTGTGT GATTCAGGAT ACTACAACTG TTTTGTATGC
 51 CTTAAATAGC TTTGATCCTA GACTTAGTGA TGACACTCAC AGACTTGGGA
101 AGCAATCACC TCTTGAAGCA GAAAATGCTC TTGGAGAATT TATTGAAGGT
151 TTGGATACAA ATAGCTTTCC TTTAGAGGAA GTTGCCATTC CCATCCTGCC
201 AGGTTATCAC CCTAAGTTTT ATTTATCTTT CATAGATAGG GACGATCAAG
251 GTGTCCACTA TGAAGTTTTA GATGGCGTAT TTTTAAAGAC AGTCGCTGCT
301 TGTATTATAG AGAACTCCTT CTTAACTGAT TCTATGAGCC CGGAGCTTCT
351 CAGCGAAGTT AAGGAAGCTC TGAAACGATG A
```

The PSORT algorithm predicts cytoplasm (0.2031).

The following *C.pneumoniae* protein (PID 4376413) was also expressed <SEQ ID 329; cp6413>:

```
  1 MAVQSIKEAV TSAATSVGCV NCSREAIPAF NTEERATSIA RSVIAAIIAV
 51 VAISLLGLGL VVLAGCCPLG MAAGAITMLL GVALLAWAIL ITLRLLNIPK
101 AEIPSPGNNG EPNERNSATP PLEGGVAGEA GRGGGSPLTQ LDLNSGAGS*
```

The cp6413 nucleotide sequence <SEQ ID 330> is:

```
  1 ATGGCTGTTC AATCTATAAA AGAAGCCGTA ACATCAGCCG CAACATCAGT
```

```
 51  AGGATGTGTA AACTGTTCTA GAGAGGCTAT ACCAGCATTT AATACAGAGG
101  AGAGAGCAAC GAGTATTGCT AGATCTGTTA TAGCAGCTAT CATTGCTGTT
151  GTAGCTATCT CCTTACTCGG ACTAGGTCTT GTAGTTCTTG CTGGTTGCTG
201  TCCTTTAGGA ATGGCTGCGG GTGCTATAAC AATGCTGCTG GGTGTAGCAT
251  TATTAGCTTG GGCAATACTG ATTACTTTGA GACTGCTTAA TATACCTAAG
301  GCTGAAATAC CGAGTCCAGG GAACAACGGT GAGCCTAATG AAAGAAATTC
351  AGCAACTCCT CCTCTAGAGG GTGGTGTTGC AGGAGAAGCC GGTCGCGGCG
401  GGGGGTCACC TTTAACCCAA CTTGATCTCA ATTCAGGGGC GGGAAGTTAG
```

The PSORT algorithm predicts inner membrane (0.6180).

The following *C.pneumoniae* protein (PID 4377391) was also expressed <SEQ ID 331; cp7391>:

```
  1  MMLRVIELPL LPIKQALEKA FVQYNSYKAK LTKVEPCFRE SPAYITSEER
 51  LQSLDQTLER AYKEYQKRFQ EPSRLESEVS GCREHLREQV KQFETQGLDL
101  IKEELIFVSD VLFRKMVSCL VSTVHVPFME FYYEYFELHR LRLRAQWMAN
151  AEIYSKVRKA FPEMLKETLE KAKAPREEEY WLLCEERKSK EKRLILNKIE
201  AAQQRVKDLE PPPIKETGKQ KRKKEYSFFI RLKS*
```

The cp7391 nucleotide sequence <SEQ ID 332> is:

```
  1  ATGATGCTTC GTGTCATAGA GCTTCCACTA CTTCCTATAA AGCAAGCGTT
 51  GGAGAAGGCT TTTGTACAAT ATAATAGCTA CAAAGCGAAG TTAACCAAGG
101  TAGAACCTTG CTTTAGAGAG AGCCCTGCCT ATATAACTAG CGAAGAGCGA
151  CTCCAGAGTT TGGATCAGAC TTTAGAACGT GCGTACAAAG AGTACCAGAA
201  GAGATTCCAG GAGCCTTCAC GTTTGGAATC GGAAGTAAGT GGATGTAGAG
251  AGCATCTTAG AGAGCAGGTA AAACAATTTG AAACTCAAGG ACTAGACTTG
301  ATCAAAGAAG AGCTTATTTT TGTTAGTGAT GTGTTATTCC GAAAAATGGT
351  CAGTTGTCTA GTGTCGACAG TGCATGTTCC CTTTATGGAG TTTTATTATG
401  AGTATTTTGA GTTGCATAGA TTGAGGTTGC GGGCCCAATG GATGGCGAAT
451  GCCGAGATTT ATAGCAAAGT TAGAAAAGCA TTCCCAGAGA TGTTGAAGGA
501  GACCTTAGAA AAAGCTAAGG CTCCCAGAGA AGAAGAGTAT TGGTTACTTT
551  GCGAGGAGAG AAAGAGTAAG GAGAAGCGTT TGATTCTCAA CAAGATAGAG
601  GCAGCTCAGC AGCGGGTAAA AGATTTAGAA CCTCCTCCTA TTAAAGAGAC
651  AGGGAAACAG AAACGGAAGA AAGAATATTC GTTTTTCATT CGATTAAAAT
701  CGTGA
```

The PSORT algorithm predicts inner membrane (0.1489).

The proteins were expressed in *E.coli* and purified as his-tag and GST-fusion products (Figure 164A; 6444=lanes 11-12; 7391=lanes 2-3; 6413=lanes 4-6). The recombinant protein was used to immunise mice, whose sera were used in Western blots (Figures 164B, 165 & 166) and for FACS analysis.

These experiments show that cp6444, cp6413 & cp7391 are surface-exposed and immunoaccessible proteins and that they are useful immunogens. These properties are not evident from the sequence alone.

Example 167 ,
Example 168 ,
Example 169 and
Example 170

The following *C.pneumoniae* protein (PID 4376463) was expressed <SEQ ID 333; cp6463>:

```
  1  MKKKVTIDEA LKEILRLEGA ATQEELCAKL LAQGFATTQS SVSRWLRKIQ
 51  AVKVAGERGA RYSLPSSTEK TTTRHLVLSI RHNASLIVIR TVPGSASWIA
101  ALLDQGLKDE ILGTLAGDDT IFVTPIDEGR LPLLMVSIAN LLQVFLD*
```

The cp6463 nucleotide sequence <SEQ ID 334> is:

```
  1  ATGAAAAAAA AAGTAACTAT AGATGAGGCT TTAAAAGAAA TTTTACGTCT
 51  TGAAGGAGCG GCAACTCAGG AGGAATTATG TGCAAAACTC TTAGCTCAAG
101  GTTTTGCTAC AACCCAGTCG TCTGTATCTC GTTGGCTACG AAAGATTCAG
151  GCTGTAAAGG TTGCTGGAGA GCGTGGTGCT CGTTATTCTT TACCCTCTTC
```

```
201  AACAGAGAAG ACCACGACCC GTCATTTGGT GCTCTCTATT CGCCATAACG
251  CCTCTCTTAT TGTAATTCGT ACGGTTCCTG GTTCAGCTTC TTGGATCGCT
301  GCTTTGTTAG ATCAAGGGCT CAAAGATGAA ATTCTTGGAA CTTTGGCAGG
351  AGATGACACG ATTTTTGTCA CTCCTATAGA TGAAGGGAGG CTCCCATTGT
401  TGATGGTTTC GATTGCAAAT TTACTGCAAG TTTTCTTGGA TTAA
```

The PSORT algorithm predicts inner membrane (0.1510).

The following *C.pneumoniae* protein (PID 4376540) was also expressed <SEQ ID 335; cp6540>:

```
  1  MSQCQSSSTS TWEWMKSFVP NWKNPTPPLS PIPSEDEFIL AYEPFVLPKT
 51  DPENAQANPP GTSTPNVENG IDDLNPLLGQ PNEQNNANNP GTSGSNPTSL
101  PAPERLPETE ENSQEEEQGS QNNEDLIG*
```

The cp6540 nucleotide sequence <SEQ ID 336> is:

```
  1  ATGTCTCAAT GTCAGAGTAG CAGTACATCT ACCTGGGAAT GGATGAAATC
 51  TTTTGTGCCA AACTGGAAGA ATCCAACTCC CCCCTTATCT CCTATACCTT
101  CTGAGGACGA ATTTATATTA GCATACGAGC CATTTGTTCT ACCGAAAACA
151  GATCCAGAAA ACGCACAAGC TAATCCTCCA GGCACATCTA CACCGAATGT
201  AGAAAACGGG ATCGATGATC TCAACCCTCT TCTGGGGCAA CCCAACGAAC
251  AAAACAATGC CAACAATCCA GGAACTTCTG GATCTAATCC TACATCTCTA
301  CCCGCCCCCG AACGACTCCC TGAAACTGAA GAGAACAGCC AAGAAGAAGA
351  ACAAGGATCT CAAAATAATG AGGATCTTAT AGGATAA
```

The PSORT algorithm predicts cytoplasm (0.3086).

The following *C.pneumoniae* protein (PID 4376743) was also expressed <SEQ ID 337; cp6743>:

```
  1  LREEGSVSFR EYFRAYMCDK IVAQKNFLFT LDAVIKQAGW RSQEKLNLFY
 51  VESQALGREI KVSLEEYIQS MVGILGSQRT KKSFKFSVDF TPLEQALQER
101  CSSDDDEDAT ATSTATGATA SPTDMHEDE*
```

The cp6743 nucleotide sequence <SEQ ID 338> is:

```
  1  TTGAGAGAAG AAGGTAGTGT TTCTTTCAGA GAATATTTCA GAGCCTATAT
 51  GTGTGATAAA ATCGTGGCAC AGAAGAACTT CTTATTTACT TTAGACGCTG
101  TAATTAAACA GGCCGGTTGG AGATCACAAG AGAAACTCAA TTTATTTTAT
151  GTTGAAAGTC AGGCTTTAGG AAGAGAAATC AAAGTCAGCT TAGAGGAATA
201  TATTCAGAGT ATGGTCGGGA TTTTGGGATC TCAGAGAACC AAGAAAAGCT
251  TTAAGTTTTC TGTCGACTTT ACCCCTTTAG AGCAGGCTCT ACAAGAAAGA
301  TGCTCTTCTG ATGATGACGA AGATGCAACA GCAACTTCGA CCGCTACAGG
351  GGCAACAGCA TCTCCGACTG ACATGCACGA AGATGAGTAA
```

The PSORT algorithm predicts cytoplasm (0.2769).

The following *C.pneumoniae* protein (PID 4377041) was also expressed <SEQ ID 339; cp7041>:

```
  1  MLMMLMMIIG ITGGSGAGKT TLTQNIKEIF GEDVSVICQD NYYKDRSHYT
 51  PEERANLIWD HPDAFDNDLL ISDIKRLKNN EIVQAPVFDF VLGNRSKTEI
101  ETIYPSKVIL VEGILVFENQ ELRDLMDIRI FVDTDADERI LRRMVRDVQE
151  QGDSVDCIMS RYLSMVKPMH EKFIEPTRKY ADIIVHGNYR QNVVTNILSQ
201  KIKNHLENAL ESDETYYMVN SK*
```

The cp7041 nucleotide sequence <SEQ ID 340> is:

```
  1  ATGTTGATGA TGCTTATGAT GATTATTGGA ATTACAGGAG GTTCTGGAGC
 51  TGGGAAAACC ACCCTAACCC AAAACATTAA AGAAATTTTC GGTGAGGATG
101  TGAGTGTTAT CTGCCAAGAT AATTATTACA AAGATAGATC TCATTATACT
151  CCTGAAGAAC GTGCCAATTT AATTTGGGAT CATCCGGACG CCTTTGATAA
201  TGACTTATTA ATTTCAGACA TAAAACGTCT AAAAAATAAT GAGATTGTCC
251  AAGCCCCAGT TTTTGATTTT GTTTTAGGTA ATCGATCTAA AACGGAGATA
301  GAAACGATCT ATCCATCTAA AGTTATTCTT GTTGAAGGTA TTCTGGTCTT
351  TGAAAATCAA GAACTTAGAG ATCTTATGGA TATTAGGATC TTTGTAGACA
401  CCGATGCTGA TGAAAGGATA CTACGCCGTA TGGTTCGAGA TGTTCAAGAA
451  CAAGGAGATA GCGTGGACTG CATCATGTCT CGTTATCTTT CTATGGTAAA
501  GCCTATGCAT GAGAAATTTA TAGAGCCGAC TCGGAAATAT GCTGATATCA
551  TTGTACATGG AAATTACCGA CAAAACGTAG TAACAAATAT TTTGTCACAG
601  AAAATTAAAA ATCATTTAGA GAATGCCCTG GAAAGCGATG AGACGTATTA
651  TATGGTCAAC TCTAAGTAA
```

The PSORT algorithm predicts inner membrane (0.1022).

The proteins were expressed in *E.coli* and purified as his-tag products (Figure 167A; 6463 = lanes 2-4; 6540 = lanes 5-7; 6743 = lanes 8-9; 7041 = lanes 10-11). The recombinant proteins were used to immunise miee, whose sera were used in Western blots (Figures 167B, 168, 169 & 170) and for FACS analysis.

These experiments show that cp6463, cp6540, cp6743 & cp7041 are surface-exposed and immunoaccessible proteins and that they are useful immunogens. These properties are not evident from the sequence alone.

Example 171 and
Example 172 and
Example 173

The following *C.pneumoniae* protein (PID 4376632) was expressed <SEQ ID 341; cp6632>:

```
  1  VQLFQYMNES GWDWLCDFDS QGEGFQLSRL VGLLHSSWAL YEAKEQFYLP
 51  EVSLLTWEEL IEMQLLSKPT KHGVAKDLCN VFEKHFQRFR QYLGSLDLNQ
101  RFENTFLNYP KYHLDRE*
```

The cp6632 nucleotide sequence <SEQ ID 342> is:

```
  1  GTGCAATTAT TTCAATATAT GAATGAGTCC GGATGGGATT GGCTTTGTGA
 51  TTTTGATTCT CAAGGCGAGG GATTCCAGTT ATCACGTCTG GTTGGGCTGT
101  TACATTCGTC CTGGGCATTA TACGAAGCAA AAGAGCAATT TTACCTTCCT
151  GAGGTTTCTC TATTGACCTG GGAAGAACTG ATAGAAATGC AGTTATTAAG
201  CAAACCAACA AAACACGGGG TTGCAAAAGA TCTTTGTAAT GTATTTGAAA
251  AACACTTTCA AAGGTTTAGA CAGTACCTAG GTTCCTTAGA TCTAAATCAA
301  AGGTTCGAAA ATACCTTCTT GAATTATCCT AAATACCATT TAGATAGGGA
351  GTGA
```

The PSORT algorithm predicts cytoplasm (0.3627).

The following *C.pneumoniae* protein (PID 4376648) was also expressed <SEQ ID 343; cp6648>:

```
  1  MPVSSAPLPT SHRPSSGNLG LMEPNSKALK AKHQDKTTKT IKLLVKILVA
 51  ILVIEVLGII AAFFIPGTPP ICLIILGGLI LTTVLCVLLL VIKLALVNKT
101  EGTTAEQQIK RKLSSKSIS*
```

The cp6648 nucleotide sequence <SEQ ID 344> is:

```
  1  ATGCCCGTGT CCTCAGCCCC CCTACCCACA AGCCACCGCC CTTCCTCTGG
 51  AAATCTAGGC CTCATGGAAC CAAATTCCAA AGCTCTAAAA GCAAAGCATC
101  AAGATAAAAC GACGAAGACG ATTAAACTTT TAGTTAAAAT CCTTGTTGCC
151  ATTCTAGTAA TAGAAGTTTT AGGAATAATT GCAGCTTTCT TTATTCCTGG
201  GACTCCTCCC ATCTGCTTGA TTATCCTAGG AGGCCTTATT CTTACAACAG
251  TACTCTGTGT GCTTCTTCTT GTTATAAAGC TTGCCCTTGT AAACAAAACC
301  GAAGGAACAA CTGCTGAACA GCAGATAAAA CGTAAACTCT CTTCTAAAAG
351  TATTTCTTAG
```

The PSORT algorithm predicts inner membrane (0.6074).

The following *C.pneumoniae* protein (PID 4376497) was also expressed <SEQ ID 345; cp6497>:

```
  1  MKPNSIIFLE NTKHYPDIFR EGFVRDRHGL MEASDWLLST EITIIRSILG
 51  AIPILGNILG AGRLYSVWYT SDEDWKKQVV *
```

The cp6497 nucleotide sequence <SEQ ID 346> is:

```
  1  ATGAAGCCAA ATAGTATTAT TTTTTTAGAA AATACTAAGC ATTATCCCGA
 51  CATCTTTCGA GAAGGATTTG TTCGTGATCG TCATGGACTA ATGGAAGCCT
101  CGGATTGGTT ACTTTCTACG GAAATTACGA TCATTCGCTC CATTCTGGGA
151  GCTATCCCTA TTTTAGGAAA TATTCTTGGA GCCGGACGAC TCTATAGCGT
```

201 TTGGTATACA AGTGACGAAG ATTGGAAAAA ACAAGTGGTT TGA

The PSORT algorithm predicts inner membrane (0.145).

The proteins were expressed in *E.coli* and purified as his-tag products (Figure 171A; 6632 = lanes 5-7; 6648 = lanes 8-10; 6497 = lanes 2-4). The recombinant proteins were used to immunise mice, whose sera were used in Western blots (Figures 171B, 172, 173) and for FACS analysis.

These experiments show that cp6632, cp6648 and cp6497 are surface-exposed and immunoaccessible proteins and that they are useful immunogens. These properties are not evident from the sequence alone.

Example 174 ,
Example 175 ,
Example 176 ,
Example 177 and
Example 178

The following *C.pneumoniae* protein (PID 4377200) was expressed <SEQ ID 347; cp7200>:

```
  1 MPVPIDNSSR NLQEVPESLE DLEQHAEESP THQSAESSSL QLSLASSAIS
 51 SRVEQLSSLV LGMENSDFSS LRDVPIFSAI YESSTHTPVP TPLVGVGYIN
101 GSQSGYYDTQ RESLHLSQLL GSRRVEVVYN QGNFMEASLL NLCPRRPRRD
151 PSPISLALLE LWEAFFLEHP PGSTFNPIFF W*
```

The cp7200 nucleotide sequence <SEQ ID 348> is:

```
  1 ATGCCCGTTC CTATAGATAA TTCCTCTCGC AACCTACAAG AAGTTCCAGA
 51 AAGCCTAGAA GACCTCGAAC AACACGCAGA AGAATCTCCT ACTCATCAAA
101 GTGCAGAAAG CAGTTCTTTG CAACTGTCTC TAGCCTCCTC AGCAATTTCT
151 AGTAGAGTAG AACAACTATC TTCCCTCGTC TTAGGAATGG AAAATTCAGA
201 TTTCTCCTCT TTAAGAGACG TTCCTATCTT CTCAGCTATC TACGAATCTT
251 CAACACACAC ACCTGTCCCC ACTCCTCTAG TTGGCGTGGG ATATATCAAC
301 GGAAGTCAAT CAGGATACTA CGATACACAA AGAGAATCTC TTCACCTCAG
351 CCAATTGTTA GGAAGCCGAA GAGTTGAAGT TGTCTATAAC CAAGGAAACT
401 TCATGGAGGC CTCTTTGCTA AATCTGTGCC CCAGAAGACC TCGAAGAGAT
451 CCCTCTCCAA TTTCTTTAGC TCTATTAGAG CTCTGGGAAG CATTTTTTTT
501 AGAACACCCC CCAGGTAGCA CTTTTAATCC AATATTTTTT TGGTAA
```

The PSORT algorithm predicts cytoplasm (0.3672).

The following *C.pneumoniae* protein (PID 4377235) was also expressed <SEQ ID 349; cp7235>:

```
  1 LNFVSTLTGS DFYAPVLEKL EEAFADTTGQ VILFSSSPDF IVHPIAQQLG
 51 ISSWYASCYR DQSAEQTIYK KCLTGDKKAQ ILSYIKKINQ ARSHTFSDHI
101 LDLPFLMLGE EKTVVRPQGR LKKMAKKYYW NIV*
```

The cp7235 nucleotide sequence <SEQ ID 350> is:

```
  1 TTGAATTTTG TATCGACTCT GACCGGCTCC GATTTTTATG CTCCTGTTTT
 51 AGAAAAACTA GAAGAAGCTT TTGCAGATAC CACAGGACAG GTGATCCTTT
101 TTTCTTCTTC TCCAGACTTT ATTGTCCACC CCATAGCGCA GCAACTCGGG
151 ATTAGTTCTT GGTATGCGTC GTGTTATCGC GATCAGTCTG CAGAACAGAC
201 GATCTATAAA AAATGTCTTA CAGGGGATAA AAAAGCGCAA ATTTTGAGTT
251 ATATTAAAAA AATTAATCAA GCAAGAAGCC ATACCTTCTC CGACCATATT
301 TTAGATCTTC CTTTTCTTAT GCTGGGAGAA GAGAAAACCG TCGTTCGCCC
351 TCAGGGACGA CTCAAGAAAA TGGCAAAAAA ATATTACTGG AATATCGTTT
401 AA
```

The PSORT algorithm predicts cytoplasm (0.3214).

The following *C.pneumoniae* protein (PID 4377268) was also expressed <SEQ ID 351; cp7268>:

```
  1 MMHRYFIPLL ALLIFSPSLV RAELQPSENR KGGWPTQLSC AEGSQLFCKF
```

```
 51  EAAYNNAIEE GKPGILVFFS ERPTPEFADL TNGSFSLSTP IAKGFNVVVL
101  CPGLISPLDF FHKMDPVILY MGSFLEMFPE VEAVSGPRLC YILIDEQGGA
151  QCQAVLPLET KN*
```

The cp7268 nucleotide sequence <SEQ ID 352> is:

```
  1  ATGATGCACC GTTATTTTAT TCCTTTATTA GCACTTCTCA TTTTCTCTCC
 51  TTCTTTAGTC AGGGCAGAGC TACAACCAAG TGAAAACAGA AAAGGGGGGT
101  GGCCTACACA ACTTTCCTGT GCAGAAGGTT CGCAACTCTT CTGTAAATTC
151  GAAGCTGCCT ATAATAATGC AATTGAGGAA GGGAAACCTG GGATTTTAGT
201  CTTTTTCTCT GAGCGACCCA CACCAGAATT TGCCGACTTA ACGAATGGTT
251  CATTTTCTCT CTCTACGCCA ATCGCCAAGG GCTTTAATGT CGTTGTGTTA
301  TGCCCCGGGC TTATCAGTCC CTTAGACTTT TTCCACAAAA TGGATCCTGT
351  GATTCTCTAT ATGGGAAGTT TTCTAGAGAT GTTCCCTGAA GTGGAGGCAG
401  TTAGTGGCCC TCGCTTATGT TATATCTTAA TAGATGAACA GGGTGGGGCT
451  CAATGTCAGG CTGTCCTGCC TTTAGAAACA AAGAATTAG
```

The PSORT algorithm predicts inner membrane (0.1235).

The following *C.pneumoniae* protein (PID 4377375) was also expressed <SEQ ID 353; cp7375>:

```
  1  MQRIIIVGID TGVGKTIVSA ILARALNAEY WKPIQAGNLE NSDSNIVHEL
 51  SGAYCHPEAY RLHKPLSPHK AAQIDNVSIE ESHICAPKTT SNLIIETSGG
101  FLSPCTSKRL QGDVFSSWSC SWILVSQAYL GSINHTCLTV EAMRSRNLNI
151  LGMVVNGYPE DEEHWLTQEI KLPIIGTLAK EKEITKTIIS CYAEQWKEVW
201  TSNHQGIQGV SGTPSLNLH*
```

The cp7375 nucleotide sequence <SEQ ID 354> is:

```
  1  ATGCAACGTA TCATCATTGT AGGAATCGAC ACTGGCGTAG GAAAAACCAT
 51  TGTCAGTGCT ATCCTTGCTA GAGCACTTAA CGCAGAATAC TGGAAACCTA
101  TACAAGCAGG GAATCTAGAA AATTCAGATA GCAATATTGT TCATGAGCTA
151  TCGGGAGCCT ACTGTCATCC CGAAGCTTAT CGATTGCATA AGCCCTTGTC
201  TCCACACAAG GCAGCGCAAA TCGATAATGT AAGTATCGAA GAGAGTCATA
251  TTTGTGCGCC AAAAACAACT TCGAATCTGA TTATTGAGAC TTCAGGAGGA
301  TTTTTATCCC CCTGCACATC AAAAAGACTT CAGGGAGATG TGTTTTCTTC
351  TTGGTCATGT TCTTGGATTT TAGTGAGCCA AGCATATCTC GGAAGTATCA
401  ATCACACCTG TTTAACGGTA GAAGCAATGC GCTCACGAAA CCTCAATATC
451  TTAGGTATGG TGGTAAATGG GTATCCAGAG GACGAAGAGC ACTGGCTAAC
501  TCAAGAAATC AAGCTTCCTA TAATCGGGAC TCTTGCCAAG GAAAAAGAAA
551  TCACAAAGAC AATCATAAGC TGTTATGCCG AACAATGGAA GGAAGTATGG
601  ACAAGCAATC ATCAGGGAAT TCAGGGTGTA TCTGGCACCC CTTCACTCAA
651  TCTGCATTAG
```

The PSORT algorithm predicts cytoplasm (0.0049).

The following *C.pneumoniae* protein (PID 4377388) was also expressed <SEQ ID 355; cp7388>:

```
  1  MQVLLSPQLP PPPQHSVGSI SSPSKLRVLA ITFLVFGMLL LISGALFLTL
 51  GIPGLSAAIS FGLGIGLSAL GGVLMISGLL CLLVKREIPT VRPEEIPEGV
101  SLAPSEEPAL QAAQKTLAQL PKELDQLDTD IQEVFACLRK LKDSKYESRS
151  FLNDAKKELR VFDFVVEDTL SEIFELRQIV AQEGWDLNFL INGGRSLMMT
201  AESESLDLFH VSKRLGYLPS GDVRGEGLKK SAKEIVARLM SLHCEIHKVA
251  VAFDRNSYAM AEKAFAKALG ALEESVYRSL TQSYRDKFLE SERAKIPWNG
301  HITWLRDDAK SGCAEKKLRD AEERWKKFRK AVFWVEEDGG FDINNLLGDW
351  GTVLDPYRQE RMDEITFHEL YEKTTFLKRL HRKCALAKTT FEKKRSKKNL
401  QAVEEANARR LKYVRDWYDQ EFQKAGERLE KLHALYPEVS VSIRENKIQE
451  TRSNLEKAYE AIEENYRCCV REQEDYWKEE EKREAEFRER GNKILSPEEL
501  ESSLEQFDHG LKNFSEKLME LEGHILKLQK EATAEVENKI LSDAESRLEI
551  VFEDVKEMPC RIEEIEKTLR MAELPLLPTK KAFEKACSQY NSCAEMLEKV
601  KPYCKESLAY VTSKERLVSL DEDLRRAYTE CQKRFQGDSG LESEVRACRE
651  QLRERIQEFE TQGLDLVEKE LLCVSSRLRN TECDCVSGVK KEAPPGKKFY
701  AQYYDEIYRV RVQSRWMTMS ERLREGVQAC NKMLKAGLSE EDKVLKEEEY
751  WLYREERKNK EKRLVGTKIV ATQQRVAAFE SIEVPEIPEA PEEKPSLLDK
801  ARSLFTREDH T
```

The cp7388 nucleotide sequence <SEQ ID 356> is:

```
  1  ATGCAAGTAC TTCTATCTCC GCAGCTACCC CCCCCCCCCC AACACTCTGT
 51  AGGGTCGATT TCTTCTCCAT CTAAACTTCG CGTTTTAGCG ATTACTTTTT
```

```
 101  TAGTTTTTGG TATGCTCTTA CTGATTTCAG GAGCTCTCTT TCTGACGTTA
 151  GGGATTCCAG GATTGAGTGC AGCAATTTCT TTTGGATTAG GCATCGGTCT
 201  CTCCGCATTA GGAGGAGTGC TGATGATTTC GGGACTACTA TGTCTTTTAG
 251  TAAAACGAGA GATTCCGACA GTACGACCAG AAGAAATTCC TGAAGGGGTT
 301  TCGCTGGCTC CTTCTGAGGA GCCAGCTCTA CAGGCAGCTC AGAAGACTTT
 351  AGCTCAGCTG CCTAAGGAAT TGGATCAGTT AGATACAGAT ATTCAGGAAG
 401  TGTTCGCATG TTTAAGAAAG CTGAAAGATT CTAAGTATGA AAGTCGAAGT
 451  TTTTTAAACG ATGCTAAGAA GGAGCTTCGA GTTTTTGACT TTGTGGTTGA
 501  GGATACCCTC TCGGAGATTT TCGAGTTGCG GCAGATTGTG GCTCAAGAGG
 551  GATGGGATTT AAACTTTTTG ATCAATGGGG GACGAAGCCT CATGATGACT
 601  GCAGAATCTG AATCGCTTGA TTTGTTTCAT GTATCGAAGC GGCTAGGGTA
 651  TTTACCTTCT GGGGATGTTC GAGGGGAGGG GTTAAAGAAA TCTGCGAAGG
 701  AGATAGTCGC TCGTTTGATG AGCTTGCATT GCGAGATTCA CAAGGTGGCG
 751  GTAGCGTTTG ATAGGAATTC CTATGCGATG GCAGAAAAGG CGTTTGCGAA
 801  AGCGTTGGGA GCTTTAGAAG AGAGTGTGTA TCGGAGTCTG ACGCAGAGTT
 851  ATAGAGATAA ATTTTTGGAG AGCGAGAGGG CGAAGATCCC ATGGAATGGG
 901  CATATAACCT GGTTAAGAGA TGATGCGAAG AGTGGGTGTG CTGAAAAGAA
 951  GCTTCGGGAT GCCGAGGAAC GTTGGAAGAA ATTTAGGAAA GCAGTCTTTT
1001  GGGTAGAAGA AGACGGGGGC TTTGACATCA ATAATCTCCT TGGAGACTGG
1051  GGGACAGTGC TTGATCCTTA TAGACAAGAG AGAATGGACG AGATAACGTT
1101  CCATGAGTTG TATGAAAAAA CTACGTTTTT GAAAAGACTG CACAGAAAGT
1151  GTGCGTTAGC GAAAACAACC TTTGAAAAGA AGAGATCTAA AAAGAATTTG
1201  CAGGCAGTCG AGGAGGCGAA TGCACGTAGG TTGAAATATG TAAGGGATTG
1251  GTATGATCAG GAGTTTCAGA AAGCAGGGGA GAGATTAGAG AAACTGCATG
1301  CTTTGTATCC TGAGGTTTCA GTCTCTATAA GAGAGAACAA AATACAAGAG
1351  ACGCGCTCTA ATTTAGAGAA AGCCTATGAG GCTATCGAAG AGAACTATCG
1401  TTGCTGTGTC CGAGAGCAAG AGGACTACTG GAAAGAAGAA GAGAAAAGGG
1451  AAGCGGAGTT TAGGGAGAGG GGAAACAAGA TTCTTTCTCC TGAGGAGCTG
1501  GAAAGTTCTT TGGAGCAATT CGACCATGGT TTGAAAAATT TTTCTGAGAA
1551  ATTAATGGAA TTGGAAGGGC ATATCTTAAA ACTTCAGAAA GAAGCCACAG
1601  CAGAGGTGGA GAATAAAATA CTTTCAGATG CAGAGAGCCG CCTTGAGATT
1651  GTATTTGAAG ATGTCAAGGA GATGCCCTGT CGAATTGAGG AGATAGAGAA
1701  GACGCTGCGT ATGGCGGAGC TGCCCCTACT TCCTACGAAG AAGGCGTTTG
1751  AGAAGGCCTG CTCACAATAT AATAGCTGCG CAGAGATGTT GGAGAAGGTG
1801  AAGCCTTACT GCAAGGAGAG CCTCGCCTAT GTGACTAGCA AAGAGCGTTT
1851  AGTGAGCTTG GATGAAGATT TACGACGAGC CTACACAGAG TGTCAGAAGA
1901  GATTCCAGGG GGATTCGGGT TTGGAGTCGG AAGTAAGAGC CTGTCGAGAG
1951  CAACTGCGAG AGCGGATCCA AGAGTTTGAA ACTCAAGGGC TGGACTTGGT
2001  GGAAAAAGAG TTGCTTTGTG TGAGTAGTAG ATTAAGAAAT ACAGAGTGCG
2051  ATTGTGTATC TGGTGTTAAG AAAGAAGCAC CTCCTGGTAA GAAGTTTTAT
2101  GCCCAGTATT ATGATGAGAT TTATCGAGTT AGAGTTCAAT CCCGATGGAT
2151  GACGATGTCT GAGAGATTGA GAGAGGGAGT TCAAGCATGC AACAAGATGT
2201  TGAAGGCAGG CCTAAGCGAA GAAGATAAGG TTCTTAAAGA AGAAGAGTAT
2251  TGGTTGTATC GAGAGGAGAG AAAGAATAAA GAGAAACGTT TGGTTGGTAC
2301  TAAGATAGTA GCAACGCAGC AGCGAGTTGC AGCATTTGAA TCCATAGAAG
2351  TTCCTGAGAT TCCTGAGGCC CCAGAGGAGA AACCGAGTTT GCTGGATAAA
2401  GCGCGTTCTT TATTTACTCG CGAGGACCAT ACCTAG
```

The PSORT algorithm predicts inner membrane (0.461).

The proteins were expressed in *E.coli* and purified as his-tag products (Figure 174: 7200=lanes 2-3; 7236=lanes 4-5; 7268=lanes 6-8; 7375=lanes 9-10; 7388=lanes 11-12). The recombinant proteins were used to immunise mice, whose sera were used in Western blots (Figures 174, 175, 176, 177 & 178) and for FACS analysis.

These experiments show that cp7200, cp7235, cp7268, cp7375 & cp7388 are surface-exposed and immunoaecessible proteins and that they are useful immunogens. These properties are not evident from the sequence alone.

Example 179

The following *C.pneumoniae* protein (PID 4376723) was expressed <SEQ ID 357; cp6723>:

```
  1 MATSVAPSPV PESSPLSHAT EVLNLPNAYI TQPHPIPAAP WETFRSKLST
 51 KHTLCFALTL LLTLGGTISA GYAGYTGNWI ICGIGLGIIV LTLILALLLA
101 IPLKNKQTGT KLIDEISQDI SSIGSGFVQR YGLMFSTIKS VHLPELTTQN
151 QEKTRILNEI EAKKESIQNL ELKITECQNK LAQKQPKRKS SQKSFMRSIK
201 HLSKNPVILF DC*
```

The cp6723 nucleotide sequence <SEQ ID 358> is:

```
  1 ATGGCAACTT CCGTAGCCCC ATCACCAGTC CCCGAGAGCA GCCCTCTCTC
 51 TCATGCTACA GAAGTTCTCA ATCTTCCTAA TGCTTATATT ACGCAGCCTC
101 ATCCGATTCC AGCGGCTCCT TGGGAGACCT TTCGCTCCAA ACTTTCCACA
151 AAGCATACGC TCTGTTTTGC CTTAACACTA CTGTTAACCT TAGGGGGAAC
201 GATCTCAGCA GGTTACGCAG GATATACTGG AAACTGGATC ATCTGTGGCA
251 TCGGCTTGGG AATTATCGTA CTCACACTGA TTCTTGCTCT TCTTCTAGCA
301 ATCCCTCTTA AAAATAAGCA GACAGGAACA AAACTGATTG ATGAGATATC
351 TCAAGACATT TCCTCTATAG GATCAGGATT TGTTCAGAGA TACGGGTTGA
401 TGTTCTCTAC AATTAAAAGC GTGCATCTTC CAGAGCTGAC AACACAAAAT
451 CAAGAAAAAA CAAGAATTTT AAATGAAATT GAAGCGAAAA AGGAATCGAT
501 CCAAAATCTT GAGCTTAAAA TTACTGAGTG CCAAAACAAG TTAGCACAGA
551 AACAGCCGAA ACGGAAATCA TCTCAGAAAT CATTTATGCG TAGTATTAAG
601 CACCTCTCCA AGAACCCTGT AATTTTGTTC GATTGCTGA
```

The PSORT algorithm predicts inner membrane (0.6095).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 179A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 179B) and for FACS analysis.

These experiments show that cp6723 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 180

The following *C.pneumoniae* protein (`PID 4376749`) was expressed <SEQ ID 359; cp6749>:

```
  1 MSYYFSLWYL KVQQHFQAAF DFTRSLCSRI SNFALGVIAL LPIIGQLYVG
 51 LDWLLSRIKK PEFPSDVDQI VRVEHVVGHD HRSRVEDILK RQRLSLEPRD
101 EGKVHGDLPS APFF*
```

The cp6749 nucleotide sequence <SEQ ID 360> is:

```
  1 ATGAGTTATT ACTTTTCTCT TTGGTATCTG AAGGTGCAAC AGCACTTTCA
 51 AGCAGCATTT GATTTTACTC GCTCCCTGTG TTCACGAATT TCTAATTTTG
101 CTTTGGGAGT GATTGCATTG CTTCCTATTA TTGGGCAGTT GTATGTAGGG
151 CTGGACTGGC TCCTCTCTAG GATAAAAAAG CCAGAATTTC CTTCCGATGT
201 GGATCAGATC GTGCGAGTAG AACACGTCGT GGGTCACGAC CATAGAAGTC
251 GAGTTGAAGA TATTCTAAAG AGACAAAGGC TCTCATTAGA GCCTAGAGAC
301 GAGGGGAAGG TTCACGGAGA TCTGCCTTCA GCTCCTTTTT TTTGA
```

The PSORT algorithm predicts inner membrane (0.2996).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 180A). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 180B) and for FACS analysis.

These experiments show that cp6749 is a surface-exposed and immunoaecessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 181 ,
Example 182 ,
Example 183 ,
Example 184 and
Example 185

The following *C.pneumoniae* protein (PID 4376301) was expressed <SEQ ID 361; cp6301>:

```
  1 LNQDLQNVYQ ECQKATGLES EVSAYRDHLR EQITEFETQG LDVIKEELLF
 51 VSSTLKSKLS YDPLIADIPC MKFYEEYYDG IDKARVQSRW LEKSERYRKA
101 KKGFQEMLKE GLFKEDQALK KAEYRLLREK RMNKEKLLIC NKIEAAQQRV
151 QEFGPSDS*
```

The cp6301 nucleotide sequence <SEQ ID 362> is:

```
  1 TTGAATCAGG ATTTACAAAA TGTATACCAA GAGTGCCAGA AGGCTACAGG
 51 TTTAGAATCG GAAGTGAGTG CATATAGAGA TCATCTTAGA GAGCAGATCA
101 CAGAGTTTGA AACTCAAGGG CTGGACGTGA TAAAAGAAGA ACTTCTTTTT
151 GTGAGTAGTA CTCTCAAAAG TAAATTGAGC TATGATCCAT TAATAGCAGA
201 CATTCCCTGT ATGAAGTTTT ATGAGGAGTA TTATGATGGC ATTGATAAAG
251 CGAGAGTTCA ATCCCGATGG CTGGAGAAGT CTGAGAGGTA TAGAAAGGCG
301 AAGAAGGGAT TCCAAGAGAT GCTGAAGGAA GGCCTATTCA AAGAAGATCA
351 GGCTTTGAAA AAAGCAGAGT ATAGATTACT TCGAGAGAAG AGAATGAATA
401 AGGAGAAGCT TTTGATTTGC AATAAGATAG AAGCAGCTCA GCAGCGAGTC
451 CAAGAATTTG GACCCTCGGA TTCATAA
```

The PSORT algorithm predicts cytoplasm (0.4621).

The following *C.pneumoniae* protein (PID 4376558) was also expressed <SEQ ID 363; cp6558>:

```
  1 MNIPAPQVPV IDEPVVNNTS SYGLSLKSSL RPITYLILAI LAIATLMSVL
 51 YFCGIISVGT FVLGMLIPLS VCSVLCVAYL FYQQSSIEKT KVFSITSPSV
101 FFSDEDLNLL LGREEDSVSA IDELLKNFPA DDFRRPKMLP YSNFLDEQGR
151 PNESREEDSH TSKIL*
```

The cp6558 nucleotide sequence <SEQ ID 364> is:

```
  1 ATGAACATAC CCGCTCCCCA AGTACCAGTC ATAGATGAGC CTGTAGTGAA
 51 CAACACAAGT AGCTATGGTC TTTCATTGAA AAGTAGTTTA AGACCGATTA
101 CTTATTTGAT TTTAGCTATC TTAGCTATAG CCACACTGAT GTCTGTTCTC
151 TACTTTTGTG GCATCATTAG TGTTGGGACG TTTGTTTTGG GCATGCTGAT
201 CCCTCTATCG GTCTGCTCTG TTCTTTGCGT TGCCTATTTA TTCTATCAGC
251 AATCTTCTAT AGAAAAGACT AAGGTCTTTT CTATAACCAG TCCTTCAGTA
301 TTTTTCTCTG ATGAGGATCT TAATTTACTC TTAGGTCGAG AAGAAGATTC
351 AGTGTCTGCA ATTGATGAAC TTCTTAAGAA CTTTCCAGCT GATGATTTCC
401 GTAGGCCGAA GATGCTTCCT TATTCAAATT TTCTAGATGA GCAGGGAAGG
451 CCTAATGAGA GTAGGGAAGA AGACTCTCAT ACTTCCAAGA TCTTATAA
```

The PSORT algorithm predicts inner membrane (0.4630).

The following *C.pneumoniae* protein (PID 4376630) was also expressed <SEQ ID 365; cp6630>:

```
  1 MSMTIVPHAL FKNHCECHST FPLSSRTIVR IAIASLFCIG ALAALGCLAP
 51 PVSYIVGSVL AFIAFVILSL VILALIFGEK KLPPTPRIIP DRFTHVIDEA
101 YGLSISAFVR EQQVTLAEFR QFSTALLCNI SPEEKIKQLP SELRSKVESF
151 GISRLAGDLE KNNWPIFEDL LSQTCPLYWL QKFISAGDPQ VCRDLGVPRE
201 CYGYYWLGPL GYSTAKATIF CKETHHILQQ LTKEDVLLLK NKALQEKWDT
251 DEVKAIVERI YTTYTARGTL KTEAGGLTKE TISKELLLLS LHGYSFDQLQ
301 LITQLPRDAW DWLCFVDNST AYNLQLCALV GALSSQNLLD ESSIDFDVNL
351 GLYVIQDLKE AVQAFSASDE PKKELGKFLL RHLSSVSKRL ESVLRQGLHR
401 IALEHGNARA RVYDVNFVTG ARIHRKTSIF FKD*
```

The ep6630 nucleotide sequence <SEQ ID 366> is:

```
  1 ATGAGCATGA CGATCGTTCC ACATGCTTTA TTTAAAAATC ATTGCGAGTG
 51 TCATTCTACC TTTCCTTTGA GTTCAAGGAC TATTGTAAGA ATAGCCATTG
101 CCAGCCTCTT TTGTATAGGT GCATTAGCAG CTTTAGGCTG TTTGGCTCCT
151 CCCGTTTCTT ATATTGTTGG GAGTGTTTTA GCTTTTATTG CCTTTGTCAT
201 TCTTTCTTTA GTAATTTTAG CTTTGATTTT TGGAGAGAAG AAGCTTCCAC
```

```
 251  CAACACCAAG AATCATTCCT GATAGATTTA CTCACGTGAT AGATGAAGCT
 301  TATGGCCTTT CAATCTCTGC ATTTGTAAGA GAACAGCAGG TAACATTAGC
 351  CGAGTTTAGA CAATTTTCTA CTGCCCTGTT GTGTAACATA TCTCCTGAAG
 401  AGAAAATCAA ACAATTGCCT TCTGAATTGC GAAGTAAAGT AGAGAGTTTT
 451  GGTATTAGCA GGCTCGCAGG TGATTTAGAA AAGAATAATT GGCCAATATT
 501  TGAAGATCTT TTAAGCCAAA CCTGCCCGTT ATATTGGCTT CAGAAATTTA
 551  TATCAGCAGG AGATCCACAA GTTTGTAGAG ACCTAGGTGT CCCTAGAGAA
 601  TGTTATGGGT ACTATTGGCT AGGGCCTTTG GGATACAGTA CAGCTAAGGC
 651  TACAATTTTT TGTAAAGAGA CGCATCATAT TCTTCAACAA TTAACGAAAG
 701  AGGACGTTCT TTTATTAAAA AACAAGGCTC TTCAAGAGAA ATGGGATACT
 751  GATGAAGTCA AAGCAATTGT AGAGCGTATC TACACTACCT ATACGGCACG
 801  AGGAACTCTA AAGACCGAAG CAGGGGGACT TACAAAAGAG ACAATCAGTA
 851  AGGAATTGCT ATTGTTGAGC TTGCATGGCT ATTCTTTTGA TCAGCTACAG
 901  CTGATCACTC AACTTCCTAG AGATGCTTGG GATTGGCTGT GTTTTGTAGA
 951  TAACAGTACC GCATACAACC TTCAGCTTTG TGCTCTTGTA GGAGCTTTGT
1001  CATCCCAAAA TCTTCTTGAC GAATCTTCTA TCGATTTTGA TGTAAACCTA
1051  GGCCTGTATG TGATTCAGGA TCTAAAAGAA GCTGTTCAAG CATTTTCTGC
1101  TTCTGATGAG CCAAAGAAAG AACTAGGTAA ATTCTTGTTA AGGCATTTGA
1151  GTTCAGTTTC TAAGCGATTA GAGAGTGTAT TAAGACAGGG TCTTCACAGA
1201  ATAGCTCTAG AGCATGGAAA TGCCAGAGCT AGGGTTTATG ACGTCAATTT
1251  TGTAACAGGA GCTAGAATTC ATAGGAAGAC GAGTATCTTC TTTAAAGACT
1301  AA
```

The PSORT algorithm predicts inner membrane (0.7092).

The following *C.pneumoniae* protein (PID 4376633) was also expressed <SEQ ID 367; cp6633>:

```
   1  MVNIQPVYRN TQVNYSQATQ FSVCQPALSL IIVSVVAAVL AIVALVCSQS
  51  LLSIELGTAL VLVSLILFAS AMFMIYKMRQ EPKELLIPKK IMELIQEHYP
 101  SIVVDFIRDQ EVSIYEIHHL ISILNKTNVF DKAPVYLQEK LLQFGIEKFK
 151  DVHPSKLPNF EEILLQHCPL HWLGRLVYPM VSDVTPGTYG YYWCGPLGLY
 201  ENAPSLFERR SLLLLKKISF GEFALLEDGL KKNTWSSSEL VQIRQNLFTR
 251  YYADKEEVDE AELNADYEQF DSLLHLIFSH KLS*
```

The cp6633 nucleotide sequence <SEQ ID 368> is:

```
   1  ATGGTTAATA TACAGCCTGT GTATAGGAAT ACCCAAGTCA ACTATAGTCA
  51  GGCTACCCAA TTTTCGGTGT GCCAGCCAGC GCTTAGCCTG ATTATCGTTT
 101  CTGTTGTTGC TGCTGTACTC GCTATTGTAG CTTTGGTATG CAGTCAATCT
 151  CTTTTATCCA TAGAGTTAGG AACTGCTCTT GTTCTAGTTT CTCTTATTCT
 201  TTTTGCTTCT GCTATGTTTA TGATTTATAA GATGAGACAA GAACCTAAGG
 251  AGTTGCTGAT CCCTAAGAAA ATCATGGAAC TCATCCAAGA ACATTATCCA
 301  AGTATTGTTG TTGATTTTAT TAGAGATCAG GAGGTTTCCA TTTATGAGAT
 351  ACATCACTTG ATCTCTATTC TTAATAAGAC GAATGTTTTC GACAAAGCAC
 401  CAGTATATTT ACAAGAAAAA CTCTTACAGT TTGGCATTGA GAAGTTCAAA
 451  GATGTACATC CAAGTAAGCT CCCTAATTTT GAAGAAATTC TTCTACAGCA
 501  TTGCCCATTG CATTGGTTGG GACGTCTGGT ATATCCCATG GTATCGGATG
 551  TCACTCCAGG AACCTATGGA TACTATTGGT GTGGTCCTTT AGGACTGTAC
 601  GAGAACGCTC CCTCTCTTTT TGAACGTCGA TCTCTTCTAT TGTTAAAGAA
 651  AATTAGCTTT GGAGAGTTTG CTCTTTTAGA AGATGGTCTC AAGAAAAACA
 701  CGTGGAGTTC TTCGGAACTC GTTCAAATCA GACAAAACCT TTTTACAAGA
 751  TATTATGCTG ATAAAGAAGA GGTAGATGAA GCAGAGTTAA ACGCTGATTA
 801  CGAACAGTTT GATTCCCTCC TTCACCTTAT TTTTTCTCAC AAGCTCTCTT
 851  GA
```

The PSORT algorithm predicts inner membrane (0.7283).

The following *C.pneumoniae* protein (PID 4376642) was also expressed <SEQ ID 369; cp6642>:

```
   1  MATISPISLT VDHPLVDTKK KSCSNFDKIQ SRILLITAIF AVLVTIGTLL
  51  IGLLLNIPVI YFLTGISFIA VVLSNFILYK RATTLLKPRA CGKHKEIKPK
 101  RVSTNLQYSS ISIAINRSKE NWEHQPKDLQ NLPAPSALLT DNPYEIWKAK
 151  HSLFSLVSLL PGGNPEHLLI SASENLGKTL LIEETSQNAP ISSYVDTTPS
 201  PKSLLNEAIQ ETRVEINTEL PAGDSGERLY WQPDFRGRVF LPQIPTTPEA
 251  IYQYYYALYV TYIQTAINTN TQIIQIPLYS LREHLYSREL PPQSRMQQSL
 301  AMITAVKYMA ELHPEYPLTI ACVERSLAQL PQESIEDLS*
```

The cp6642 nucleotide sequence <SEQ ID 370> is:

```
   1  ATGGCTACAA TCTCACCCAT ATCTTTAACT GTAGATCATC CCCTAGTAGA
```

```
  51  CACTAAAAAA AAATCCTGCA GCAACTTTGA TAAGATTCAG TCTCGAATTC
 101  TATTGATTAC TGCAATCTTT GCTGTCTTAG TTACTATAGG GACCCTACTT
 151  ATTGGTTTGC TTTTAAATAT TCCTGTTATC TATTTCCTCA CAGGAATTTC
 201  ATTTATTGCT GTTGTTCTTA GCAACTTTAT CCTTTATAAA CGAGCAACCA
 251  CCCTCTTAAA ACCGCGTGCT TGTGGCAAAC ACAAAGAAAT AAAACCAAAA
 301  AGGGTCTCCA CCAACCTACA GTATTCTTCT ATCTCTATCG CAATCAATCG
 351  TTCTAAAGAA AACTGGGAAC ACCAACCCAA GGACCTACAG AATCTCCCCG
 401  CACCCTCTGC ATTACTCACA GATAACCCTT ACGAGATATG GAAAGCTAAA
 451  CATTCACTGT TTTCCCTAGT ATCCCTCCTA CCGGGAGGCA ATCCAGAACA
 501  TCTCTTAATT TCAGCTTCCG AAAATTTAGG AAAGACTCTG TTAATTGAAG
 551  AAACCTCGCA AAATGCGCCT ATATCCTCCT ACGTAGATAC CACTCCCTCC
 601  CCAAAATCCT TGCTCAATGA GGCAATTCAG GAAACCAGGG TAGAAATAAA
 651  TACAGAACTC CCTGCGGGAG ATTCAGGAGA ACGTTTATAC TGGCAACCCG
 701  ATTTCCGAGG CCGCGTCTTC CTCCCACAAA TACCAACAAC TCCTGAAGCC
 751  ATCTACCAAT ACTACTATGC ACTCTATGTC ACTTATATCC AGACTGCGAT
 801  CAATACGAAC ACCCAAATTA TCCAAATCCC TTTATACAGC TTGAGGGAGC
 851  ATCTCTATTC TAGAGAATTG CCCCCGCAAT CAAGAATGCA ACAATCTTTG
 901  GCTATGATTA CAGCAGTAAA ATACATGGCC GAGCTGCACC CAGAATATCC
 951  GCTAACTATT GCTTGTGTTG AAAGATCCTT AGCCCAACTA CCTCAAGAAA
1001  GTATTGAGGA TCTCTCTTAG
```

The PSORT algorithm predicts inner membrane (0.5288).

The proteins were expressed in *E.coli* and purified as GST-fusion products. The recombinant proteins were used to immunise mice, whose sera were used in Western blots (Figures 181-185) and for FACS analysis.

These experiments show that cp6301, cp6558, cp6630, cp6633 and cp6642 are surface-exposed and immunoaccessible proteins, and that they are useful immunogens. These properties are not evident from their sequences alone.

Example 186

The following *C.pneumoniae* protein (PID 4376389) was expressed <SEQ ID 371; cp6389>:

```
  1  MSEVKPLFLK NDSFDLATQR FQNLINMLQE QAEIYNEYEE KNARVQNEIK
 51  EQKDFVKRCI EDFEARGLGV LKEELASLTR DFHDKAKAET SMLIECPCIG
101  FYYSIHQEEQ RQRQERLQKM AERYRDCKQV LEAVQVEQKD MISSRVVVDD
151  SYFEEEKEEQ KVDNRKKEQD *
```

The cp6389 nucleotide sequence <SEQ ID 372> is:

```
  1  ATGTCAGAAG TGAAGCCTTT GTTTTTAAAG AATGACTCTT TTGATTTGGC
 51  AACTCAGAGA TTCCAGAATC TAATTAACAT GCTACAAGAG CAAGCCGAGA
101  TATATAACGA GTATGAAGAA AAGAATGCTA GGGTTCAGAA TGAGATTAAG
151  GAGCAAAAGG ACTTTGTGAA AAGATGCATA GAGGACTTTG AAGCCAGAGG
201  ACTGGGGGTG CTAAAAGAAG AGCTTGCATC TTTGACGCGT GATTTCCATG
251  ATAAAGCAAA AGCAGAGACT TCTATGCTCA TTGAATGTCC TTGTATTGGT
301  TTTTATTATA GTATTCATCA GGAGGAACAA AGGCAAAGGC AAGAAAGGCT
351  TCAAAAGATG GCTGAGCGCT ATAGGGACTG TAAACAAGTC TTGGAGGCTG
401  TCCAGGTGGA GCAAAAAGAT ATGATATCTT CTAGAGTCGT TGTCGATGAC
451  AGCTACTTTG AAGAAGAAAA AGAAGAACAA AAGGTGGATA ACAGAAAGAA
501  AGAACAGGAC TAG
```

The PSORT algorithm predicts cytoplasm (0.3193).

The protein was expressed in *E.coli* and purified as a GST-fusion product (Figure 186A) and also in his-tagged form. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 186B) and for FACS analysis.

These experiments show that cp6389 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 187

The following *C.pneumoniae* protein (PID 4376792) was expressed <SEQ ID 373; cp6792>:

```
  1  VLQEHFFLSE DVITLAQQLL GHKLITTHEG LITSGYIVET EAYRGPDDKA
 51  CHAYNYRKTQ RNRAMYLKGG SAYLYRCYGM HHLLNVVTGP EDIPHAVLIR
101  AILPDQGKEL MIQRRQWRDK PPHLLTNGPG KVCQALGISL ENNRQRLNTP
151  ALYISKEKIS GTLTATARIG IDYAQEYRDV PWRFLLSPED SGKVLS*
```

The cp6792 nucleotide sequence <SEQ ID 374> is:

```
  1  GTGCTACAAG AACATTTTTT TCTATCGGAA GATGTAATTA CACTAGCGCA
 51  ACAGCTTTTA GGACATAAAC TCATCACAAC ACATGAGGGT CTGATAACTT
101  CAGGTTACAT TGTAGAAACC GAAGCGTATC GTGGCCCTGA TGACAAAGCA
151  TGCCACGCCT ACAACTACAG AAAAACTCAG AGGAACAGAG CGATGTACCT
201  GAAAGGAGGC TCTGCTTACC TCTACCGTTG CTATGGCATG CATCACCTAT
251  TGAATGTTGT CACTGGACCT GAGGACATTC CCCATGCCGT CCTGATCCGG
301  GCCATCCTTC CTGATCAAGG CAAAGAACTT ATGATCCAAC GCCGCCAATG
351  GAGAGATAAA CCCCCACACC TTCTCACCAA TGGACCCGGA AAAGTGTGCC
401  AAGCTCTAGG AATCTCTTTG GAAAACAATA GGCAACGCCT AAATACCCCA
451  GCTCTCTATA TCAGCAAAGA AAAAATCTCT GGGACTCTAA CAGCAACTGC
501  CCGGATCGGC ATCGATTATG CTCAAGAGTA TCGTGATGTC CCATGGAGAT
551  TTCTCCTATC CCCAGAAGAT TCGGGAAAAG TTTTATCTTA A
```

The PSORT algorithm predicts cytoplasm (0.180).

The protein was expressed in *E.coli* and purified as a his-tagged product (Figure 187A; lanes 2-4). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 187B) and for FACS analysis.

These experiments show that cp6792 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 188

The following *C.pneumoniae* protein (PID 4376868) was expressed <SEQ ID 375; cp6868>:

```
  1  MVETVLHNFQ RYLSKYLYRV FRFPCRKKTF LSSHRVLARP SFPVDYCPGK
 51  IYDLQEIYEE LNAQLFQGAL RLQIGWFGRK ATRKGKSVVL GLFHENEQLI
101  RIHRSLDRQE IPRFFMEYLV YHEMVHSVVP REYSLSGRSI FHGKKFKEYE
151  QRFPLYDRAV AWEKANAYLL RGYKKRVGGG YGRA*
```

The cp6868 nucleotide sequence <SEQ ID 376> is:

```
  1  ATGGTTGAAA CAGTACTTCA TAATTTCCAA CGTTATCTGA GCAAGTATCT
 51  CTATAGGGTA TTTCGCTTCC CATGTCGTAA AAAGACGTTC CTATCTTCGC
101  ACAGGGTTCT TGCTCGTCCT TCATTCCCAG TAGACTACTG TCCGGGAAAG
151  ATCTATGATT TGCAGGAGAT CTATGAGGAA TTGAATGCGC AGTTATTTCA
201  AGGTGCACTG CGTTTACAGA TTGGTTGGTT CGGAAGGAAA GCTACCAGAA
251  AAGGCAAGAG TGTTGTCTTG GGATTGTTTC ATGAAAATGA ACAGTTAATT
301  CGAATTCATC GTTCTTTAGA TCGGCAGGAA ATCCCAAGAT TTTTTATGGA
351  ATATCTTGTG TATCATGAAA TGGTTCATAG TGTAGTCCCT AGAGAGTATT
401  CTCTATCGGG GCGTTCGATT TTTCATGGTA AAAAGTTTAA AGAATACGAA
451  CAACGTTTCC CCTTGTATGA TCGTGCTGTT GCTTGGGAAA AGGCAAACGC
501  TTATTTATTG CGAGGGTATA AAAAAAGAGT AGGTGGAGGA TATGGCAGGG
551  CATAG
```

The PSORT algorithm predicts bacterial cytoplasm (0.325).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 188A; lanes 2-3). The recombinant protein was used to immunise mice, whose sera were used in a Western blot (Figure 188B) and for FACS analysis.

These experiments show that cp6868 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 189

The following *C.pneumoniae* protein (PID 4376894) was expressed <SEQ ID 377; cp6894>:

```
  1 MYKRCVLDKI LKGIVAGSLI LLYWSSDLLE RDIKSIKGNV RDIQEDIREI
 51 SRVVKQQQTS QAIPAAPGVM LAPKLVRDEA FALLFGDPSY PNLLSLDPYK
101 QQTLPELLGT NFHPHGILRT AHVGKPENLS PFNGFDYVVG FYDLCIPSLA
151 SPHVGKYEEF SPDLAVKIEE HLVEDGSGDK EFHIYLRPNV FWRPIDPKAL
201 PKHVQLDEVF QRPHPVTAHD IKFFYDAVMN PYVATMRAVA LRSCYEDVVS
251 VSVENDLKLV VRWKAHTVIN EEGKEERKVL YSAFSNTLSL QPLPRFVYQY
301 FANGEKIIED ENIDTYRTNS IWAQNFTMHW ANNYIVSCGA YYFAGMDDEK
351 IVFSRNPDFY DPLAALIDKR FVYFKESTDS LFQDFKTGKI DISYLPPNQR
401 DNFYSFMKSS AYNKQVAKGG AVRETVSADR AYTYIGWNCF SLFFQSRQVR
451 CAMNMAIDRE RIIEQCLDGQ GYTISGPFAS SSPSYNKQIE GWHYSPEEAA
501 RLLEEEGWID TDGDGIREKV IDGVIVPFRF RLCYYVKSVT AHTIADYVAT
551 ACKEIGIECS LLGLDMADLS QAFDEKNFDA LLMGWCLGIP PEDPRALWHS
601 EGAMEKGSAN VVGFHNEEAD KIIDRLSYEY DLKERNRLYH RFHEIIHEEA
651 PYAFLFSRHC SLLYKDYVKN IFVPTHRTDL IPEAQDETVN VTMVWLEKKE
701 DPCLSTS*
```

The cp6894 nucleotide sequence <SEQ ID 378> is:

```
   1 ATGTATAAAA GATGTGTGCT AGATAAAATT TTAAAGGGGA TTGTCGCCGG
  51 TTCTTTAATT TTGTTATACT GGTCCTCAGA CCTACTTGAA AGAGACATTA
 101 AGTCGATAAA AGGTAACGTA AGAGATATTC AAGAAGACAT TCGTGAAATC
 151 TCACGCGTAG TGAAACAACA GCAGACATCA CAAGCTATCC CTGCGGCACC
 201 TGGGGTGATG CTCGCTCCTA AGCTCGTCAG AGACGAAGCT TTTGCTCTAC
 251 TCTTTGGAGA TCCTAGTTAT CCTAATTTAC TTTCCCTAGA CCCCTATAAA
 301 CAGCAGACTC TTCCTGAACT TCTAGGAACA AATTTCCACC CTCATGGTAT
 351 CCTACGCACT GCCCATGTCG GAAAACCCGA AAATCTGAGC CCTTTTAATG
 401 GCTTTGATTA TGTCGTGGGC TTTTACGATC TCTGTATTCC TAGTTTAGCT
 451 TCTCCCCACG TAGGGAAATA CGAAGAATTT TCTCCAGATC TCGCTGTGAA
 501 AATAGAAGAA CATCTTGTTG AAGATGGTTC TGGGGATAAA GAGTTTCACA
 551 TCTATCTGAG GCCGAATGTT TTTTGGCGTC CTATAGATCC TAAGGCCCTT
 601 CCAAAACACG TTCAGTTAGA CGAAGTATTT CAACGTCCTC ATCCTGTGAC
 651 AGCTCATGAT ATTAAGTTTT TCTACGACGC TGTTATGAAC CCTTATGTAG
 701 CAACCATGCG AGCAGTGGCT CTGCGCTCTT GTTATGAAGA TGTGGTTTCT
 751 GTCTCAGTAG AAAACGATTT AAAATTAGTA GTCAGATGGA AAGCACACAC
 801 GGTAATCAAT GAAGAAGGAA AGGAAGAGCG CAAAGTGCTC TACTCTGCAT
 851 TTTCTAATAC CTTAAGCTTG CAGCCCCTCC CTAGATTTGT ATATCAGTAT
 901 TTTGCTAACG GGGAAAAAAT CATTGAAGAT GAGAATATCG ATACCTACCG
 951 AACCAATTCC ATTTGGGCGC AAAACTTCAC TATGCATTGG GCAAACAACT
1001 ATATTGTAAG TTGTGGAGCC TACTACTTTG CAGGGATGGA TGATGAGAAA
1051 ATCGTGTTTT CTAGAAATCC TGACTTCTAT GATCCTCTTG CGGCTCTTAT
1101 TGACAAGCGT TTCGTCTATT TTAAGGAAAG CACAGACTCC CTATTCCAAG
1151 ATTTTAAGAC AGGGAAAATA GACATCTCTT ACCTTCCACC CAACCAAAGA
1201 GATAATTTCT ATAGTTTTAT GAAAAGCTCC GCTTATAACA AACAGGTAGC
1251 TAAGGGAGGA GCCGTCCGTG AAACAGTCTC AGCAGATCGA GCATATACGT
1301 ACATAGGATG GAATTGCTTT TCATTATTTT TCCAAAGCCG ACAGGTGCGC
1351 TGTGCTATGA ACATGGCAAT CGATAGAGAG AGGATTATCG AACAGTGCTT
1401 GGATGGCCAA GGCTATACGA TTAGTGGGCC TTTTGCTTCG AGTTCTCCTT
1451 CTTATAATAA ACAGATCGAA GGGTGGCATT ATTCTCCAGA AGAAGCAGCT
1501 CGTCTCCTGG AAGAAGAGGG ATGGATAGAT ACCGATGGCG ATGGAATCCG
1551 AGAAAAAGTT ATCGATGGTG TGATTGTCCC GTTCCGTTTC CGTTTATGCT
1601 ATTATGTAAA GAGTGTCACC GCTCATACCA TTGCAGATTA CGTAGCTACT
1651 GCTTGTAAGG AAATCGGAAT CGAGTGTAGC CTTCTAGGAC TAGATATGGC
1701 CGATCTTTCG CAAGCTTTTG ATGAAAAGAA TTTCGATGCT CTTTTAATGG
1751 GATGGTGTTT AGGAATTCCT CCTGAGGATC CTAGGGCTTT ATGGCATTCT
```

```
1801  GAAGGGGCTA TGGAAAAGGG TTCAGCGAAT GTTGTAGGTT TCCATAATGA
1851  AGAAGCTGAT AAAATCATAG ACAGACTCAG CTACGAATAC GATCTGAAAG
1901  AACGTAATCG CCTGTACCAC CGTTTCCATG AAATTATTCA TGAGGAAGCT
1951  CCTTATGCTT TCTTGTTCTC ACGACATTGT TCCTTACTTT ATAAGGATTA
2001  TGTAAAAAAT ATTTTCGTAC CTACACATAG AACAGATTTA ATTCCTGAAG
2051  CTCAGGATGA GACTGTCAAC GTAACTATGG TATGGCTTGA GAAGAAGGAG
2101  GATCCGTGCT TAAGTACATC CTAA
```

The PSORT algorithm predicts inner membrane (0.162).

The protein was expressed in *E.coli* and purified as a his-tag product (Figure 189A) and also in GST/his form. The recombinant proteins were used to immunise mice, whose sera were used in a Western blot (Figure 189B) and for FACS analysis.

These experiments show that cp6894 is a surface-exposed and immunoaccessible protein, and that it is a useful immunogen. These properties are not evident from the sequence alone.

Example 190

The following *C.pneumoniae* protein (PID 4377193) was identified in the 2D-PAGE experiment <SEQ ID 379; cp7193>:

```
  1  MKRVIYKTIF CGLTLLTSLS SCSLDPKGYN LETKNSRDLN QESVILKENR
 51  ETPSLVKRLS RRSRRLFARR DQTQKDTLQV QANFKTYAEK ISEQDERDLS
101  FVVSSAAEKS SISLALSQGE IKDALYRIRE VHPLALIEAL AENPALIEGM
151  KKMQGRDWIW NLFLTQLSEV FSQAWSQGVI SEEDIAAFAS TLGLDSGTVA
201  SIVQGERWPE LVDIVIT*
```

A predicted leader peptide is underlined.

The cp7193 nucleotide sequence <SEQ ID 380> is:

```
  1  ATGAAAAGAG TCATTTATAA AACCATATTT TGCGGGTTAA CTTTACTTAC
 51  AAGTTTGAGT AGTTGTTCCC TGGATCCTAA AGGATATAAC CTAGAGACAA
101  AAAACTCGAG GGACTTAAAT CAAGAGTCTG TTATACTGAA GGAAAACCGT
151  GAAACACCTT CTCTTGTTAA GAGACTCTCT CGTCGTTCTC GAAGACTCTT
201  CGCTCGACGT GATCAAACTC AGAAGGATAC GCTGCAAGTG CAAGCTAACT
251  TTAAGACCTA CGCAGAAAAG ATTTCAGAGC AGGACGAAAG AGACCTTTCT
301  TTCGTTGTCT CGTCTGCTGC AGAAAAGTCT TCAATTTCGT TAGCTTTGTC
351  TCAGGGTGAA ATTAAGGATG CTTTGTACCG TATCCGAGAA GTCCACCCTC
401  TAGCTTTAAT AGAAGCTCTT GCTGAAAACC CTGCCTTGAT AGAAGGGATG
451  AAAAAGATGC AAGGCCGTGA TTGGATTTGG AATCTTTTCT TAACACAATT
501  AAGTGAAGTA TTTTCTCAAG CTTGGTCTCA AGGGGTTATC TCTGAAGAAG
551  ATATCGCCGC ATTTGCCTCC ACCTTAGGTT TGGACTCCGG GACCGTTGCG
601  TCCATTGTCC AAGGGGAAAG GTGGCCCGAG CTTGTGGATA TAGTGATAAC
651  TTAA
```

The PSORT algorithm predicts periplasmic (0.925).

This shows that cp7193 is an immunoaccessible protein in the EB and that it is a useful immunogen. These properties are not evident from the protein's sequence alone.

It will be appreciated that the invention has been described by way of example only and that modifications may be made whilst remaining within the spirit and scope of the invention.

TABLE II – sequences of the primers used to amplify Cpn genes.

Orf ID	N-terminus final primer	C-terminus final primer
CP0014P	GCGTC CCG GGTCATATG AAGTCTTCTTTCCCCA	GCGT CTC GAG ATGAAAGAGTTTTTGCG
CP0015P	GCGTCCCGGGTCATATG TCAGCTCTGTTTTCTGA	GCGT CTC GAG GAATTGGTATTTTGCTC
CP0016P	GCGTCCCGGGTCATATG GCCGATCTCACATTAG	GCGT CTC GAG GTCCAAGTTAAGGTAGCA
CP0017P	GCGT CCG GGTCATATG GGTATCAAGGGAACTG	GCGT CTC GAG AAATCCGAATCTTCC
CP0019P	GCGTCCCGGGTCAT ATGCAAGACTCTCAAGACTATAG	GCGT CTC GAG AAATCGGTATTTACCC
CP6260P	GCGTC CCG GGT GCTAGCACTACGATTTCTTTAACCC	GCGT CTC GAG AAAACGAAATTTGCTTC
CP6397P	GCGTC CCG GGTCATATGTTTAAACTGCTAAAAAATCTATT	GCGT CTC GAG ATGAAAGAAGAGTCCTCG
CP6456P	GCGTC CCG GGT CATATG TCATCTCCTGTAAATAACA	GCGT CTC GAG CTGACCATCTCCTGTT
CP6466P	GCGTC CCG GGT CAT ATG TGCAAGGAGTCCAGT	GCGT CTC GAG ATTTTCCTTAGCATAACG
CP6467P	GCGTC CCG GGT CAT ATG TGTTCCCCATCCCAA	GCGT CTC GAG TAGTTTTTCTATAAAACGAAAGTCT
CP6468P	GCGTC CCG GGT CAT ATG TGCTCCTCCTACTCTTC	GCGT CTC GAG GGGGAAATAGGTATATTTGA
CP6469P	GCGTC CCG GGT CAT ATG AGCTGCTCAAAGCAA	GCGT CTC GAG ACTTAAGATATCGATATTTTTGA
CP6552P	GCGTC CCG GGT CAT ATG TGCCATAAGGAAGATG	GCGT CTC GAG ACCATTGTCTTGAGTCAT
CP6567P	GCGTC CCG GGT CAT ATG ACCTCACCGATCCCC	GCGT CTC GAG AGAAGCCGGTAGAGGC
CP6576P	GCGTC CCG GGT CAT ATG ACTGAAAAAGTTAAAGAAGG	GCGT CTC GAG GAA CATGCCCCCTAA
CP6727P	GCGTC CCG GGT CATATGCTACATCCACTAATGGC	GCGT CTC GAG GAAAGAATAACGAGTTCC
CP6729P	GCGTC CCG GGT CAT ATGGCAGATGCTTCTTTATC	GCGT CTC GAG GAATGAGTATCTTAGCC
CP6731P	GCGTC CCG GGT CATATGGCTGTTGTTGAAATCAAT	GCGTC CAT GGC GGC CGC GAACTGGAACTTACCTCC
CP6736P	GCGTC CCG GGT GCT AGCGTAGAAGTTATCATGCCTT	GCGTC CAT GGC GGC CGC AAATCGTAATTTGCTTC
CP6737P	GCGT GGA TCC CAT ATG GAGACTAGACTCGGAGG	GCGT CTC GAG AAATGTGGATTTTAGTCC
CP6751P	GCGTC CCG GGT GCT AGC AATGAAGGTCTCCAACT	GCGT CTC GAG AAATCTCATTCTACTCGC
CP6752P	GCGTGA ATT CAT ATGTTCGGGATGACTCCT	GCGT CTC GAG GAATTTTAAGGTACTTCCTG
CP6753P	GCGTC CCG GGT GCT AGCACTCCCTACTCTCATAGAG	GCGT CTC GAG AAACTTAAAGGTCGTTC
CP6767P	GCGTC CCG GGT CAT ATG ATAAAACAAATAGGCCGT	GCGT CTC GAG TTCGTAAGCAACTTCAGA
CP6829P	GCGTC CCG GGT CAT ATG AAGCAGATGCGTCTTT	GCGTC CAT GGC GGC CGC GAAACTAAGGGAGAGGC
CP6830P	GCGTC CCG GGT CAT ATG GATCCCGCGTCTGTT	GCGTC CAT GGC GGC CGC GAATACAAACCGGATCC
CP6832P	GCGTC CCG GGT CAT ATG CATAAAGTAATAGTTTTCATTT	GCGT CTC GAG TAAACTAGAAAAAGTCGTC
CP6848P	GCGTC CCG GGT CAT ATG TCATCAAATCTACATCCC	GCGT CTC GAG AACGCGAGCTATTTTAC
CP6849P	GCGTC CCG GGT GCT AGC AGCGGGGGTATAGAG	GCGT CTC GAG ATACACGTGGGTATTTTC
CP6850P	GCGTC CCG GGT CAT ATG TGCCGCATTGTAGAT	GCGT CTC GAG CTGTTTGCATCTGCC
CP6854P	GCGTC CCG GGT GCT AGC TCAATAGCTATTGCAAG	GCGT CTC GAG TTATCGAAATGTCTTTG
CP6879P	GCGTC CCG GGT CAT ATG GCAACACCCGCTCAA	GCGTC CAT GGC GGC CGC TCCTTGAAATTGCTCTTGC
CP6894P	GCGTC CCG GGT CAT ATG TATAAAAGATGTGTGCTAGA	GCGT CTC GAG GGATGTACTTAAGCACG
CP6900P	GCGTC CCG GGT CAT ATG AAGATAAAATTTTCTTGGAAG	GCGT AAG CTT GGGAAGACGATACCG
CP6952P	GCGTC CCG GGT CAT ATG CTCTCGGATCAATATATAGG	GCGT CTC GAG TCGAATTTCTTTTTTAGC
CP7034P	GCGTC CCG GGT CAT ATG AAAAAACAGGTATATCAATG	GCGT AAG CTT AAACGCTGAAATTATACC
CP7090P	GCGTC CCG GGT CAT ATG TGTAGCCTTTCCCCT	GCGT CTC GAG GCGTGCATGAATCTTA
CP7091P	GCGTC CCG GGT CAT ATG GAAGAATTAGAAGTTGTTGT	GCGT CTC GAG TAGTGTTCTCTTTATCGGT
CP7170P	GCGTC CCG GGT CAT ATG CTAGGGGCTGGAAACC	GCGT AAG CTT AAACTGCAGACCTGACG
CP7228P	GCGTC CCG GGT CAT ATG ACTGCTGTTCTTATTCTTACA	GCGT CTC GAG ATCTGAAAGCGGAGG
CP7249P	GCGTC CCG GGT CAT ATG ATCCCATCCCCTACC	GCGT CTC GAG ATCAGGTTGCTGAGACTT
CP7250P	GCGTC CCG GGT CAT ATG AATCTTTCAAACAGGTCT	GCGT CTC GAG ATTTTTTCTAGAGAGACTCTC
CP0018P	GTGCGT CATATG GCAACCACTCCACTAA	ACTCGCTA GCGGCCGC TAATGAGGTCCCCAG
CP6270P	GTGCGT CATATG AATTTATTAGGAGCTGCT	ACTCGCTA GCGGCCGC AAATTTGATTTTGCTACC
CP6735P	GTGCGT CATATG GCAGCACAAGTTGTATAT	ACTCGCTA GCGGCCGC TGGCGTAGAAGTGATC
CP6998P	GTGCGT CATATG TTGCCTGTAGGGAAC	ACTCGCTA GCGGCCGC GAATCTGAACTGACCAGA
CP7033P	GTGCGT CATATG GTTAATCCTATTGGTCCA	ACTCGCTA GCGGCCGC TTGGAGATAACCAGAATATA
CP7287P	GTGCGT CATATG TTACACAGCTCAGAACTAGA	ACTCGCTA GCGGCCGC GAAAATAATACGGATACCA
CP0010P	GTGCGT CATATG GCAACTGCTGAAAATATA	GCGT CTCGAG GAATTGGAACTTACCC
CP0468P	GTGCGT GCTAGC ATTTTTTATGACAAACTCTAT	GCGT CTCGAG AAATGTGCAATGACTCT
CP6272P	GTGCGT CATATG TTGACTCATCAAGAGGCT	GCGT CTCGAG GAAGGGAGGTTTTTTAGGT
CP6273P	GTGCGT CATATG ACATATCTGGAAGCTC	ACTCGCTA GCGGCCGC CTCCACAATTTTTATG
CP6362P	GTGCGT CATATG CCCTTTGATATTACTTATTATACA	GCGT CTCGAG TCGTTTCCAAATCCA
CP6372P	GTGCGT CATATG AAACAACACTATTCTCTAAATA	GCGT CTCGAG TTTCTTGTGGTTTTTCT
CP6390P	GTGCGT CATATG CGAGAGGTGCCTAAG	ACTCGCTA GCGGCCGC TCTCCTAGACAGCCTT
CP6402P	GTGCGT CATATG AATGTTGCGGATCTCCTTT	GCGT CTCGAG GAAGGGGTTGGCCGT
CP6446P	GTGCGT CATATG TGTAATCAAAAGCCCTCTT	GCGT CTCGAG GGGCTGAGGAGGAAC
CP6520P	GTGCGT GCTAGC AAACACTACCTATCATTTTCT	GCGT CTCGAG CAGAAAGGCTTTTCTTT
CP6577P	GTGCGT CATATG AATTTAGGCTATGTTAATTTA	GCGT CTCGAG GTTTTGTTTTTTGAAAGA
CP6602P	GTGCGT CATATG GCAGCATCAGGAGGCA	GCGT CTCGAG TGACCAAGGATAGGGTTTAG

CP6607P	GTGCGT CATATG CCTCGTGGTGACACTTT	GCGT CTCGAG CGCTGCTTCTTGCTC
CP6615P	GTGCGT CATATG TGCTCTCAAAAAACGACAA	GCGT CTCGAG TGAAGAGGCGCCATC
CP6624P	GTGCGT CATATG GATGCGAAAATGGGA	GCGT CTCGAG TCTTTGACATTCAAGAGC
CP6672P	GTGCGT CATATG ATTCCTACCATGTTAATG	GCGT CTCGAG GTCATACAATTTCCTTATATA
CP6679P	GTGCGT CATATG TGCACTCACTTAGGCT	GCGT CTCGAG CGAGTAGTTAGCACAAAC
CP6717P	GTGCGT GCTAGC AAGACAATCGTAGCTTCA	ACTCGCTA GCGGCCGC GGCTGGCATATAGGT
CP6784P	GTGCGT GCTAGC AAATCAAGATGTTCTATTGATA	GCGT CTCGAG TCCAAAACAACCCTCT
CP6802P	GTGCGT CATATG TGCGTAAGTTATATTAATTCCTT	GCGT CTCGAG CAGTCGGGCTTGTTG
CP6847P	GTGCGT CATATG TCGGATCTTTTACGAG	GCGT CTCGAG TTTTCTACACTGTTGTAATAAA
CP6884P	GTGCGT CATATG AATCAGCTGCTTTCT	GCGT CTCGAG AGAGAAGGTAATTGTACC
CP6886P	GTGCGT CATATG TGTCTACTTATTATCTATCTCTAC	GCGT CTCGAG TTCAGAAAAATGGCT
CP6890P	GTGCGT CATATG TCCCCACGACGACAA	GCGT CTCGAG TCCTGCAGCATTTAGC
CP6960P	GTGCGT CATATG TGTGACGTACGGTCTA	ACTCGCTA GCGGCCGC TTCACCTTGATTTCCT
CP6968P	GTGCGT CATATG TGCGATGCAAAAC	ACTCGCTA GCGGCCGC GGAAGTATGCTTAGATATT
CP6969P	GTGCGT CATATG TGCTGTGGTTACTCTATT	ACTCGCTA GCGGCCGC AAAAAGGTCATAGTATACCT
CP7005P	GTGCGT CATATG AAAACTGTGATATTGAACA	GCGT CTCGAG CTGAGCTTCTATTTCTATTAT
CP7072P	GTGCGT CATATG CCCATTTATGGGAAA	GCGT CTCGAG GTTGAGCAAAGGTTTG
CP7101P	GTGCGT CATATG TATTCGTGTTACAGCAA	GCGT CTCGAG GAAAAATTCTTTAGGGAG
CP7102P	GTGCGT CATATG GCCGCTAAAGCAAAT	GCGT CTCGAG TGAAAATGAAAGGATGGT
CP7105P	GTGCGT GCTAGC AGTCTATATCAAAAATGGTG	GCGT CTCGAG ATCTTTCATTTGGTTATCT
CP7106P	GTGCGT CATATG AAAGATTTGGGGACTCT	GCGT CTCGAG GAATCCTAAGGCATACCTA
CP7107P	GTGCGT GCTAGC AGTATAGTCAGAAATTCTGCA	GCGT CTCGAG GAAGCTAAGATTATAGCTACTTT
CP7108P	GTGCGT GCTAGC GCGGCCCTTTCCA	ACTCGCTA GCGGCCGC TTTATGTATATGGAACAGATAGG
CP7109P	GTGCGT CATATG GGACATTTTATTGATATTG	ACTCGCTA GCGGCCGC ATCATCAAGGTAGATAAAG
CP7110P	GTGCGT CATATG GGTTATTGCTATGTAATTACA	GCGT CTCGAG TTCTGATTGGACTCCA
CP7127P	GTGCGT CATATG GTGGCTTTAACGATAGC	ACTCGCTA GCGGCCG GCAGCCATCGTATTC
CP7130P	GTGCGT CATATG TTCAATATGCGAGG	GCGT CTCGAG CTTCTTATTTGAACTTTG
CP7140P	GTGCGT CATATG ACAGCCGGAGCAGCT	GCGT CTCGAG AGCACCCTCAATTTCATTG
CP7182P	GTGCGT CATATG GGATATGTTTTCTATGTGATC	GCGT CTCGAG GCTACTAAATCGAATCGA
CP6262P	GTGCGT CATATG ATCCCTGGATTAAGTTCA	ACTCGCTA GCGGCCGC TTCACTGGGAGCTTGA
CP6269P	GTGCGT CATATG TACCAGGAGAATCTAAGAT	ACTCGCTA GCGGCCGC GATTTCTTCTTCAGCTC
CP6296P	GTGCGT CATATG GAGGAGGTGTCTGAGTAT	ACTCGCTA GCGGCCGC ATGTTTCTTTTACTCTTTCT
CP6419P	GTGCGT CATATG GCTCCAGTCCGTGTT	GCGT CTCGAG AAGTGTTCGTTGGAAGT
CP6601P	GTGCGT CATATG AATAAGCTACTCAATTTCGT	GCGT CTCGAG GAAAATCTGAATTCTTCCT
CP6639P	GTGCGT CATATG TTAAATTCAAGCAATTCA	GCGT CTCGAG AGGAACTAAAACCTCATCT
CP6664P	GTGCGT GCTAGC GTTTTATTTCATGCTCAA	ACTCGCTA GCGGCCGC CTTAGAAAGACTATTTTCTAAGTA
CP6696P	GTGCGT CATATG TGCGTGATAATGGG	GCGT CTCGAG ATTCATCTTCGTAAAGAAT
CP6757P	GTGCGT CATATG GCAGTTGGTGGCGT	ACTCGCTA GCGGCCGC CTGTCCCTCTGGAGC
CP6790P	GTGCGT GCTAGC AGTGAACACAAAAAATCA	ACTCGCTA GCGGCCGC CTTATCGTCGTTATCAATA
CP6814P	GTGCGT CATATG CATGACGCACTTCTAAG	GCGT CTCGAG TACAGCTGCGCGA
CP6834P	GTGCGT CATATG GTTATGGGAACCTATATCG	GCGT CTCGAG TACATTTGTATTGATTTCAG
CP6878P	GTGCGT CATATG AACGTCCCTGATTCC	GCGT CTCGAG GCTAGCGGCTCTTTC
CP6892P	GTGCGT CATATG CAGAAGCATCCTTCCT	ACTCGCTA GCGGCCGC TCCTCTTTAGGAAATGG
CP6909P	GTGCGT CATATG TCCTCTTTAGGAAATGG	GCGT CTCGAG CAGTGCCAAGTAGGGA
CP7015P	GTGCGT CATATG GCAGTACGATTAATTGTTG	GCGT CTCGAG TTTATTGTAGTCTATTTTATATTTC
CP7035P	GTGCGT GCTAGC AGCAGAAAAGACAATGA	GCGT CTCGAG ATTTTGAGTGTCTTGCA
CP7073P	GTGCGT CATATG ATTACCATAAATCACGTG	GCGT CTCGAG TATCCATCGACTTATAGC
CP7085P	GTGCGT GCTAGC TGTATTTTCCCTTACGTA	ACTCGCTA GCGGCCGC GGATTCTGCATACTCTG
CP7092P	GTGCGT CATATG TCTCCTCTTCCTAAAAAA	GCGT CTCGAG GGATTCATTACTGACCA
CP7093P	GTGCGT CATATG AAATACCGCTTCACG	GCGT CTCGAG ATTCTGTAGGGCTACGT
CP7094P	GTGCGT CATATG GTACACTTCTCTCATAACCC	GCGT CTCGAG TAAGTTTGTATTGCGGTAT
CP7132P	GTGCGT CATATG TTGTTATTAGGGACTTTAGGA	GCGT CTCGAG TTTCCCAACCGCA
CP7133P	GTGCGT CATATG GCTGCGAATGCTC	GCGT CTCGAG TAATTTAATACTCTTTGAAGG
CP7177P	GTGCGT CATATG CCTACTCAAGTTAAAACAGA	GCGT CTCGAG AAGTTTATATTTCAGCACTT
CP7184P	GTGCGT GCTAGC CATATAGGATTTTGCCA	GCGT CTCGAG GTACTTAGCAAAGCGAT
CP7206P	GTGCGT GCTAGC AAGAAGCTATATCACCCTA	GCGT CTCGAG CACACCGAGGAAAC
CP7222P	GTGCGT CATATG GTAGTTTCAGAAGAAAAAGTC	GCGT CTCGAG ACGTATGCGCAACTG
CP7223P	GTGCGT CATATG GAAGTATTAGACCGCTCT	GCGT CTCGAG CGAGAAAAAGCTTCC
CP7224P	GTGCGT CATATG ATGAAGAAAATTCGAAA	ACTCGCTA GCGGCCGC TAAGCATTCACAAATGA
CP7225P	GTGCGT CATATG CATATTTTGCTTGATCGT	GCGT CTCGAG TCTTTTAACTAAATCTTGTTCTT
CP7303P	GTGCGT CATATG CTTGTCTATTGTTTTGATCC	GCGT CTCGAG AAAATATACGGAACTCGC
CP7304P	GTGCGT GCTAGC GAAGTTTATAGTTTTTCCC	GCGT CTCGAG TTTTTGATTCCTTAAGAAG
CP7305P	GTGCGT CATATG GAAGTTTATAGTTTTCACCCT	GCGT CTCGAG ACTCCTTGAGAAGGGAA
CP7307P	GTGCGT CATATG CTTAATCATGCTAAAAAGC	ACTCGCTA GCGGCCGC CTCTTTTATTTTAGGAAGCT

CP7342P	GTGCGT CATATG AAAAAAAAATTTATTTTCTACT	ACTCGCTA GCGGCCGC CACACTCTGTTCTTCTG
CP7347P	GTGCGT CATATG TTTTCTAAGGATTTGACTAA	GCGT CTCGAG CGAAGCAGAAGTCGT
CP7353P	GTGCGT CATATG AATATGCCTGTTCCTTCT	GCGT CTCGAG GGGGCGTAGGTTGTA
CP7193P	GTGCGT CATATG TGTTCCCTGGATCCT	ACTCGCTA GCGGCCGC AGTTATCACTATATCCACAAG
CP7248P	GTGCGT GCTAGC CTTGAACATTCTAAACAAGAT	GCGT CTCGAG ACGTAGTTTAAGAGCAGACT
CP7261P	GTGCGT CATATG TGTCTATCTGCCTACATAG	GCGT CTCGAG TTTTGATGCTTCTTTCA
CP7280P	GTGCGT CATATG GACCAGAAAATTGAAAA	GCGT CTCGAG AGAGGTCTTCTGAGTGC
CP7302P	GTGCGT CATATG AATTTCCATTGTAGTGTAGT	GCGT CTCGAG GAACAGTTCGATTTGTG
CP7306P	GTGCGT CATATG CTTCCTTTATCAGGGCA	ACTCGCTA GCGGCCGC TTCTTCAGGTTTCAGG
CP7367P	GTGCGT GCTAGC CGTTATGCCGAGGTC	GCGT CTCGAG TTCGTGCATTTGGTG
CP7408P	GTGCGT CATATG TTGAAAATCCAGAAAAA	GCGT CTCGAG ATTCATTTTCGGAAGAG
CP7409P	GTGCGT CATATG AGACGTTATCTTTTCATGGT	GCGT CTCGAG CCCTTTGCTCTTTACATAG
CP6733P	GTGCGT ACTAGT TGTCACCTACAGTCACTAG	GCGT CTCGAG GAATCGGAGTTTGGTA
CP6728P	GTGCGT ACTAGT AAGTCCTCTGTCTCTTGG	GCGT CTCGAG GAAACAAAACTTAGAGCCC

TABLE III – Proteins with best results in FACS analysis

cp number	Molecular Weight (kDa)		Fusion type
	Theoretical	Western Blot	
6260	97.5	94; 70	GST
6270	87.5	-	GST
6272	78.0	90	GST
6273	58.6	74; 64; 50	GST
6296	31.1	-	GST
6390	88.9	102	GST
6456	42.5	89; 67,45	GST
6466	57.5	59; 56	His
6467	59.0	67	GST
6552	28.4	50; 27	GST
6576	86.0	79; 70; 62; 45	GST
6577	17.3	12	GST
6602	43.4	53; 42; 34	GST
6664	54.5	104; 45	GST
6696	47.9	95; 53	GST
6727	130.0-142.9	123; 61; 39	His
6729	94.8	multiple bands	GST
6731	95.5	97	GST
6733	97.1	104	His
6736	100.1	98; 93; 66; 60	GST
6737	101.2	multiple bands	GST
6751	100.2	95; 71	GST
6752	102.1	97; 48	His
6767	29.1	28	GST
6784	32.9	35	GST
6790	71.3	multiple bands	His
6802	29.7	-	GST
6814	29.6	28	GST

6830	177.4	174; 91; 13	GST
6849	57.3	multiple bands	GST
6850	7.4-9.4	61; 14; 8	GST
6854	42.2	-	GST
6878	40.4	-	GST
6900	28.0	-	GST
6960	25.6	75; 35	GST
6968	34.6	83; 53; 35	GST
6998	39.3	multiple bands	GST
7033	68.2	multiple bands	GST
7101	113	105	GST
7102	63.4	-	GST
7105	29.2	30	GST
7106	39.5	72;46	GST
7107	71.4	67; 31	His
7108	35.9	35	GST
7111	46.1	51	GST
7132	17.9	57; 47; 17	His
7140	36.2-29.8	50; 38; 34	GST
7170	34.4	77; 33	GST
7224	39.4	40	GST
7287	167.3	180	GST
7306	50.1	50	GST

TABLE IV – FACS-positive proteins not found in *C.trachomatis*

cp7105	cp6390
cp7106	cp6784
cp7107	cp6296
cp7108	

TABLE V – Proteins identified by MALDI-TOF following 2D electrophoresis

cp6270	cp6733	cp6900
cp6552	cp6736	cp6960
cp6576	cp6737	cp6998
cp6577	cp6752	cp7033
cp6602	cp6767	cp7108
cp6664	cp6784	cp7111
cp6727	cp6790	cp7170
cp6728	cp6830	cp7287
cp6729	cp6849	cp7306

CLAIMS

1. A protein comprising an amino acid sequence selected from the group consisting of SEQ IDs 97, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, & 377.

2. A protein having 50% or greater sequence identity to a protein according to claim 1.

3. A protein comprising a fragment of an amino acid sequence selected from the group consisting of SEQ IDs 97, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, & 377.

4. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.

5. A nucleic acid molecule according to claim 4, comprising a nucleotide sequence selected from the group consisting of SEQ IDs 98, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,

320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, & 378.

6. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of SEQ IDs 98, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, & 378.

7. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to any one of claims 4 to 6.

8. A nucleic acid molecule comprising a nucleotide sequences having 50% or greater sequence identity to a nucleic acid molecule according to any one of claims 4 to 7.

9. A nucleic acid molecule which can hybridise to a nucleic acid molecule according to any one of claims 4 to 8 under high stringency conditions.

10. A composition comprising a protein or a nucleic acid molecule according to any preceding claim.

11. A composition according to claim 10 being a vaccine composition.

12. A composition according to claim 10 or claim 11 for use as a pharmaceutical.

13. The use of a composition according to claim 10 in the manufacture of a medicament for the treatment or prevention of infection due to *Chlamydia* bacteria, particularly *Chlamydia pneumoniae*.

FIGURE 1

FIG. 1A

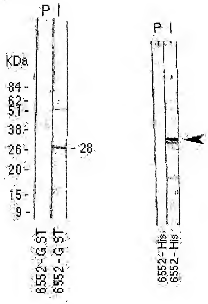


FIG. 1B

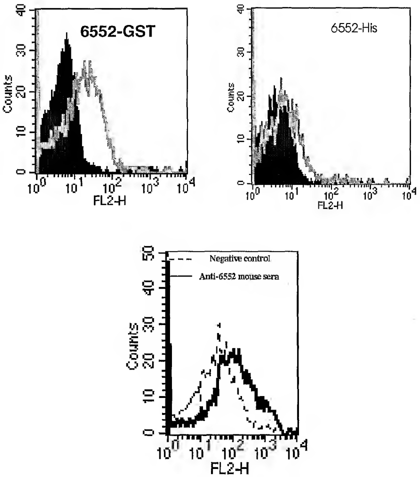


FIG. 1C

FIGURE 2

FIG. 2A

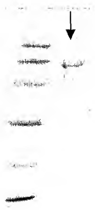


FIG. 2B

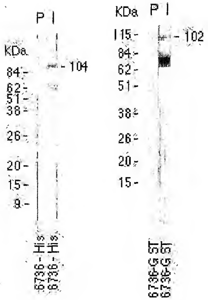


FIG. 2C

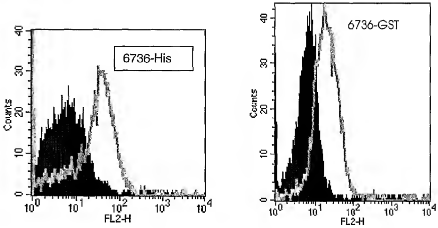


FIGURE 3

FIG. 3A

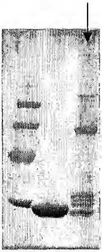


FIG. 3B

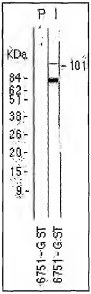


FIG. 3C

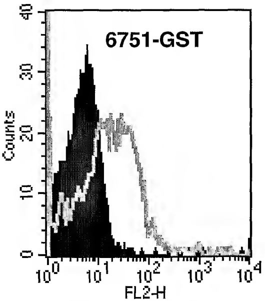


FIGURE 4

FIG. 4A

FIG. 4B

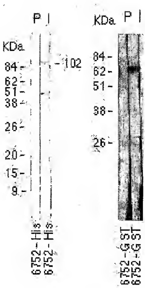


FIG. 4C

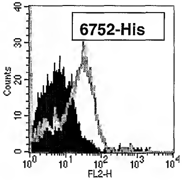


FIGURE 5

FIG. 5A

FIG. 5B

FIG. 5C

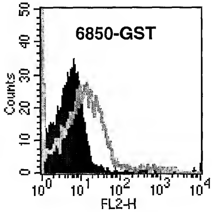


FIGURE 6

FIG. 6A

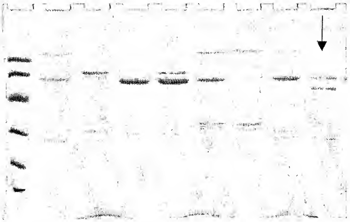


FIG. 6B

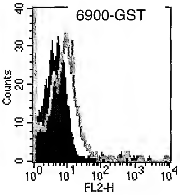


FIG. 6C

FIGURE 7

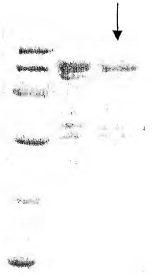


FIG. 7A

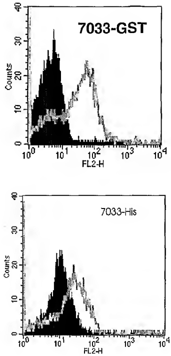


FIG. 7B

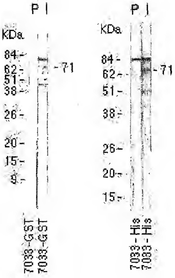


FIG. 7C

FIGURE 8

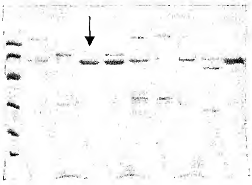


FIG. 8A

FIG. 8B

FIG. 8C

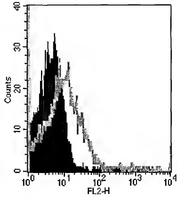


FIGURE 9

Fig. 9A

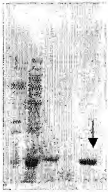


Fig. 9B

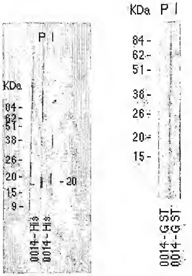


Fig. 9C

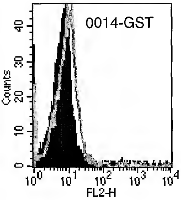


FIGURE 10

FIG. 10A

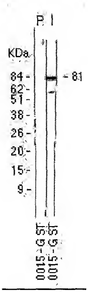


FIG. 10B

FIGURE 11

FIG. 11A

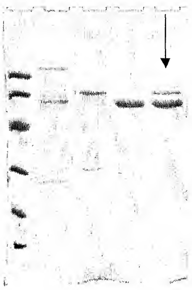


FIG. 11B

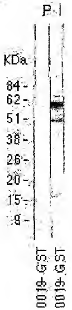


FIG. 11C

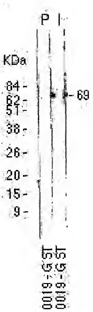


FIGURE 12

FIG. 12A

FIG. 12B

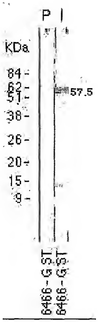


FIG. 12C

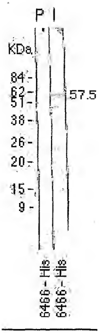


FIGURE 13

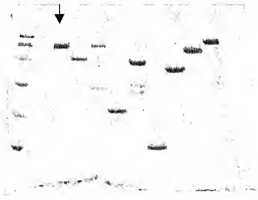


FIG. 13A

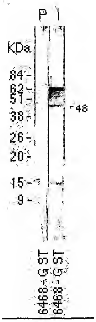


FIG. 13B

FIGURE 14

FIG. 14A

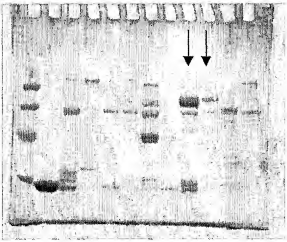


FIG. 14B

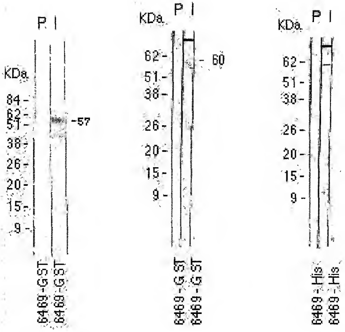


FIGURE 15

FIG. 15A

FIG. 15B

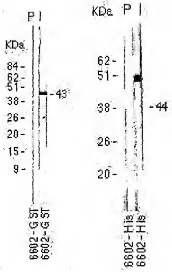


FIG. 15C

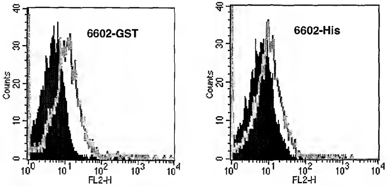


FIGURE 16

Fig. 16A

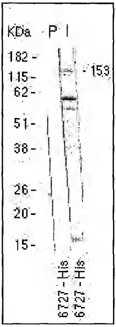


Fig. 16B

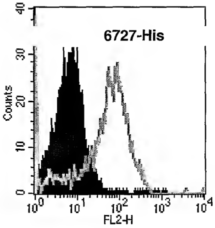


Fig. 16C

FIGURE 17

Fig. 17A

Fig. 17B

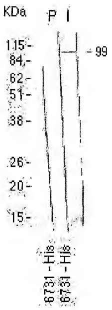


Fig. 17C

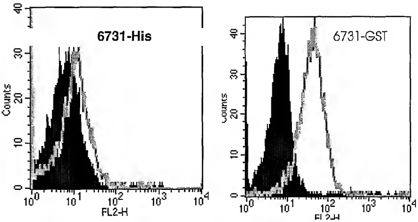


FIGURE 18

FIG. 18A

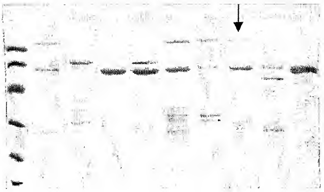


FIG. 18B

FIG. 18C

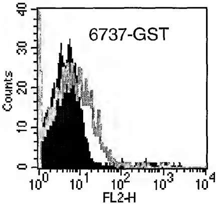


FIGURE 19

FIG. 19A

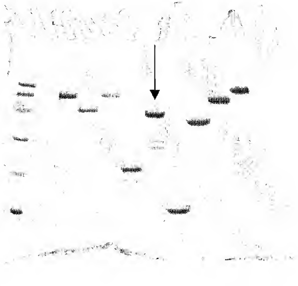


FIG. 19B

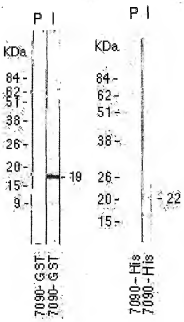


FIGURE 20

FIG. 20A

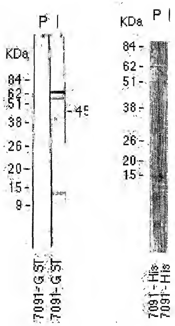


FIG. 20B

FIGURE 21

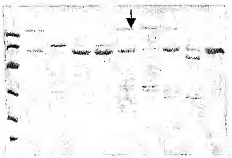


FIG. 21A

FIG. 21B

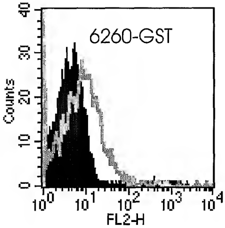


FIG. 21C

FIGURE 22

FIG. 22A

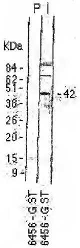


FIG. 22B

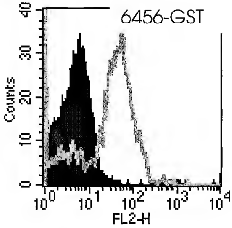


FIG. 22C

FIGURE 23

FIG. 23A

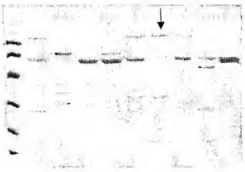


FIG. 23B

FIG. 23C

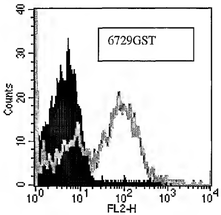


FIGURE 24

FIG. 24A

FIG. 24B

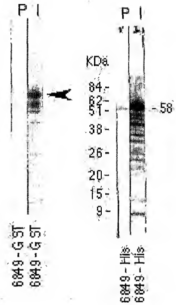


FIG. 24C

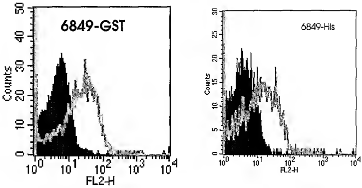


FIGURE 25

FIG. 25A

FIG. 25B

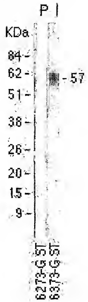


FIG. 25C

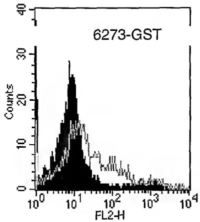


FIGURE 26

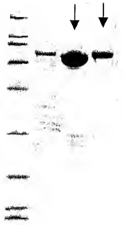


FIG. 26A

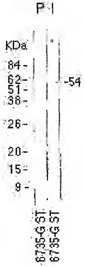


FIG. 26B

FIGURE 27

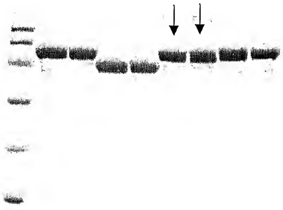


FIG. 27A

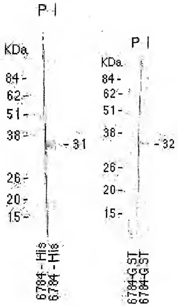


FIG. 27B

FIG. 27C

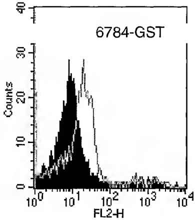


FIGURE 28

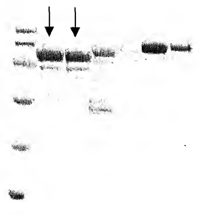


FIG. 28A

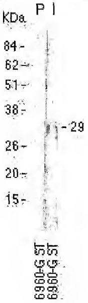


FIG. 28B

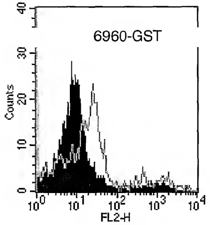


FIG. 28C

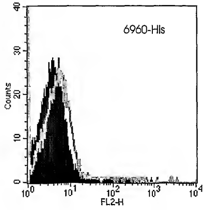


FIGURE 29

FIG. 29A

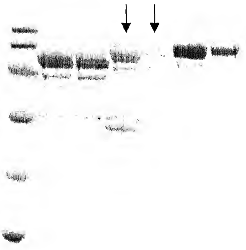


FIG. 29B

FIG. 29C

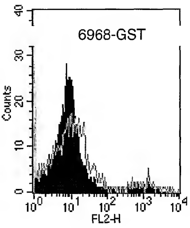


FIGURE 30

FIG. 30A

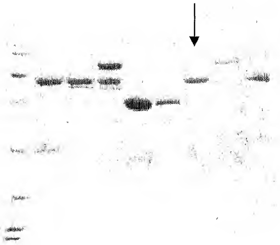


FIG. 30B

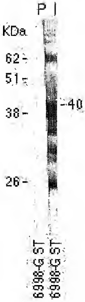


FIG. 30C

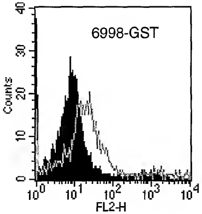


FIGURE 31

FIG. 31A

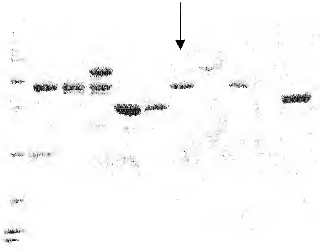


FIG. 31B

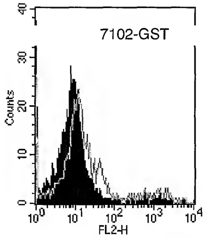


FIGURE 32

FIG. 32A

FIG. 32B

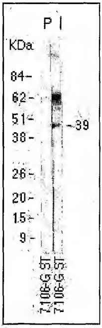


FIG. 32C

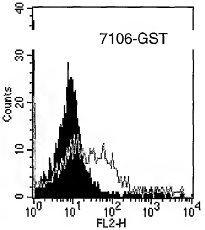


FIGURE 33

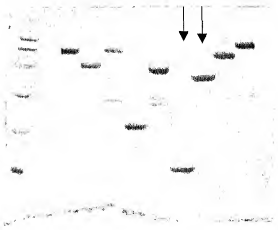


FIG. 33A

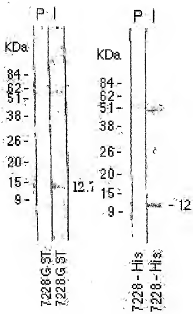


FIG. 33B

FIGURE 34

FIG. 34A

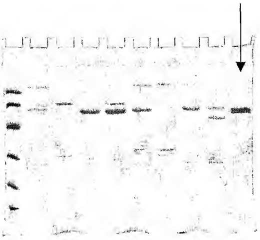


FIG. 34B

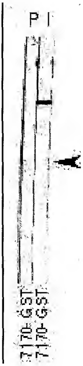


FIG. 34C

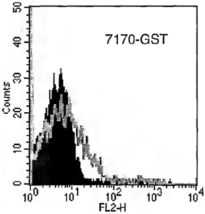


FIGURE 35

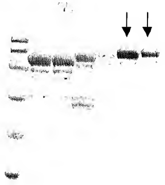


FIG. 35A

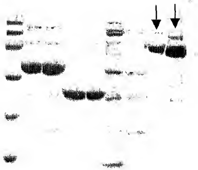


FIG. 35B

FIG. 35C

FIGURE 36

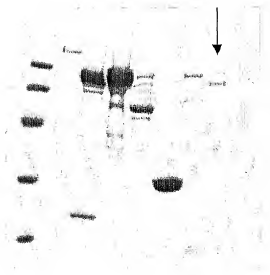


FIG. 36A

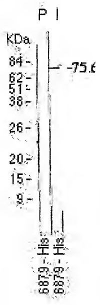


FIG. 36B

FIGURE 37

FIG. 37A

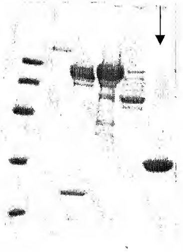


FIG. 37C

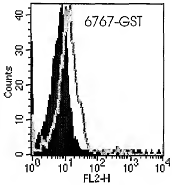


FIG. 37B

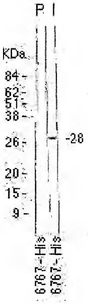


FIG. 37D

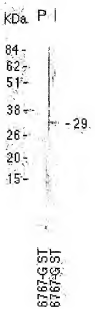


FIGURE 38

FIG. 38A

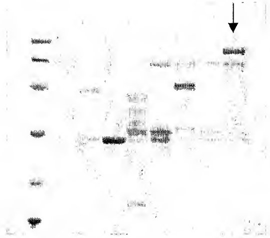


FIG. 38B

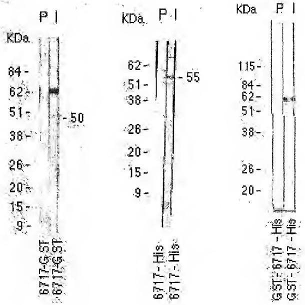


FIGURE 39

FIG. 39A

FIG. 39B

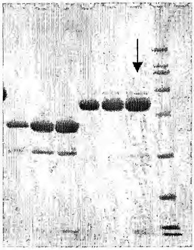


FIG. 39C

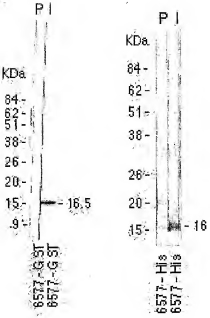


FIG. 39D

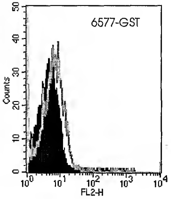


FIGURE 40

FIG. 40A

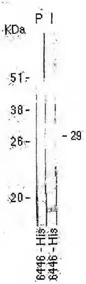


FIG. 40B

FIGURE 41

FIG. 41A

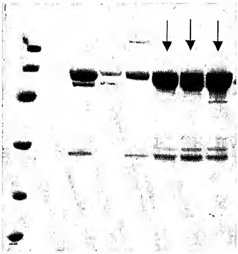


FIG. 41B

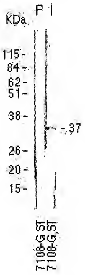


FIG. 41C

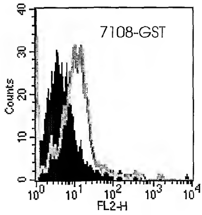


FIGURE 42

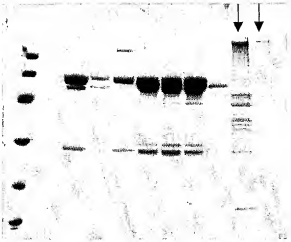


FIG. 42A

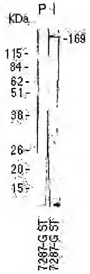


FIG. 42B

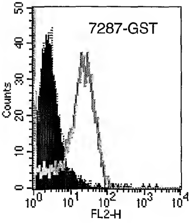


FIG. 42C

FIGURE 43

FIG. 43A

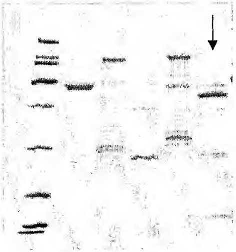


FIG. 43B

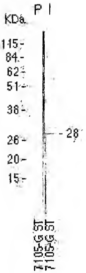


FIG. 43C

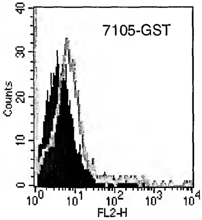


FIGURE 44

FIG. 44A

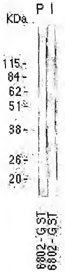


FIG. 44B

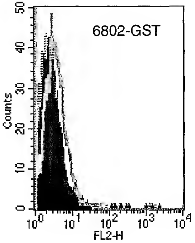


FIG. 44C

FIGURE 45

FIG. 45A

FIG. 45B

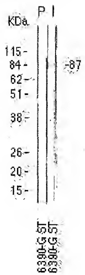


FIG. 45C

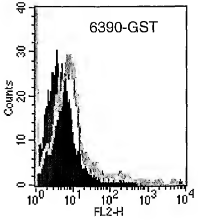


FIGURE 46

Fig. 46A

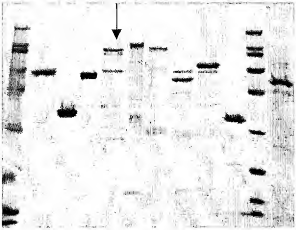


Fig. 46B

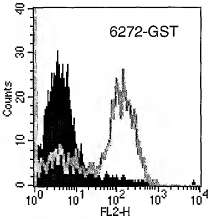


FIGURE 47

Fig. 47A

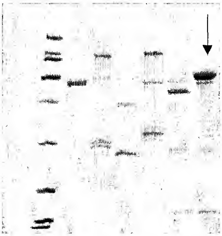


Fig. 47B

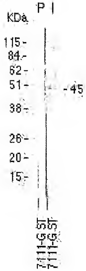


Fig. 47C

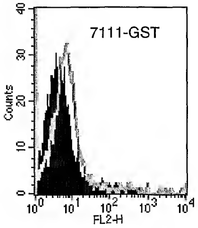


FIGURE 48

FIG. 48A

FIG. 48B

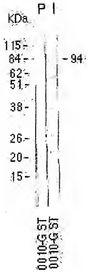


FIG. 48C

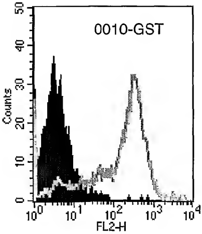


FIGURE 49

FIG. 49A

FIG. 49B

FIG. 49C

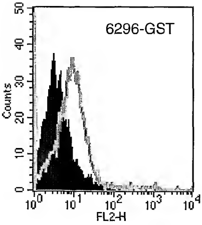


FIGURE 50

FIG. 50A

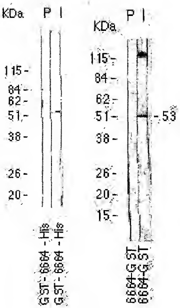


FIG. 50B

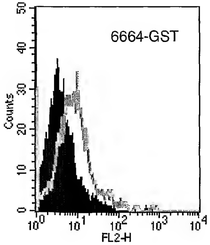


FIG. 50C

FIGURE 51

FIG. 51A

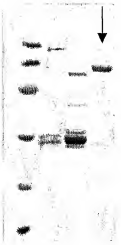


FIG. 51B

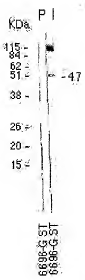


FIG. 51C

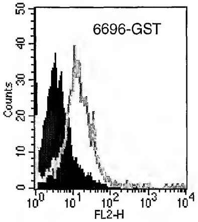


FIGURE 52

FIG. 52A

FIG. 52B

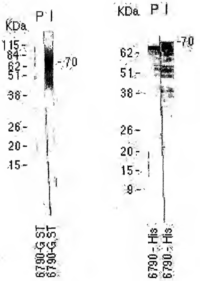


FIG. 52C

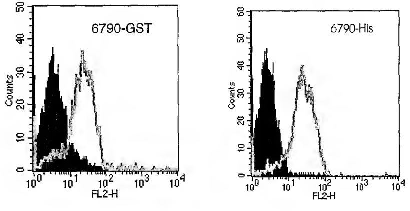


FIGURE 53

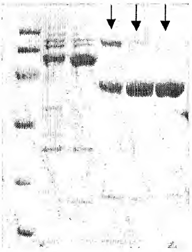


FIG. 53A

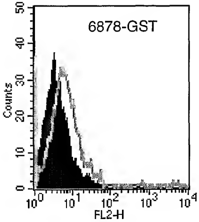


FIG. 53B

FIGURE 54

FIG. 54A

FIG. 54B

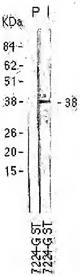


FIG. 54C

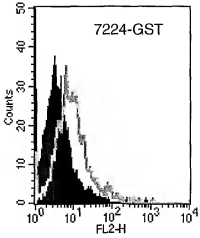


FIGURE 55

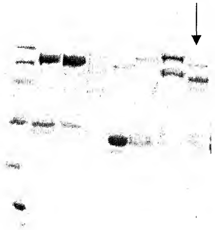


FIG. 55A

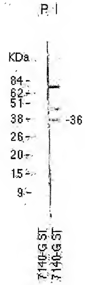


FIG. 55B

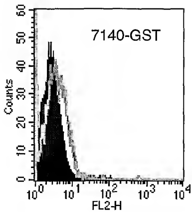


FIG. 55C

FIGURE 56

FIG. 56A

FIG. 56B

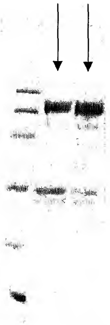


FIG. 56C

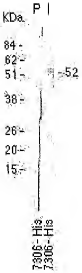


FIG. 56D

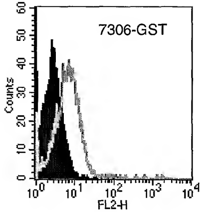


FIGURE 57

FIG. 57A

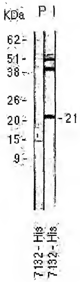


FIG. 57B

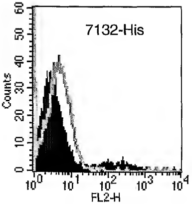


FIG. 57C

FIGURE 58

FIG. 58A

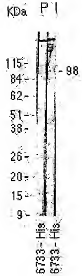


FIG. 58B

FIG. 58C

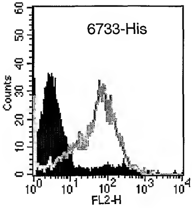


FIGURE 59

FIG. 59A

FIG. 59B

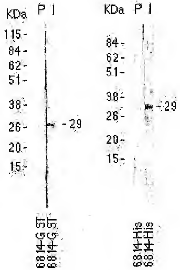


FIG. 59C

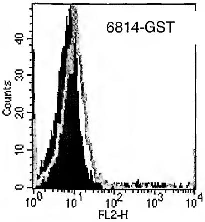


FIGURE 60

FIG. 60A

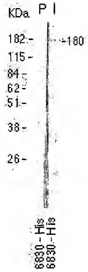


FIG. 60B

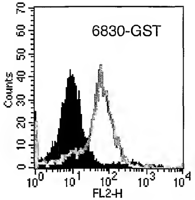


FIG. 60C

FIGURE 61

FIG. 61A

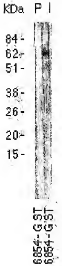


FIG. 61B

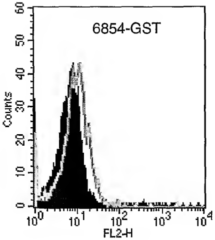


FIG. 61C

FIGURE 62

FIG. 62A

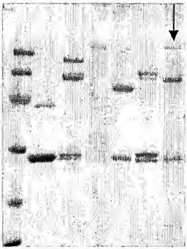


FIG. 62C

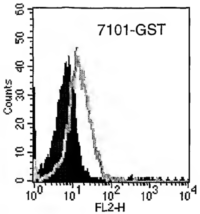


FIG. 62B

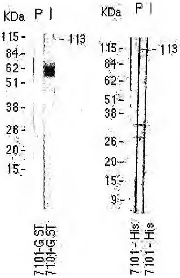


FIGURE 63

FIG. 63A

FIG. 63B

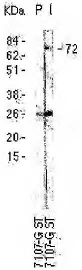


FIG. 63C

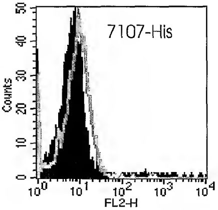


FIGURE 64

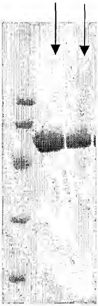


FIG. 64A

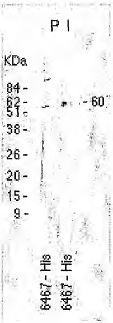


FIG. 64B

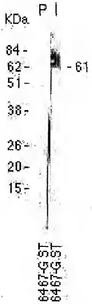


FIG. 64C

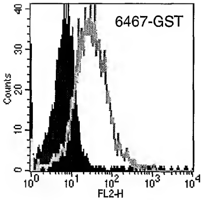
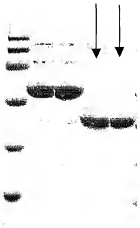


FIG. 64D

FIGURE 65

FIG. 65A



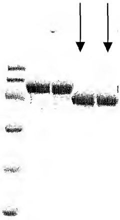


FIG. 65B

FIG. 65C

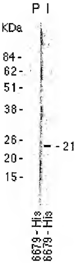


FIGURE 66

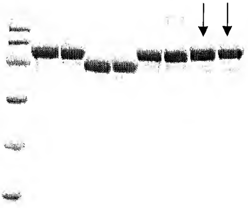


FIG. 66A

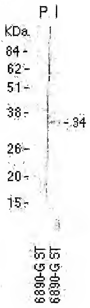


FIG. 66B

FIGURE 67

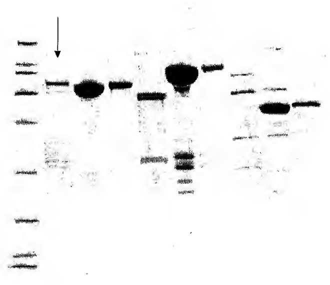


FIG. 67A

FIG. 67B

FIGURE 68

FIG. 68A

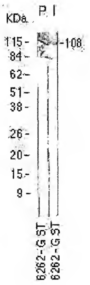


FIG. 68B

FIGURE 69

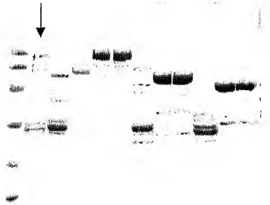


Fig. 69A

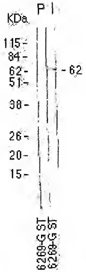


Fig. 69B

FIGURE 70

FIG. 70A

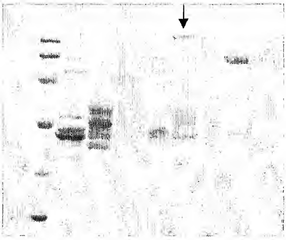


FIG. 70B

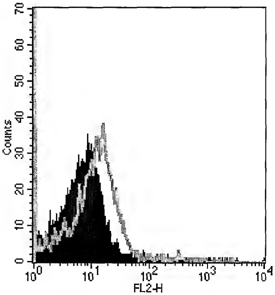


FIGURE 71

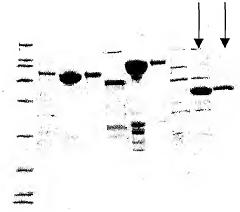


FIG. 71A

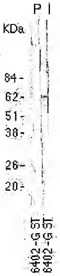


FIG. 71B

FIGURE 72

Fig. 72A

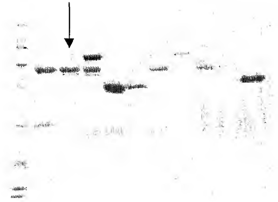


Fig. 72B

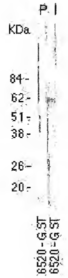


FIGURE 73

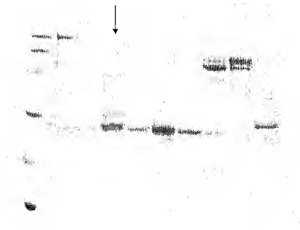


FIG. 73A

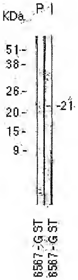


FIG. 73B

FIGURE 74

Fig. 74A

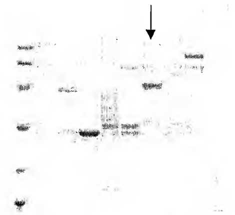


Fig. 74B

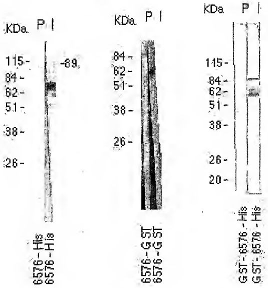


Fig. 74C

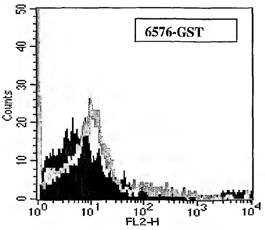


FIGURE 75

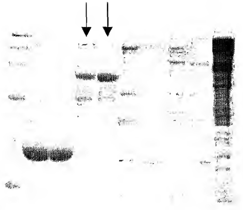


FIG. 75A

FIG. 75B

FIGURE 76

FIG. 76A

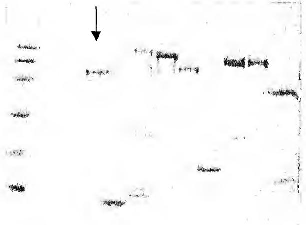


FIG. 76B

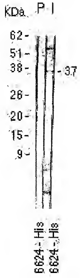


FIGURE 77

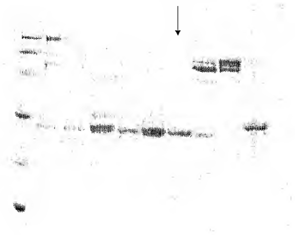


FIG. 77A

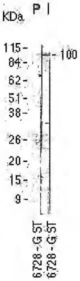


FIG. 77B

FIGURE 78

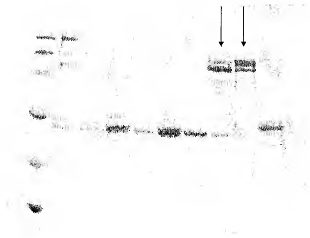


FIG. 78A

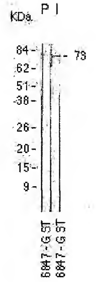


FIG. 78B

FIGURE 79

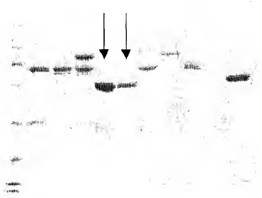


FIG. 79A

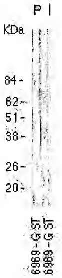


FIG. 79B

FIGURE 80

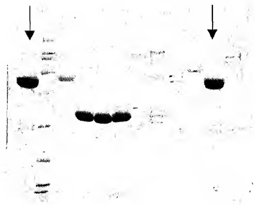


FIG. 80A

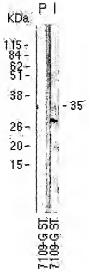


FIG. 80B

FIGURE 81

FIG. 81A

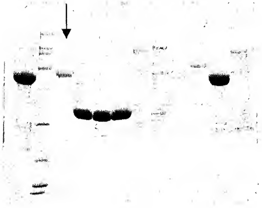


FIG. 81B

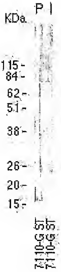


FIGURE 82

Fig. 82A

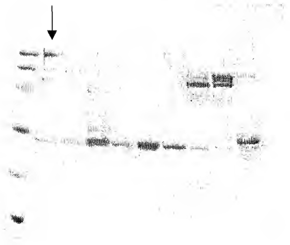


Fig. 82B

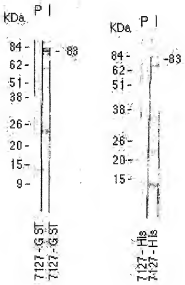


FIGURE 83

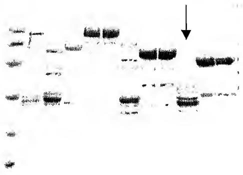


FIG. 83A

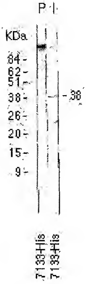


FIG. 83B

FIGURE 84

FIG. 84A

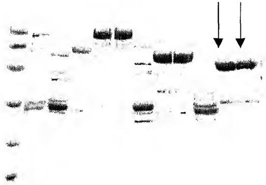


FIG. 84B

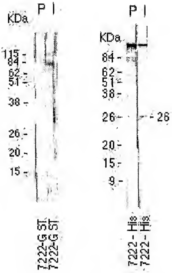


FIGURE 85

FIG. 85A

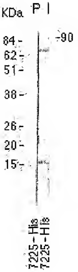


FIG. 85B

FIGURE 86

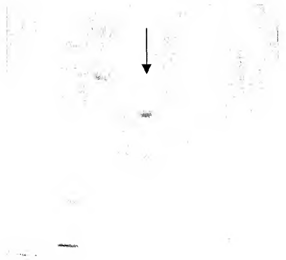


FIG. 86A

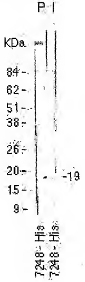


FIG. 86B

FIGURE 87

FIG. 87A

FIG. 87B

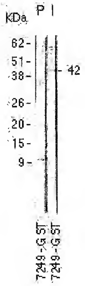


FIGURE 88

FIG. 88A

FIG. 88B

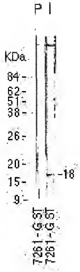


FIGURE 89

FIG. 89A

FIG. 89B

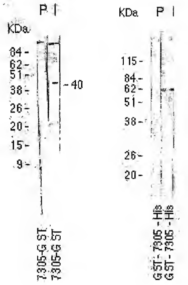


FIGURE 90

FIG. 90A

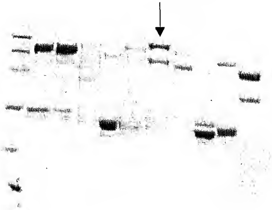


FIG. 90B

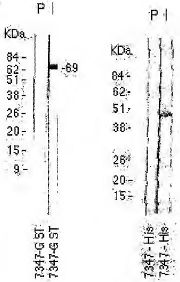


FIGURE 91

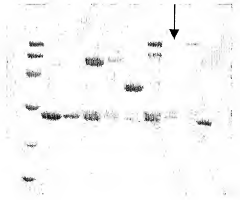


FIG. 91A

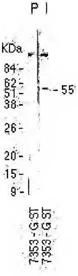


FIG. 91B

FIGURE 92

FIG. 92A

FIG. 92B

FIGURE 93

FIG. 93A

FIG. 93B

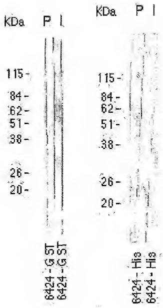


FIG. 93C

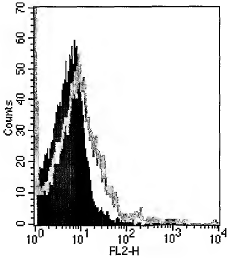


FIGURE 94

FIG. 94A

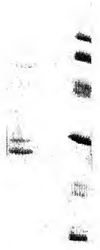


FIG. 94B

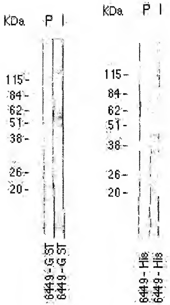


FIG. 94C

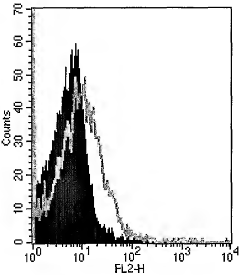


FIGURE 95

Fig. 95A

Fig. 95B

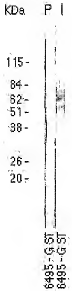


Fig. 95C

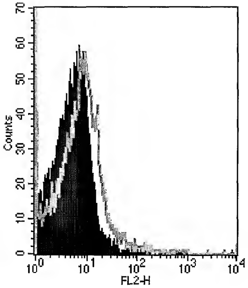


FIGURE 96

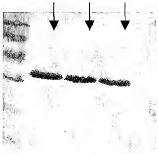


FIG. 96A

FIG. 96B

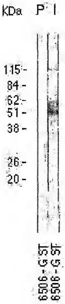


FIG. 96C

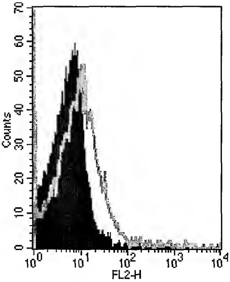


FIG. 96D

FIGURE 97

FIG. 97A

FIG. 97B

FIG. 97C

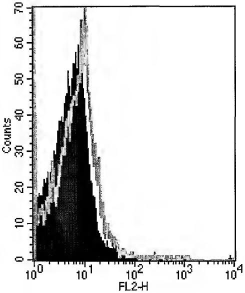


FIGURE 98

FIG. 98A

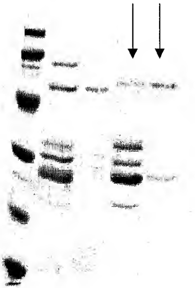


FIG. 98B

FIG. 98C

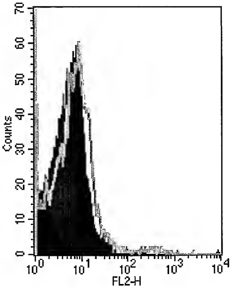


FIGURE 99

FIG. 99A

FIG. 99B

FIG. 99C

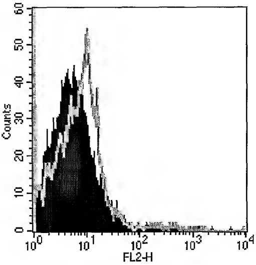


FIGURE 100

Fig. 100A

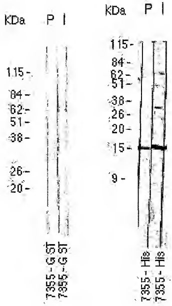


Fig. 100B

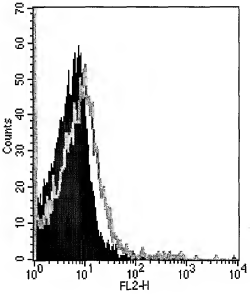


Fig. 100C

FIGURE 101

Fig. 101A

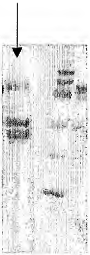


Fig. 101B

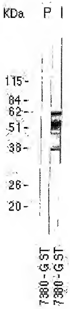


Fig. 101C

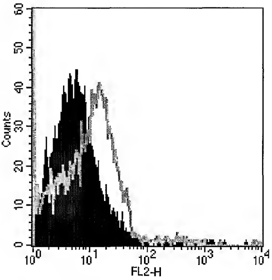


FIGURE 102

FIG. 102A

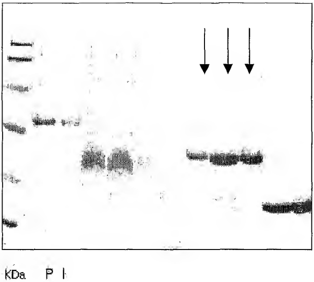


FIG. 102B

FIGURE 103

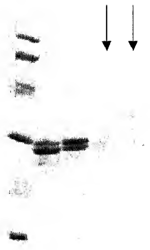


FIG. 103A

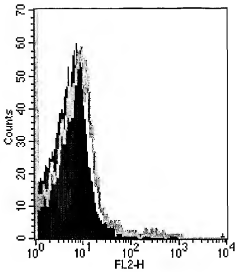


FIG. 103C

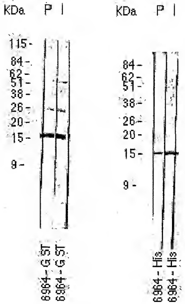


FIG. 103B

FIGURE 104

FIG. 104A

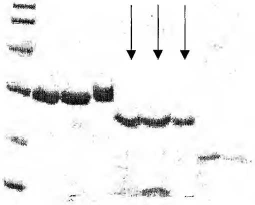


FIG. 104B

FIG. 104C

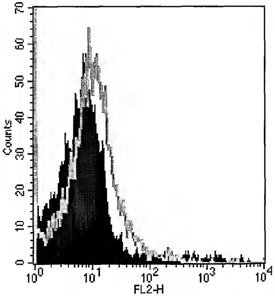


FIGURE 105

FIG. 105A

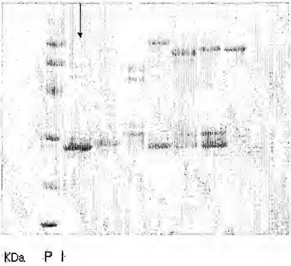


FIG. 105B

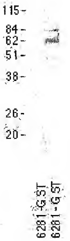


FIGURE 106

FIG. 106A

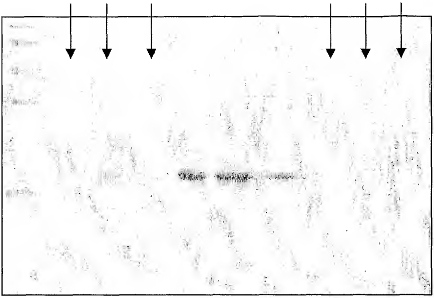


FIG. 106B

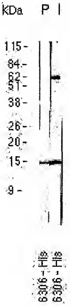


FIGURE 107

FIGURE 108

FIG. 108A

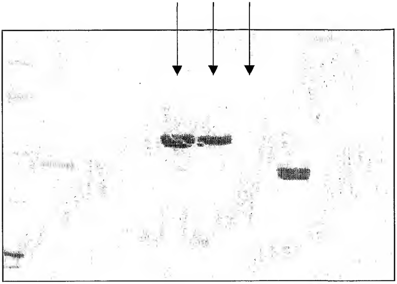


FIG. 108B

FIGURE 109

Fig. 109A

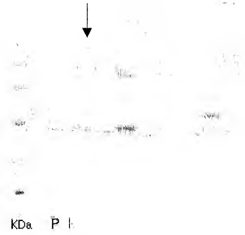


Fig. 109B

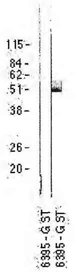


FIGURE 110

FIG. 110A

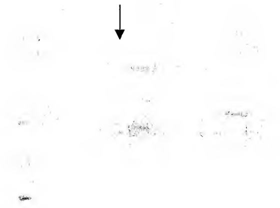


FIG. 110B

FIGURE 111

FIG. 111A

FIG. 111B

FIGURE 112

FIG. 112A

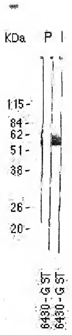


FIG. 112B

FIGURE 113

FIG. 113A

FIG. 113B

FIGURE 114

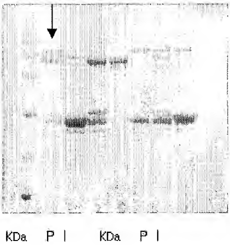


FIG. 114A

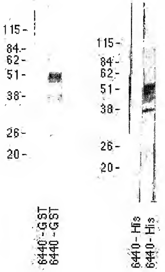


FIG. 114B

FIGURE 115

FIG. 115A

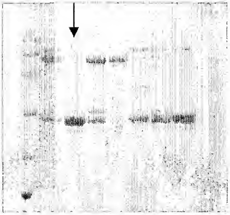


FIG. 115B

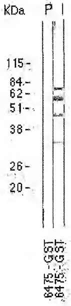


FIGURE 116

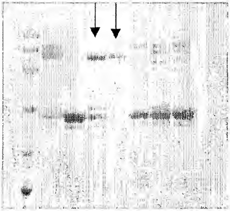


FIG. 116A

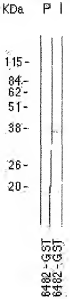


FIG. 116B

FIGURE 117

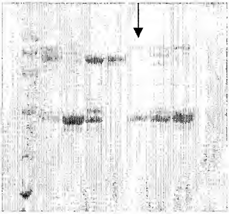


FIG. 117A

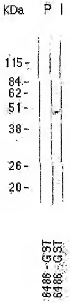


FIG. 117B

FIGURE 118

FIG. 118A

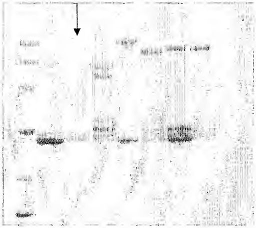


FIG. 118B

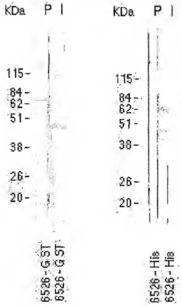


FIGURE 119

FIG. 119A

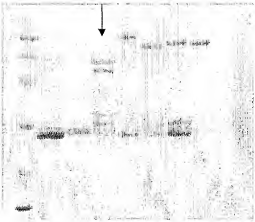


FIG. 119B

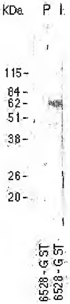


FIGURE 120

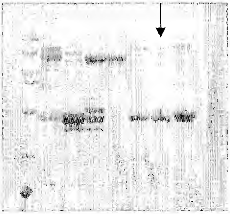


FIG. 120A

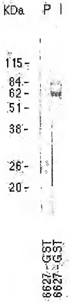


FIG. 120B

FIGURE 121

FIG. 121A

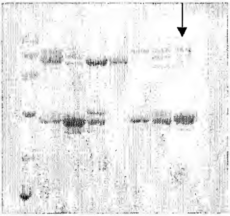


FIG. 121B

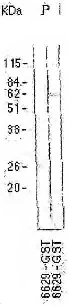


FIGURE 122

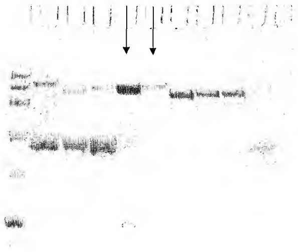


FIG. 122A

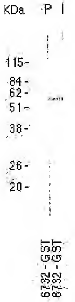


FIG. 122B

FIGURE 123

Fig. 123A

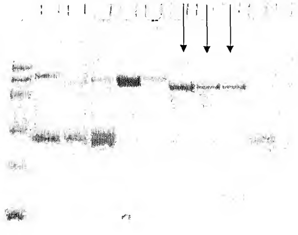


Fig. 123B

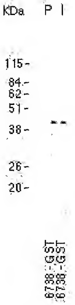


FIGURE 124

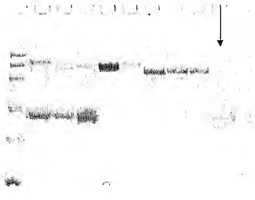


FIG. 124A

FIG. 124B

FIGURE 125

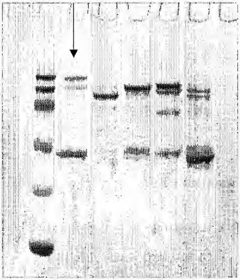


Fig. 125A

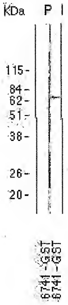


Fig. 125B

FIGURE 126

FIG. 126A

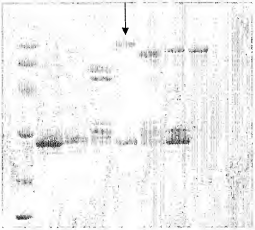


FIG. 126B

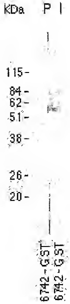


FIGURE 127

FIG. 127A

FIG. 127B

FIGURE 128

FIG. 128A

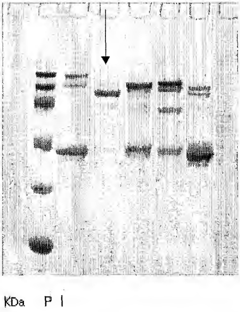


FIG. 128B

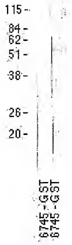


FIGURE 129

FIG. 129A

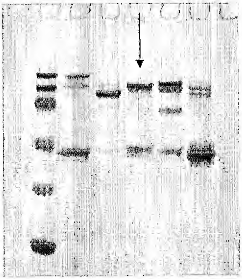


FIG. 129B

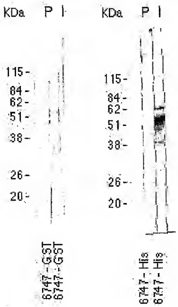


FIGURE 130

FIG. 130A

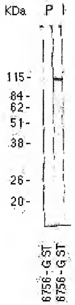


FIG. 130B

FIGURE 131

FIG. 131A

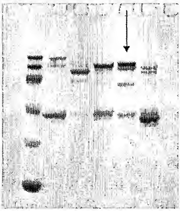


FIG. 131B

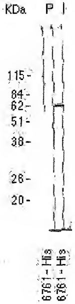


FIGURE 132

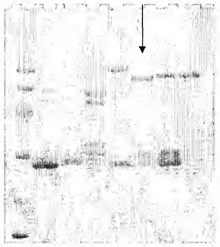


FIG. 132A

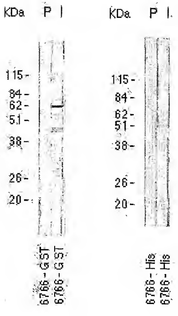


FIG. 132B

FIGURE 133

FIG. 133A

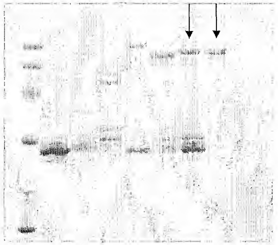


FIG. 133B

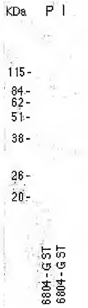


FIGURE 134

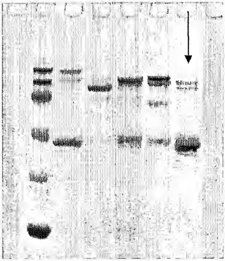


FIG. 134A

FIG. 134B

FIGURE 135

FIG. 135A

FIG. 135B

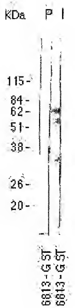


FIGURE 136

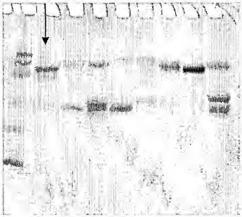


FIG. 136A

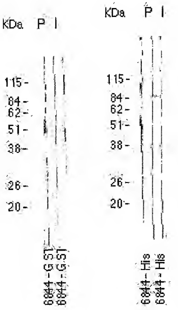


FIG. 136B

FIGURE 137

FIG. 137A

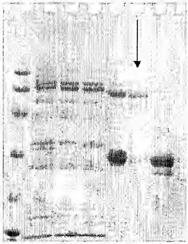


FIG. 137B

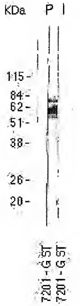


FIGURE 138

FIG. 138A

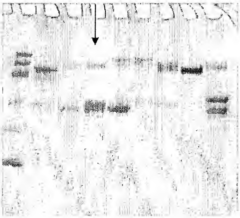


FIG. 138B

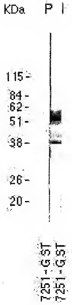


FIGURE 139

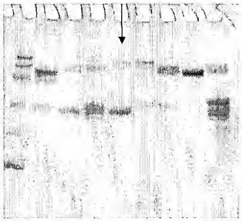


FIG. 139A

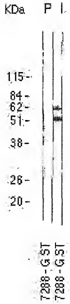


FIG. 139B

FIGURE 140

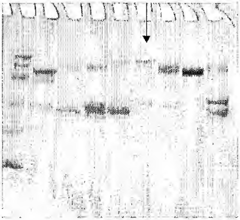


FIG. 140A

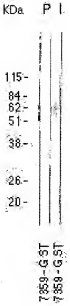


FIG. 140B

FIGURE 141

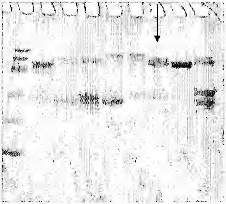


FIG. 141A

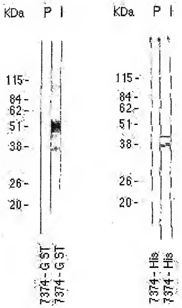


FIG. 141B

FIGURE 142

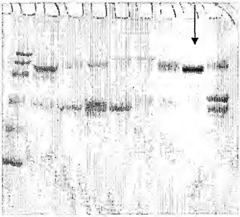


FIG. 142A

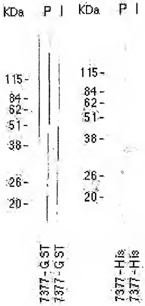


FIG. 142B

FIGURE 143

Fig. 143A

Fig. 143B

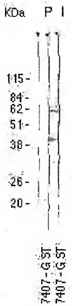


FIGURE 144

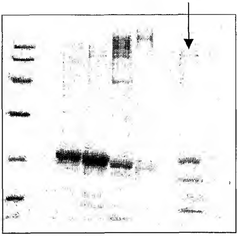


FIG. 144A

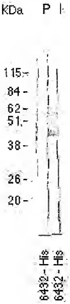


FIG. 144B

FIGURE 145

FIG. 145A

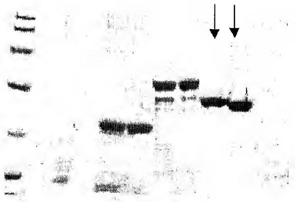


FIG. 145B

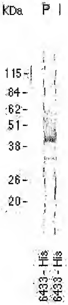


FIGURE 146

FIG. 146A

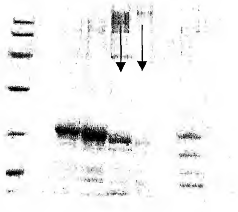


FIG. 146B

FIGURE 147

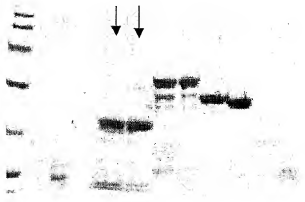


FIG. 147A

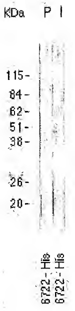


FIG. 147B

FIGURE 148

FIG. 148A

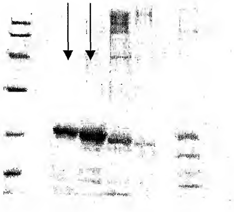


FIG. 148B

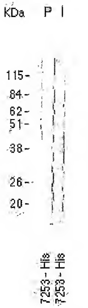


FIGURE 149

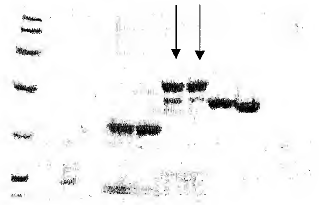


FIG. 149A

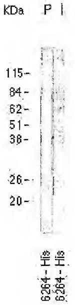


FIG. 149B

FIGURE 150

FIG. 150A

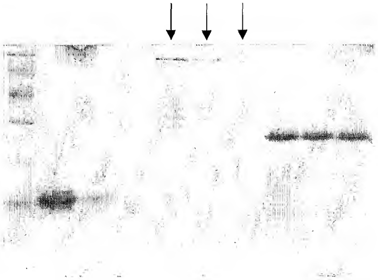


FIG. 150B

FIGURE 151

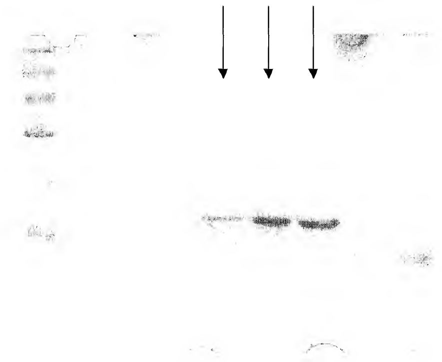


FIG. 151A

FIG. 151B

FIGURE 152

FIG. 152A

FIG. 152B

FIGURE 153

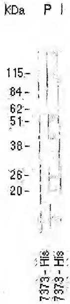


FIGURE 154

FIG. 154A

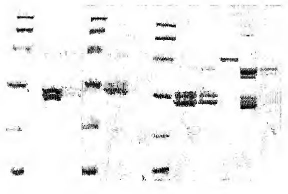


FIG. 154B

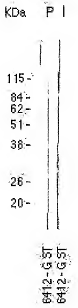


FIGURE 155

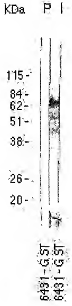


FIGURE 156

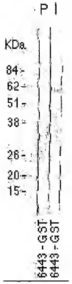


FIGURE 157

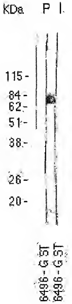


FIGURE 158

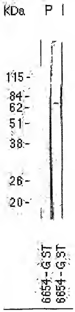


FIGURE 159

FIG. 159A

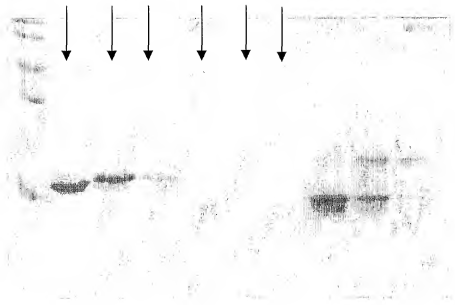


FIG. 159B

FIGURE 160

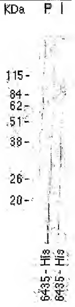


FIGURE 161

Fig. 161A

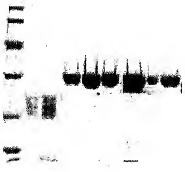


Fig. 161B

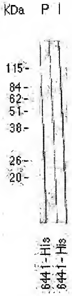


FIGURE 162

FIGURE 163

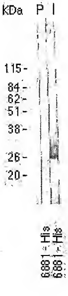


FIGURE 164

FIG. 164A

FIG. 164B

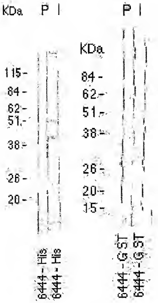


FIGURE 165

FIGURE 166

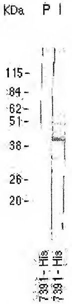


FIGURE 167

FIG. 167A

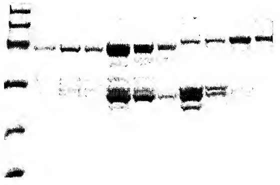


FIG. 167B

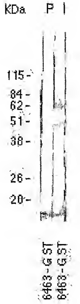


FIGURE 168

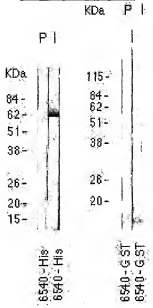


FIGURE 169

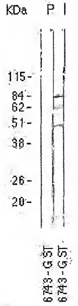


FIGURE 170

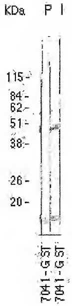


FIGURE 171

FIG. 171A

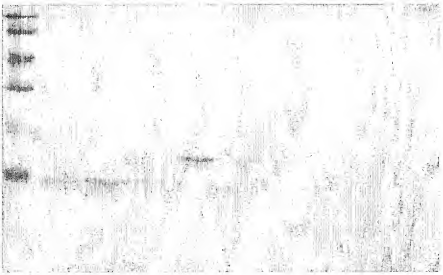


FIG. 171B

FIGURE 172

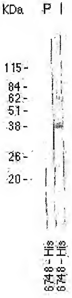


FIGURE 173

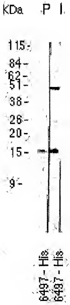


FIGURE 174

Fig. 174A

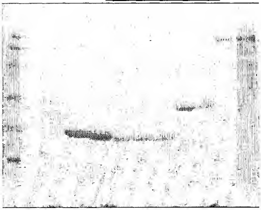


Fig. 174B

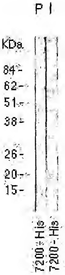


FIGURE 175

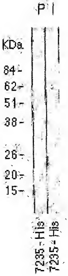


FIGURE 176

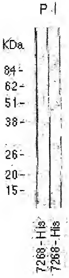


FIGURE 177

FIGURE 178

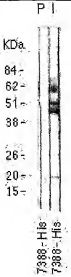


FIGURE 179

FIG. 179A

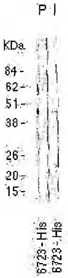


FIG. 179B

FIGURE 180

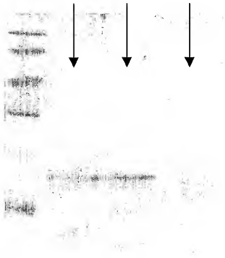


FIG. 180A

FIG. 180B

FIGURE 181

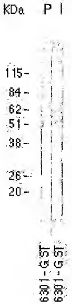


FIGURE 182

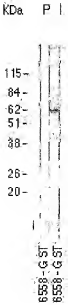


FIGURE 183

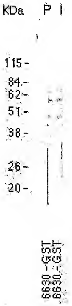


FIGURE 184

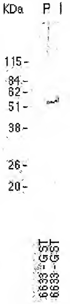


FIGURE 185

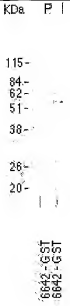


FIGURE 186

FIG. 186A

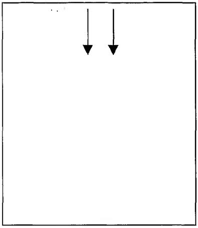


FIG. 186B

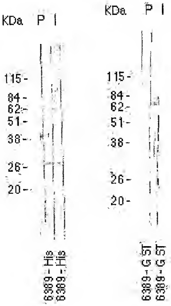


FIGURE 187

FIG. 187A

FIG. 187B

FIGURE 188

FIG. 188A

FIG. 188B

FIGURE 189

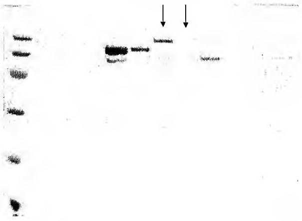


FIG. 189A

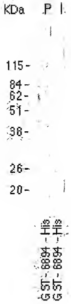


FIG. 189B

FIGURE 190

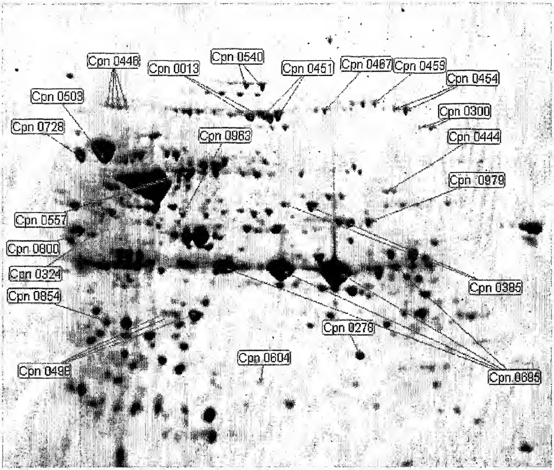


FIGURE 191

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SVIVG.VSTNSEHRYHAFQYADGQMVDLGTLGGPESYAQGVSGDGK
KVIVG.HSTRTDGEYRAFKYVDGRMIDLGTLGGSASFAFGVSDDGK
KVIVG.RSETYYGEVHAFCHKNGVMSDLGTLGGSYSAAKGVSATGK
KVIVG.WSTTNNGETHAFMHKDETMHDLGTLGGGFSVATGVSADGR
TIIVGSMESTITRKTTAVKWVNNVPTYLGTLGGDASTGLYISGDGT
```